

File S1

Supporting Material

I. Antagonistic pleiotropy at an X-linked locus.

Under X-linked inheritance, and assuming $h = h_1 = h_2 \leq 1/2$ (as in the main text), the allele frequency change in females and males (respectively) will be:

$$\Delta q_f \approx q(1-q)\{s_1 + s_1s_2h^2(1-2q) - (s_1 + s_2)[h + q(1-2h)]\}$$

and

$$\Delta q_m = \frac{q(1-q)(s_1 - s_2)}{1 - s_1 + q(s_1 - s_2)} \approx q(1-q)(s_1 - s_2)$$

Ignoring recurrent mutation, the expected allele frequency change per generation is:

$$\Delta q \approx \frac{1}{3}q(1-q)\{3s_1 - s_2 + 2s_1s_2h^2(1-2q) - 2(s_1 + s_2)[h + q(1-2h)]\}$$

Under conditions for balancing selection, the deterministic equilibrium is:

$$\hat{q} = \frac{3s_1 - s_2 - 2h(s_1 + s_2 - s_1s_2h)}{2(s_1 + s_2)(1-2h) + 4s_1s_2h^2}$$

When $h \rightarrow 0$ (complete dominance reversal), the model is equivalent to one of overdominant selection in females and directional selection in males (as long as $s_1 \neq s_2$; otherwise, the alleles are neutral in males). In this case, the allele frequency trajectory is:

$$\Delta q \approx \frac{2}{3}q(1-q)(s_1 + s_2)(\hat{q} - q)$$

where $\hat{q} = (3s_1 - s_2)/(2s_1 + 2s_2)$. Balancing selection occurs when:

$$s_2/3 < s_1 < 3s_2$$

which (given small selection coefficients, as stated) compares well with prior results by Pamilo (1979; see his Table 2).

With additive allelic effects ($h = 0.5$), the allele frequency trajectory is:

$$\Delta q \approx \frac{1}{3}s_1s_2q(1-q)(\hat{q} - q)$$

where $\hat{q} = (2s_1 - 2s_2 + s_1s_2/2)/s_1s_2$. Here, as with the autosomal model (see eq. 7a), the frequency change is a function of the product of the homozygous selection coefficients. However, the conditions for balancing selection are more restrictive than in the autosomal case. Balancing selection requires that:

$$s_2/(1 + s_2/4) < s_1 < s_2/(1 - s_2/4)$$

Overall, conditions for balancing selection are more restrictive on the X than the autosomes, though the difference is not too great unless dominance reversals are extreme (Fig. S1).

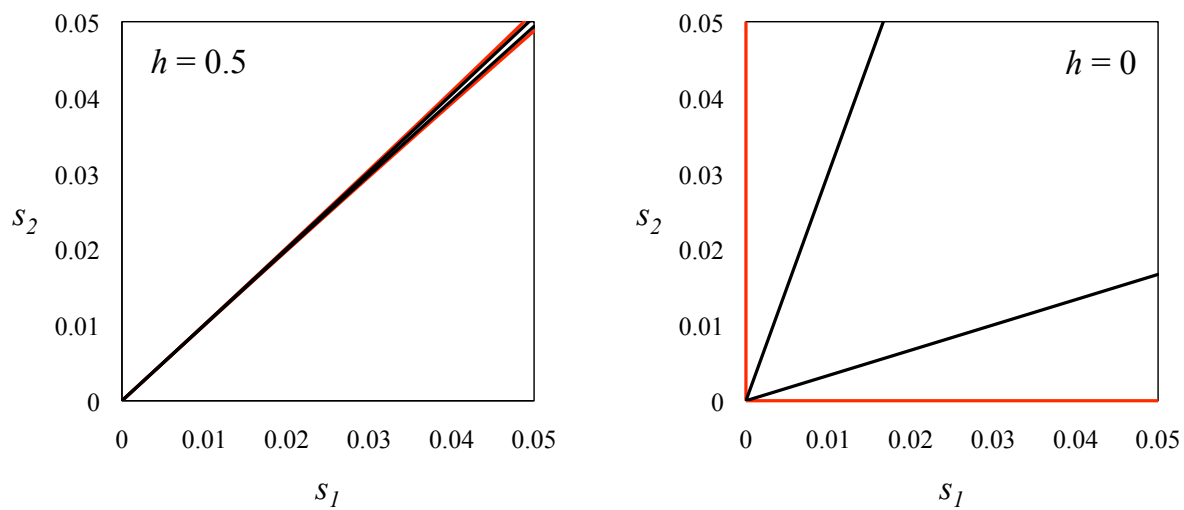


Figure S1 Parameter space conducive to balanced polymorphism under antagonistic pleiotropy: X versus autosome linkage. The parameter space under X-linkage is between the black lines. Autosomal parameter space is delineated by the red lines.

II. Sexual antagonism and constant dominance at an autosomal locus.

Under constant dominance between the sexes ($h_f = 1 - h_m$, such that the same allele is dominant in each sex, based on the parameterization in Table 1), the allele frequency change due to selection in males and selection in females will be:

$$\Delta q \approx \frac{q(1-q)[h_f + q(1-2h_f)]}{2} \{s_m(1+s_m) - s_f - q(s_f^2 + s_m^2)[2h_f + q(1-2h_f)]\}$$

The criteria for balancing selection is $-s_f^2 < s_f - s_m < s_m^2$, which is independent of the particular dominance coefficient, and identical to the additive case presented in the main text. In the absence of recurrent mutation, the equilibrium under balancing selection will be:

$$\hat{q} = \begin{cases} \frac{s_m(1+s_m) - s_f}{s_f^2 + s_m^2} & \text{for } h_f = 0.5 \\ \frac{h_f - \sqrt{h_f^2 + \frac{(1-2h_f)[s_m(1+s_m) - s_f]}{s_f^2 + s_m^2}}}{2h_f - 1} & \text{for } h_f \neq 0.5 \end{cases}$$

For the same set of selection coefficients, male-beneficial alleles reach slightly higher equilibrium frequencies when they are recessive in both sexes and lower when they are dominant in both sexes (Fig. S2).

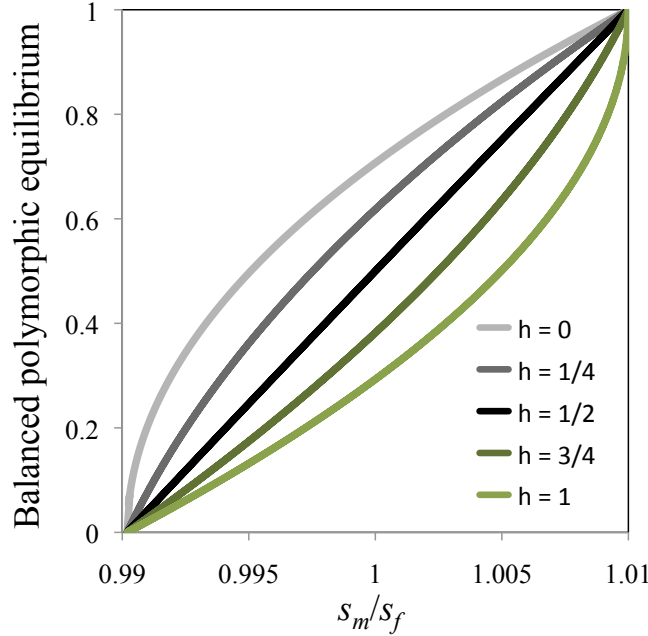


Figure S2 Balanced polymorphic equilibria for the male beneficial allele under constant dominance between the sexes ($h = h_f = 1 - h_m$). Results are shown for $s_f = 0.01$.

For the case of net directional selection we focus on the case of purifying selection against the male beneficial allele (given the symmetry of the model, these results also apply to positive selection for A_m when $s_m > s_f(1 + s_f)$ with h_m substituted for h_f). When $s_f > s_m(1 + s_m)$, and assuming very weak mutation relative to net directional selection [$(s_f^2 + s_m^2)h_f^2 \gg u$], the mutation-selection balance equilibrium is approximated:

$$q_{eq} \approx \frac{\sqrt{[s_m(1 + s_m) - s_f]^2 + 16u(s_f^2 + s_m^2)} - s_f + s_m(1 + s_m)}{4(s_f^2 + s_m^2)h_f}$$

Substituting $h_f = 1/2$ and $\hat{q} = [s_m(1 + s_m) - s_f]/(s_m^2 + s_f^2)$ leads to the first result in eq. (4b) from the main text. Conditional on net directional selection against male-beneficial alleles, A_m reaches higher equilibrium frequency when recessive in both sexes and lower frequency when dominant in both sexes (Fig. S3).

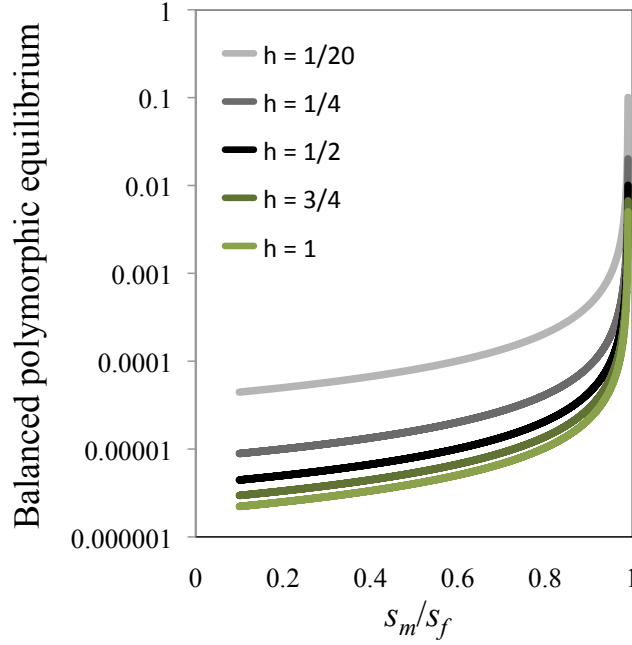


Figure S3 Male-beneficial alleles at a balance between recurrent mutation and net purifying selection. Results are shown for $s_f = 0.01$ and $u = 10^{-8}$.

The effects of finite population are also similar to the strict additive model. Under net directional selection with $|s_f - s_m(1 + s_m)| \gg s_m^2, s_f^2$, the change due to selection is approximately:

$$\Delta q \approx \frac{q(1-q)[h_f + q(1-2h_f)](s_m - s_f)}{2}$$

The effective size of a population will not have much of an impact on equilibrium variation when $N_e(s_m - s_f) \gg 1$. Under balancing selection with s_m approaching s_f in magnitude, the change due to selection is roughly:

$$\Delta q \approx \frac{q(1-q)[h_f + q(1-2h_f)]}{2} \{s_m^2 - q(s_f^2 + s_m^2)[2h_f + q(1-2h_f)]\}$$

which depends on the squared selection terms. As was the case for the strictly additive model, we expect the efficacy of balancing selection to be weak and on the order of $N_e(s_m^2 + s_f^2)$.

III. Approximations in eqs. (4-7) compared to numerical evaluation of the deterministic equilibria.

To test the quality of the deterministic approximations, we used Newton's Method to calculate allele frequency equilibria under the same parameter restrictions (*e.g.*, small selection coefficients and weak mutation; see the main text for details). The method involves iteration to convergence of the recursion equation:

$$q_{n+1} = q_n - \frac{q_n(1-q_n)(\hat{q}-q_n)f(s_i, s_j, h) + u(1-2q_n)}{f(s_i, s_j, h)[3q_n^2 - 2q_n(1+\hat{q}) + \hat{q}] - 2u}$$

where terms \hat{q} and $f(s_i, s_j, h)$ are defined in the main text. Iterations were initiated with starting frequency $q_0 = q_{eq}$ from the approximations. For each model, the approximations were excellent across the entire range of parameter space. The following example, for autosomal additive sexual antagonism, with $\max(s_m, s_f) = 0.01$, $h = 0.5$, and $u = 10^{-8}$, provides a representative contrast between the approximations and numerical results:

