In this section, we argue that in general it is not possible to rescale the Poisson model such that it gives reasonable approximations to one of the other offspring-number models with respect to both population dynamics and genetics, even if we both linearly rescale the population-size parameters and change the growth parameter. Given an offspring-number model $M$ with critical population size $a$, carrying capacity $k_1$, target population size $z$, founder population size $N_0$, growth parameter $r$, $\nu = \var{N_{t+1}|N_t} / \mathbb{E}(N_{t+1}|N_t)$, and relative strength of genetic drift $c$, we will attempt to determine scaling parameters $s$ and $\rho$ such that a Poisson model $M'$ with parameters $a' = s \cdot a, k_1' = s \cdot k_1, z' = s \cdot z, N_0' = s \cdot N_0$, and $r' = \rho \cdot r$ approximates the original model.

In our argument, we will be guided by the following theorem on a time change in diffusion processes (Durrett 1996, Theorem 6.1 on p. 207): If we speed up a diffusion process by a factor $\rho$, we obtain the same process as when we multiply both its infinitesimal mean and its infinitesimal variance by a factor $\rho$. In this study, we do not consider diffusion processes, but processes in discrete time and with a discrete state space. Furthermore, we cannot manipulate mean and variance independently. Therefore, the theorem cannot hold exactly for the models in this study. Nevertheless, it yields good approximations to the population dynamics under the the binomial, Poisson-Poisson, and Poisson-geometric model (Figure S2). Specifically, a Poisson model $M'$ with $r' = \rho \cdot r$ runs $\rho$ times as fast but otherwise exhibits approximately the same population dynamics as a model $M''$ with growth parameter $r$ and $\nu = \var{N_{t+1}|N_t} / \mathbb{E}(N_{t+1}|N_t) = 1/\rho$, given that all other parameters are the same, i.e. $a'' = a', k_1'' = k_1, z'' = z'$ and $N_0'' = N_0$. However, due to the difference in time scale, the genetic drift experienced by populations under the two models may be very different.

To determine whether the offspring-number model $M$ can be approximated by a Poisson model $M'$, we will check whether it is possible to simultaneously fulfill two conditions, one on the population dynamics and one on the genetic aspect of the models. These two conditions are not sufficient to ensure that the models behave the same in every respect, but they appear necessary. If we can show that it is not possible to fulfill them simultaneously, not even in the unconditioned model, then the population dynamics and/or genetics of successful populations should be different under the two models.

First, we will specify a condition required to match the population dynamics. Since the success or failure of a population and other qualitative features of the population dynamics do not depend on the time scaling and since it is easier to compare models with the same growth parameter, we will use the model $M''$ instead of model $M'$ here. To match the relative strength of stochastic vs. deterministic forces in the population dynamics, we will require that the standard deviation of the population size in the next generation relative to the corresponding expected value is equal in both
Figure S2  Comparison of Poisson models with growth parameter $r' = 0.1 \cdot \rho$ to other offspring-number models, the binomial model (A), the Poisson-Poisson model (B), and the Poisson-geometric model (C), all with growth parameter $r'' = 0.1$. Each subplot shows the average number of generations that successful populations with an Allee effect (AE) or without (no AE) under the various models spend at different population sizes from 1 to $z-1$ before reaching the target population size $z$. In each case, we set $\rho = 1/\nu$ (see Table 1, and using $\nu \approx 1/2$ for the binomial model) and divided the times spent at the different population sizes under the respective other offspring model by $\rho$ to account for the change in time scale. The dotted vertical line indicates the critical size $a$ of Allee-effect populations, here $a = 50$. $k_1 = 1000$, $z = 100$.

Given the properties of the model $M''$ and $M$ stated above, this is equivalent to

$$\frac{1}{\sqrt{\rho}} \cdot E[N_{t+1}'|N_t' = n'''] = \sqrt{\nu} \cdot E[N_{t+1}|N_t = n].$$

(S24)

$$\Leftrightarrow \frac{1}{\sqrt{\rho}} \cdot E[N_{t+1}'|N_t' = n'''] = \sqrt{\nu} \cdot E[N_{t+1}|N_t = n].$$

(S25)

$$\Leftrightarrow \frac{1}{\sqrt{\rho}} \cdot n''' \cdot \phi\left(\frac{n'''}{k_1}\right) = \sqrt{\nu} \cdot n \cdot \phi\left(\frac{n}{k_1}\right).$$

(S26)

where

$$\phi(x) = e^{-r \cdot (1 - x)} \cdot \left(1 - \frac{x}{k_1}\right)^{r \cdot (1 - x)}.$$  

(S27)

is the expected per-capita number of surviving offspring in a population whose current size is a fraction $x$ of the carrying
capacity (see equation (1)). Since $n''/k''_1 = n/k_1$, (S26) reduces to

$$\frac{1}{\nu} = \frac{\rho \cdot n''}{n} = \frac{\rho \cdot s}{n}.$$  

(S28)

This is our first condition.

Second, both models should have the same strength of genetic drift at corresponding population sizes $n$ and $n'$.

Specifically, we require that the heterozygosity maintained over a corresponding time span is equal in both models:

$$\left(1 - \frac{1}{n'}\right)^{1/\rho} = \left(1 - \frac{c}{n}\right),$$  

(S29)

which corresponds approximately to the condition

$$\frac{1}{\frac{\rho}{n'}} = \frac{c}{n},$$  

(S30)

as long as $n$ and $n'$ are not too small. Here, we need the exponent $1/\rho$ because—as we have seen above and in Figure S2—multiplying the growth parameter by a factor $\rho$ effectively speeds up the process by the same factor such that there is less time for genetic drift to act. Using $n' = s \cdot n$, (S30) simplifies to

$$\frac{1}{c} = \frac{\rho \cdot s}{n}.$$  

(S31)

This is our second condition.

Combining (S28) and (S31) shows that the two conditions can only be fulfilled simultaneously if $\nu = c$, which is not the case for the offspring-number models we consider in this study (see Table 1). The mismatch between $\nu$ and $c$ in our models is related to the way in which the diploid individuals form pairs to sexually reproduce. In a haploid and asexual model, in which individuals independently produce identically distributed numbers of offspring, $\text{Var}[N_{t+1}|N_t] = N_t \cdot \text{Var}[X]$ and $\mathbb{E}[N_{t+1}|N_t] = N_t \cdot \mathbb{E}[X]$, where $X$ is a random variable representing the number of offspring produced by a single individual. In analogy to (S22), we can then quantify the strength of genetic drift as

$$c = \mathbb{E}[X^*] - 1 = \frac{\text{Var}[X]}{\mathbb{E}[X]} + \mathbb{E}[X] - 1 = \frac{\text{Var}[N_{t+1}|N_t]}{\mathbb{E}[N_{t+1}|N_t]} + \mathbb{E}[X] - 1 = \nu + \mathbb{E}[X] - 1.$$  

(S32)

This shows that in equilibrium, i.e. for $\mathbb{E}[X] = 1$, there would be no mismatch between $c$ and $\nu$ in such a haploid model. In other situations, however, especially if we condition on the success of a small Allee-effect population, there could still be a mismatch. Furthermore, as discussed above, conditions (S28) and (S31) may not be sufficient to ensure that two processes behave similarly. Especially if we condition on an unlikely event, the higher moments characterizing the tail of

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the offspring-number distribution may be important and they are not necessarily matched even if mean and variance are. We therefore suggest that the strong differences among offspring-number distributions in the genetic consequences of the Allee effect can only in special cases be resolved by rescaling the parameters of the Poisson model.