

Supplementary Information

The effect of the timing of selection on the mutation load, inbreeding depression and population size.

Table 1

File S1: Domain of validity for the expressions for population size, numerical and genetic loads and inbreeding depression

File S2: Equations for the change in the number of individuals

File S3: Genotypic frequencies at equilibrium

File S4: Proofs for population size at equilibrium

Model	Variable
Mating success	N_{mut}
Λ	$N_{eq} \frac{(1-\mu)^2(2+h^4(1+\mu)^2s^2-2h(4+H_1)+2h^2(4+s+2\mu s+2H_1)-h^3s(4+8\mu+(1+\mu)H_1))}{2(1-2h)^2}$
L	$1 - \frac{(1-\mu)^2(2+h^4(1+\mu)^2s^2-2h(4+H_1)+2h^2(4+s+2\mu s+2H_1)-h^3s(4+8\mu+(1+\mu)H_1))}{2(1-2h)^2}$
δ	$\frac{h^2\mu^2s+\mu(2-h(H_1+4))-h(hs-H_1)}{2(1-2h)}$
Fecundity	N_{mut}
Λ	$\frac{(1-h)(H_1-hs)-\mu(3h^2s-h(s+4)+2)}{4(1-\mu)(1-h(2-hs))}$
L	$N_{eq} \frac{(1-\mu)(2+h^2(1+\mu)s-h(4+H_1))}{2(1-2h)}$
δ	$\frac{h^2\mu^2s+\mu(2-h(H_1+4))-h(hs-H_1)}{2-4h}$
Survival	N_{mut}
Λ	$\frac{(1-h)(H_1-hs)-\mu(3h^2s-h(s+4)+2)}{4(1-\mu)(1-h(2-hs))}$
δ	$N_{eq} \frac{(1-\mu)(2+h^2(1+\mu)s-h(4+H_1))}{2(1-2h)}$
	L
	Λ
	δ
Fundamental model	L
δ	$\frac{2(1+\mu)-h(4+4\mu-h(s+2s\mu)+\sqrt{s(4\mu(1+\mu)-8h\mu(1+\mu)+s(h+2h\mu)^2)})}{(2-4h)(1+\mu)^2}$
	δ
	$\frac{(1-2h)\mu(h(s+2s\mu)+\sqrt{s(4\mu(1+\mu)-8h\mu(1+\mu)+s(h+2h\mu)^2)}-2\mu)}{2(2\mu+h(h(s+2s\mu)+\sqrt{s(4\mu(1+\mu)-8h\mu(1+\mu)+s(h+2h\mu)^2)}-4\mu))}$

Table 1: Explicit solutions at mutation-selection balance for population size N_{mut} , genetic load L , inbreeding depression δ for values of dominance h between 0 and 1 different than 0.5. $H_1 = \sqrt{s((4-8h)\mu + h^2(1+\mu)^2s)}$. The deterministic fixation of a occurs for $\mu \geq \frac{(1-h)s}{1-hs}$ in our models and for $\mu \geq \frac{(1-h)s}{1-s}$ in the fundamental model. The domain of validity of these expressions is addressed in more detail in File S1. An empty cell indicates that the expression is too long to be represented.

File S1

Domain of validity for the expressions for population size, numerical and genetic loads and inbreeding depression

Full expressions for all measured variables (population size, the numerical and genetic load, and inbreeding depression) can be found in Table S1. These equations are valid for all values of dominance h between 0 and 1, but not codominant mutations ($h = 0.5$); expressions for co-dominant mutations can be found in Table 2 of the main text. The validity of these equations depends on the threshold value of the mutation rate $\mu_{fix} = \frac{(1-h)s}{1-hs}$ for the deterministic fixation of the deleterious allele a and on the validity of $H_1 = \sqrt{s((4-8h)\mu + h^2(1+\mu)^2s)}$. Figure S1 is a graphical representation of the domains of validity for each of the limitations. For H_1 to be in the domain of real numbers, and hence for the expressions to be biologically realistic, s must be greater than $\frac{(8h-4)\mu}{h^2(1+\mu)^2}$. This limitation does not interfere with the domain of validity for the expressions, as it is always below the domain of validity imposed by the deterministic fixation of a ($\mu > \frac{(1-h)s}{1-hs}$).

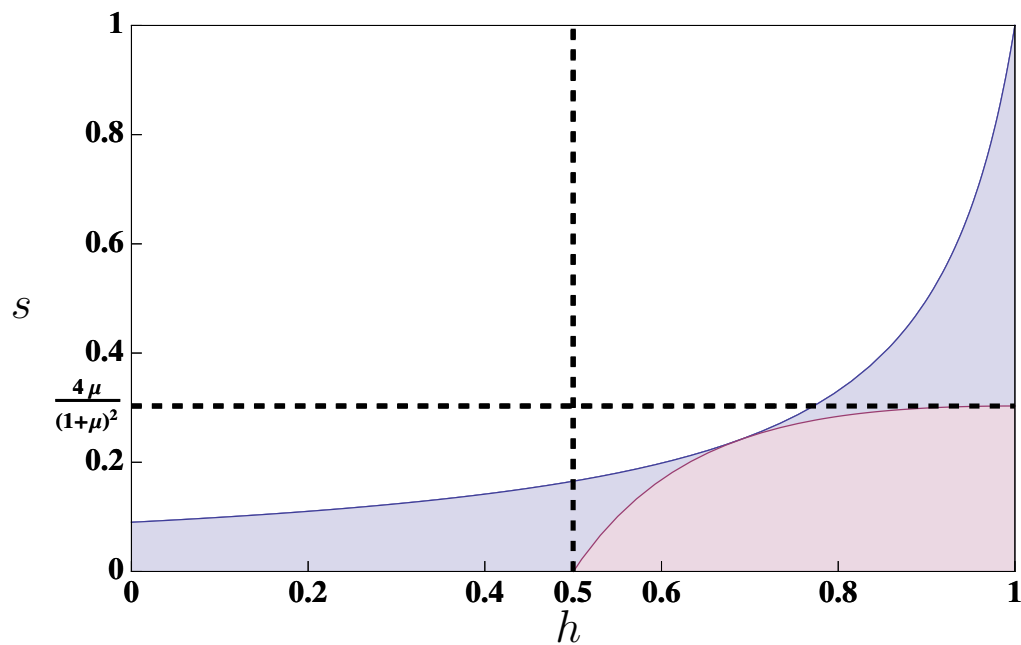


Figure 1: Limitations for the validity of the expressions in Table S1. The area below the blue (respectively red) curve depicts all values of s and h for which the expressions are not valid as mutations are deterministically fixed (respectively as the expression H_1 is not in the domain of real numbers) for $\mu = 10^{-2}$.

File S2

Equations for the change in the number of individuals

Here we provide the full general equations for the change in the number of individuals of each genotype for all three models of selection (mating success, fecundity and survival). The expressions presented in Table S1 as well as the genotypic frequencies of X , Y and Z and mutation selection balance presented below are obtained by solving for the steady state of these differential equations ($\frac{dX_t}{N_t} = \frac{dY_t}{N_t} = \frac{dZ_t}{N_t} = 0$). These expressions were obtained using Wolfram's Mathematica 9.0.

Selection on mating success

$$\begin{aligned}
\frac{dX_t}{N_t} &= \frac{b}{N_t} \left((1-s)^2 X_t^2 + 2(1-s)X_t Z_t \mu + Z_t^2 \mu^2 + (1-s)(1-hs)X_t Y_t (1+\mu) \right. \\
&\quad \left. + (1-hs)Y_t Z_t \mu (1+\mu) + \frac{1}{4}(1-hs)^2 Y_t^2 (1+\mu)^2 \right) - d \frac{N_t}{K} X_t \\
&= \frac{b}{N_t} (r^X)^2 - d \frac{N_t}{K} X_t \tag{S1a}
\end{aligned}$$

$$\begin{aligned}
\frac{dY_t}{N_t} &= \frac{b}{N_t} \left((1-s)(1-hs)X_t Y_t (1-\mu) + 2(1-s)X_t Z_t (1-\mu) + 2Z_t^2 (1-\mu)\mu \right. \\
&\quad \left. + \frac{1}{2}(1-hs)^2 Y_t^2 (1-\mu)(1+\mu) + 2(1-hs)Y_t Z_t \left(\frac{1}{2}(1-\mu)\mu + \frac{1}{2}(1-\mu)(1+\mu) \right) \right) \\
&\quad - d \frac{N_t}{K} Y_t \\
&= \frac{2b}{N_t} (r^X r^Y) - d \frac{N_t}{K} Y_t \tag{S1b}
\end{aligned}$$

$$\begin{aligned}
\frac{dZ_t}{N_t} &= \frac{b}{N_t} \left(\frac{1}{4}(1-hs)^2 Y_t^2 (1-\mu)^2 + (1-hs)Y_t Z_t (1-\mu)^2 + Z_t^2 (1-\mu)^2 \right) - d \frac{N_t}{K} Z_t \\
&= \frac{b}{N_t} (r^Z)^2 - d \frac{N_t}{K} Z_t \tag{S1c}
\end{aligned}$$

where

$$r^X = \left((1-s)X_t + (1-hs)Y_t \frac{(1+\mu)}{2} + Z_t \mu \right) \tag{S2a}$$

and

$$r^Z = \left(Z_t (1-\mu) + (1-hs)Y_t \frac{(1-\mu)}{2} \right). \tag{S2b}$$

Selection on fecundity

$$\begin{aligned}
\frac{dX_t}{N_t} &= \frac{b}{(1-s)X_t + (1-hs)Y_t + Z_t} \left((1-s)^2 X_t^2 + 2(1-s)X_t Z_t \mu + Z_t^2 \mu^2 \right. \\
&\quad \left. + (1-s)(1-hs)X_t Y_t (1+\mu) + (1-hs)Y_t Z_t \mu (1+\mu) + \frac{1}{4}(1-hs)^2 Y_t^2 (1+\mu)^2 \right) \\
&\quad - d \frac{N_t}{K} X_t \\
&= \frac{b}{N_t - sX_t - hsY_t} (r^X)^2 - d \frac{N_t}{K} X_t \tag{S3a}
\end{aligned}$$

$$\begin{aligned}
\frac{dY_t}{N_t} &= \frac{b}{(1-s)X_t + (1-hs)Y_t + Z_t} \left((1-s)(1-hs)X_t Y_t (1-\mu) + 2(1-s)X_t Z_t (1-\mu) \right. \\
&\quad \left. + 2Z_t^2 (1-\mu)\mu + \frac{1}{2}(1-hs)^2 Y_t^2 (1-\mu)(1+\mu) \right. \\
&\quad \left. + 2(1-hs)Y_t Z_t \left(\frac{1}{2}(1-\mu)\mu + \frac{1}{2}(1-\mu)(1+\mu) \right) \right) - d \frac{N_t}{K} Y_t \\
&= \frac{2b}{N_t - sX_t - hsY_t} (r^X r^Z) - d \frac{N_t}{K} Y_t \tag{S3b}
\end{aligned}$$

$$\begin{aligned}
\frac{dZ_t}{N_t} &= \frac{b}{(1-s)X_t + (1-hs)Y_t + Z_t} \left(\frac{1}{4}(1-hs)^2 Y_t^2 (1-\mu)^2 + (1-hs)Y_t Z_t (1-\mu)^2 + Z_t^2 (1-\mu)^2 \right) \\
&\quad - d \frac{N_t}{K} Z_t \\
&= \frac{b}{N_t - sX_t - hsY_t} (r^Z)^2 - d \frac{N_t}{K} Z_t \tag{S3c}
\end{aligned}$$

where

$$r^X = \left((1-s)X_t + (1-hs)Y_t \frac{(1+\mu)}{2} + Z_t \mu \right) \tag{S4a}$$

and

$$r^Z = \left(Z_t (1-\mu) + (1-hs)Y_t \frac{(1-\mu)}{2} \right). \tag{S4b}$$

Selection on zygote survival

$$\begin{aligned}
\frac{dX_t}{N_t} &= \frac{b(1-s)}{N_t} \left(X_t^2 + 2X_tZ_t\mu + Z_t^2\mu^2 + X_tY_t(1+\mu) + Y_tZ_t\mu(1+\mu) + \frac{1}{4}Y_t^2(1+\mu)^2 \right) \\
&\quad - d\frac{N_t}{K}X_t \\
&= \frac{b(1-s)}{N_t}(r^X)^2 - d\frac{N_t}{K}X_t
\end{aligned} \tag{S5a}$$

$$\begin{aligned}
\frac{dY_t}{N_t} &= \frac{b(1-hs)}{N_t} \left(X_tY_t(1-\mu) + 2X_tZ_t(1-\mu) + 2Z_t^2(1-\mu)\mu + \frac{1}{2}Y_t^2(1-\mu^2) \right. \\
&\quad \left. + Y_tZ_t(1+\mu-2\mu^2) \right) - d\frac{N_t}{K}Y_t \\
&= \frac{b(1-hs)}{N_t}(r^X r^Z) - d\frac{N_t}{K}Y_t
\end{aligned} \tag{S5b}$$

$$\begin{aligned}
\frac{dZ_t}{N_t} &= \frac{b}{N_t} \left(\frac{1}{4}Y_t^2(1-\mu)^2 + Y_tZ_t(1-\mu)^2 + Z_t^2(1-\mu)^2 \right) - d\frac{N_t}{K}Z_t \\
&= \frac{b}{N_t}(r^Z)^2 - d\frac{N_t}{K}Z_t
\end{aligned} \tag{S5c}$$

where

$$r^X = \left(X_t + Y_t \frac{(1+\mu)}{2} + Z_t\mu \right) \tag{S6a}$$

and

$$r^Z = \left(Z_t(1-\mu) + Y_t \frac{(1-\mu)}{2} \right). \tag{S6b}$$

Selection on adult survival

$$\begin{aligned}
\frac{dX_t}{N_t} &= \frac{b}{(1-s)X_t + (1-hs)Y_t + Z_t} \left((1-s)^2 X_t^2 + 2(1-s)X_t Z_t \mu + Z_t^2 \mu^2 \right. \\
&\quad \left. + (1-s)(1-hs)X_t Y_t (1+\mu) + (1-hs)Y_t Z_t \mu (1+\mu) + \frac{1}{4}(1-hs)^2 Y_t^2 (1+\mu)^2 \right) \\
&\quad - d \frac{(1-s)X_t + (1-hs)Y_t + Z_t}{K} X_t \\
&= \frac{b}{N_t - sX_t - hsY_t} (r^X)^2 - d \frac{(1-s)X_t + (1-hs)Y_t + Z_t}{K} X_t \quad (\text{S7a})
\end{aligned}$$

$$\begin{aligned}
\frac{dY_t}{N_t} &= \frac{b}{(1-s)X_t + (1-hs)Y_t + Z_t} \left((1-s)(1-hs)X_t Y_t (1-\mu) + 2(1-s)X_t Z_t (1-\mu) \right. \\
&\quad \left. + 2Z_t^2 (1-\mu)\mu + \frac{1}{2}(1-hs)^2 Y_t^2 (1-\mu)(1+\mu) \right. \\
&\quad \left. + 2(1-hs)Y_t Z_t \left(\frac{1}{2}(1-\mu)\mu + \frac{1}{2}(1-\mu)(1+\mu) \right) \right) - d \frac{(1-s)X_t + (1-hs)Y_t + Z_t}{K} Y_t \\
&= \frac{2b}{N_t - sX_t - hsY_t} (r^X r^Z) - d \frac{(1-s)X_t + (1-hs)Y_t + Z_t}{K} Y_t \\
&\hspace{15em} (\text{S7b})
\end{aligned}$$

$$\begin{aligned}
\frac{dZ_t}{N_t} &= \frac{b}{(1-s)X_t + (1-hs)Y_t + Z_t} \left(\frac{1}{4}(1-hs)^2 Y_t^2 (1-\mu)^2 + (1-hs)Y_t Z_t (1-\mu)^2 + Z_t^2 (1-\mu)^2 \right) \\
&\quad - d \frac{(1-s)X_t + (1-hs)Y_t + Z_t}{K} Z_t \\
&= \frac{b}{N_t - sX_t - hsY_t} (r^Z)^2 - d \frac{(1-s)X_t + (1-hs)Y_t + Z_t}{K} Z_t \quad (\text{S7c})
\end{aligned}$$

where

$$r^X = \left((1-s)X_t + (1-hs)Y_t \frac{(1+\mu)}{2} + Z_t \mu \right) \quad (\text{S8a})$$

and

$$r^Z = \left(Z_t(1 - \mu) + (1 - hs)Y_t \frac{(1 - \mu)}{2} \right). \quad (\text{S8b})$$

File S3

Genotypic frequencies at equilibrium

Hardy-Weinberg genotypic frequencies at equilibrium

We will prove that in our model, the expectations at Hardy-Weinberg equilibrium are met when there is no selection or mutation.

Proposition 1. *When there is no selection or mutation (s and $\mu = 0$), the genotypic frequencies in our model are at Hardy-Weinberg equilibrium.*

Proof of Proposition 1. Let q be the frequency of allele a , defined by

$$q = \frac{2X_{eq} + Y_{eq}}{2N_{eq}}, \quad (\text{S9})$$

and $1 - q$ is the frequency of A .

First, at Hardy-Weinberg equilibrium the frequency of each genotype is q^2 , $2q(1 - q)$ and $(1 - q)^2$ for genotypes aa , Aa and AA respectively. From the expected genotype frequencies, q can be expressed as a function of the frequency of heterozygotes (F^{Aa}).

From $F^{Aa} = 2q(1 - q)$ we obtain the expected frequency of a :

$$p = \frac{1 \pm \sqrt{1 - 2FAa}}{2} \quad (\text{S10})$$

Let us consider our model and prove that we have the same frequency of the allele a . Equilibrium is defined by $\frac{dV_i}{dt} = 0$, where V represents X , Y and Z . When there is no mutation or selection, the number of homozygous individuals in the population (either X_{eq} or Z_{eq} , both noted H_{eq}) can be written as a function of the number of number of Y_{eq} (or heterozygous) individuals:

$$\frac{b}{N_{eq}} \left(H_{eq}^2 + Y_{eq} H_{eq} + \frac{1}{4} Y_{eq}^2 \right) - d \frac{N_{eq}}{K} H_{eq} = 0.$$

By using equation 6 from the main text we can simplify the previous equation to:

$$\frac{Y_{eq}^2}{4N_{eq}} + H_{eq} \left(\frac{Y_{eq}}{N_{eq}} - 1 \right) + \frac{H_{eq}^2}{N_{eq}} = 0.$$

This gives us a quadratic equation in H_{eq} with discriminant

$$\Delta = \left(1 - 2 \frac{Y_{eq}}{N_{eq}} \right) \geq 0$$

This gives two possible solutions, corresponding to frequencies of homozygous individuals greater or smaller than $\frac{1}{4} N_{eq}$:

$$H_{eq} = \frac{1}{2} \left(N_{eq} - Y_{eq} \pm N_{eq} \sqrt{1 - 2 \frac{Y_{eq}}{N_{eq}}} \right) \quad (\text{S12})$$

If we replace X_{eq} with equation S12 in equation S9, then we find that

$$q = \frac{N_{eq} \pm N_{eq} \sqrt{1 - 2 \frac{Y_{eq}}{N_{eq}}}}{2N_{eq}}.$$

Which is equation S10 and the proposition is proved. \square

Genotypic frequencies at mutation-selection balance

The genotypic frequencies of aa , Aa and AA individuals are given by the expressions $F^{X_{mut}}$, $F^{Y_{mut}}$ and $F^{Z_{mut}}$ respectively. For each of the models, we provide the expressions for all values of the dominance h of the deleterious allele a between 0 and 1 and different than 0.5, as well as the separate expressions for $h = 0.5$. The domain of validity of these equations depends on the threshold value of the mutation rate for the deterministic fixation of the deleterious allele a $\mu_{fix} = \frac{(1-h)s}{1-hs}$ and on the validity of $H_1 = \sqrt{s((4-8h)\mu + h^2(1+\mu)^2s)}$ (see File S1 for more details). These expressions were obtained using Wolfram's Mathematica 9.0.

Selection on mating success, fecundity and adult survival

For $h \neq 0.5$:

$$F^{X_{mut}} = \frac{(2-4h)\mu + h^2(1+\mu)^2s - hH_1 - h\mu H_1}{2(1-2h)^2s}$$

$$F^{Y_{mut}} = \frac{\mu(h(4-s+H_1) - 2) - (1-h)(hs - H_1) - h^2\mu^2s}{(1-2h)^2s}$$

$$F^{Z_{mut}} = \frac{(2-h(6-5h))s + h^2\mu^2s - (2-3h)H_1 + \mu(2-h(4-2(1-h)s+H_1))}{2(1-2h)^2s}$$

For $h = 0.5$

$$F^{X_{mut}} = \frac{4\mu^2}{(1 + \mu)^2 s^2}$$

$$F^{Y_{mut}} = \frac{4\mu(s - \mu(2 - s))}{(1 + \mu)^2 s^2}$$

$$F^{Z_{mut}} = \frac{(s - \mu(2 - s))^2}{(1 + \mu)^2 s^2}$$

Selection on zygote survival

For $h \neq 0.5$

$$F^{X_{mut}} = \frac{(1 - s)(2\mu - 4h\mu + h^2(1 + \mu)s - hH_1)}{2(1 - 2h)(1 - m)s(1 - h(2 - hs))}$$

$$F^{Y_{mut}} = \frac{2(1 - hs)((1 - h)(H_1 - hs) - \mu(2 - h(4 - s + H_1))) - h^2\mu^2 s}{(1 - 2h)(1 - \mu)s(2 + h^2(1 + \mu)s - h(4 + H_1))}$$

$$F^{Z_{mut}} = \frac{(2 - h(6 - 5h))s + h^2\mu^2 s - (2 - 3h)H_1 + \mu(2 - h(4 - 2(1 - h)s + H_1))}{(1 - 2h)(1 - \mu)s(2 + h^2(1 + \mu)s - h(4 + H_1))}$$

For $h = 0.5$

$$F^{X_{mut}} = \frac{4\mu^2(1 - s)}{(1 - \mu^2)s^2}$$

$$F^{Y_{mut}} = \frac{2\mu(2 - s)(s - \mu(2 - s))}{(1 - \mu^2)s^2}$$

$$F^{Z_{mut}} = \frac{(s - \mu(2 - s))^2}{(1 - \mu^2)s^2}$$

File S4

Proofs for population size at equilibrium

General expressions for population size at equilibrium found in Table S1 are obtained using Wolfram's Mathematica 9.0 by solving for the steady state solutions of the differential equations $\frac{dN_t}{dt} = \frac{dX_t}{dt} = \frac{dY_t}{dt} = \frac{dZ_t}{dt} = 0$. Expressions and the proofs for population size at equilibrium without selection and for recurrent recessive mutations are presented in this section.

No selection

When there is no selection, the expression for population size at equilibrium N_{eq} is given by equation 6 in the main text.

Proposition 2. *At equilibrium and when there is no selection ($s = 0$), the equation $\frac{dN_t}{dt} = \frac{dX_t}{dt} = \frac{dY_t}{dt} = \frac{dZ_t}{dt} = 0$ admits a unique attractive non-trivial solution N_{eq} (equation 6 in the main text).*

Proof of proposition 2. Population size is at equilibrium when

$$R_t^X + R_t^Y + R_t^Z - M_t^X - M_t^Y - M_t^Z = 0. \quad (\text{S13})$$

When this condition is met, then population size is noted N_{eq} , and X_{eq} ,

Y_{eq} and Z_{eq} are the numbers of individuals carrying each genotype, with

$N_{eq} = X_{eq} + Y_{eq} + Z_{eq}$. Equation S13 therefore gives:

$$\frac{b}{N_{eq}} (X_{eq}^2 + Y_{eq}^2 + Z_{eq}^2 + 2X_{eq}Y_{eq} + 2Y_{eq}Z_{eq} + 2X_{eq}Z_{eq}) - d \frac{N_{eq}}{K} (X_{eq} + Y_{eq} + Z_{eq}) = 0.$$

leading to equation 6. □

Mutation-selection balance

Population size at mutation-selection balance N_{mut} (s and $\mu \neq 0$) can be presented as a function of population size at equilibrium with no or neutral mutations N_{eq} . For each model of selection (mating success, fecundity and survival), we find two attractive non-trivial solutions, one for a polymorphic population (with X , Y and Z individuals) and one which is monomorphic as the deleterious allele a is fixed (for $\mu \geq \frac{(1-h)s}{1-hs}$). Proofs for N_{mut} for recessive mutations ($h = 0$) can be found in the following section for selection on mating success, fecundity and zygote survival.

Selection on mating success

Proposition 3. *There are two expressions for N_{mut} when mutations are recessive:*

$$N_{mut} = N_{eq}(1 - \mu \wedge s)^2 \quad (\text{S15})$$

$$\mu \wedge s = \min(\mu, s)$$

Proof of proposition 3. At equilibrium, $\frac{dN_t}{dt} = \frac{dX_t}{dt} = \frac{dY_t}{dt} = \frac{dZ_t}{dt} = 0$. From equations S1 and S2 in File S2, we find:

$$\begin{aligned} 0 &= \frac{b}{N_{mut}}((r^X)^2 + 2(r^X)(r^Z) + (r^Z)^2) - d(X_{mut} + Y_{mut} + Z_{mut})\frac{N_{mut}}{K} \\ \Leftrightarrow 0 &= \frac{b}{N_{mut}}(r^X + r^Z)^2 - d\frac{N_{mut}^2}{K} \\ \Leftrightarrow 0 &= \frac{b}{N_{mut}}((1-s)X_{mut} + Y_{mut} + Z_{mut})^2 - d\frac{N_{mut}^2}{K} \\ \Leftrightarrow 0 &= \frac{b}{N_{mut}}(N_{mut} - sX_{mut})^2 - d\frac{N_{mut}^2}{K} \end{aligned}$$

$N_{mut} = 0$ is a trivial solution, else N_{mut} satisfies

$$N_{mut} = \frac{bK}{d} \left(1 - \frac{sX_{mut}}{N_{mut}}\right)^2. \quad (\text{S16})$$

A second equation for N_{mut} can be obtained by finding an expression for the change in the number of A alleles at mutation-selection $\frac{dN^A}{dt} = 0$, where

$N^A = 2Z_t + Y_t$. From equations S1 and S2, and for $Z_{mut} + Y_{mut} \neq 0$ we find:

$$\begin{aligned}
0 &= \frac{b}{N_{mut}} 2r^Z (r^X + r^Z) - d(2Z_{mut} + Y_{mut}) \frac{N_{mut}}{K} \\
\Leftrightarrow 0 &= \frac{b(1-\mu)}{N_{mut}} (2Z_{mut} + Y_{mut})(N_{mut} - sX_{mut}) - d(2Z_{mut} + Y_{mut}) \frac{N_{mut}}{K} \\
\Leftrightarrow 0 &= (2Z_{mut} + Y_{mut}) \left(b(1-\mu) \left(1 - \frac{sX_{mut}}{N_{mut}} \right) - d \frac{N_{mut}}{K} \right) \\
\Leftrightarrow 0 &= \left(b(1-\mu) \left(1 - \frac{sX_{mut}}{N_{mut}} \right) - d \frac{N_{mut}}{K} \right) \\
\Leftrightarrow N_{mut} &= \frac{bK}{d} (1-\mu) \left(1 - \frac{sX_{mut}}{N_{mut}} \right). \tag{S17}
\end{aligned}$$

Using equations S16 and S17 we find:

$$b \left(1 - \frac{sX_{mut}}{N_{mut}} \right)^2 = b(1-\mu) \left(1 - \frac{sX_{mut}}{N_{mut}} \right)$$

which implies

$$\left(1 - \frac{sX_{mut}}{N_{mut}} \right) = (1-\mu).$$

By using this equality in equation S16 or S17, we obtain equation S15

If $N_{mut} = X_{mut}$, we consider that there is fixation of the a allele. Using this information in equation S16, we find that

$$N_{mut} = N_{eq}(1-s)^2 \tag{S19}$$

as proposed in equation S15. □

Selection on fecundity

Proposition 4. *When selection is on fecundity*

$$N_{mut} = N_{eq}(1 - \mu \wedge s) \quad (\text{S20})$$

Proof of proposition 4. Using similar calculations as in Proposition 3, we find an expression for N_{mut} using the expression for N^A . From equations S3 and S8 we find:

$$\begin{aligned} 0 &= 2(R_{mut}^Z - dZ_{mut} \frac{N_{mut}}{K}) + (R_{mut}^Y - dY_{mut} \frac{N_{mut}}{K}) \\ \Leftrightarrow 0 &= \frac{b(1 - \mu)}{N_{mut} - sX_{mut}} (2Z_{mut} + Y_{mut})(N_{mut} - sX_{mut}) - d(2Z_{mut} + Y_{mut}) \frac{N_{mut}}{K} \\ \Leftrightarrow 0 &= (2Z_{mut} + Y_{mut})(b(1 - \mu) - d \frac{N_{mut}}{K}) \end{aligned}$$

which implies for $Z_{mut} + Y_{mut} \neq 0$

$$N_{mut} = N_{eq}(1 - \mu). \quad (\text{S21})$$

If $N_{mut} = X_{mut}$, then the mutant allele a has gone to fixation, implying that

$Z_{mut} = Y_{mut} = 0$. This gives

$$\begin{aligned} 0 &= \frac{b}{(1 - s)X_{mut}} ((1 - s)X_{mut})^2 - d \frac{X_{mut}^2}{K} \\ \Leftrightarrow 0 &= b(1 - s) - d \frac{X_{mut}}{K} \end{aligned}$$

$$N_{mut} = N_{eq}(1 - s) \quad (\text{S22})$$

as proposed in equation S20. \square

Selection on zygote survival

Proposition 5. *When mutations are recessive*

$$N_{mut} = N_{eq}(1 - \mu \wedge s) \quad (\text{S23})$$

Proof of proposition 5. The number of A alleles is noted N^A and expressed using equation ?? and as in Proposition 3, from equations S5 and S6 we find:

$$\begin{aligned} 0 &= \frac{b}{N_{mut}} 2r^Z (r^X + r^Z) - d(2Z_{mut} + Y_{mut}) \frac{N_{mut}}{K} \\ \Leftrightarrow 0 &= b(1 - \mu)(2Z_{mut} + Y_{mut}) - d(2Z_{mut} + Y_{mut}) \frac{N_{mut}}{K} \\ \Leftrightarrow b(1 - \mu) &= d \frac{N_{mut}}{K} \end{aligned}$$

providing $N_{mut} = N_{eq}(1 - \mu)$.

If we consider that there is fixation of the a allele, then the entire population is made of X individuals, then Y_{mut} and $Z_{mut} = 0$,

$$0 = \frac{b}{N_{mut}} (1 - s) N_{mut}^2 - d \frac{N_{mut}^2}{K}$$

gives

$$N_{mut} = N_{eq}(1 - s) \tag{S24}$$

if $N_{mut} \neq 0$.

□