# Coexistence of sexually antagonistic alleles

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# 1 Abstract

Sexually antagonistic selection (SAS) occurs when the selection in the traits or loci differs between the sexes. This sexual conflict offers the opportunity for maintaining polymorphism in a population, but it often results in the eventual fixation of the fitter allele. However, the effects of SAS have generally been studied under strong simplifying assumptions, such as constant populations and homogeneous environments, which could considerably change the expected outcomes of SAS. Thus, in this study, we examined how fluctuations in selection and population sizes contributed to the coexistence of sexually antagonistic alleles by adopting an ecological framework that allowed us to examine evolutionary dynamics through the same lens as the coexistence of competing species. We performed simulations of alleles invading a population while allowing selection and populations sizes to fluctuate over time. Then, we quantified coexistence outcomes and the relative contribution of each type of fluctuation to each alleles' invasion growth rate. Our results showed that environmental fluctuations can dramatically increase the expected genetic variation under SAS. The positive contribution of fluctuations, however, depended on the sex and allele where invasion occurred. This study contributes to the growing body of work that shows the importance of non-constant environments on the maintenance of genetic diversity.

# 2 Introduction

The question of how genetic variation is maintained despite the effects of selection and drift is central within evolutionary biology (Walsh & Lynch, 2018). Classical explanations include overdominance (heterozygote advantage) or frequency-dependent selection (Hedrick, 2007), but in the modern era of genomic data, all patterns of variation that exceed the expected variation under neutrality tend to be categorized broadly as balancing selection, regardless of the evolutionary mechanism (Mitchell-Olds *et al.*, 2007). In species with separate sexes, balancing selection can arise due to sexually antagonistic selection (Connallon & Clark, 2014), which occurs when the direction of natural selection on traits or loci differs between the sexes (Lande, 1980; Arnqvist & Rowe, 2013).

Sexually antagonistic selection can maintain polymorphisms of otherwise disadvantageous alleles in a population (Gavrilets, 2014), which in turn can result in phenotypically distinct sexes that express different morphological, physiological, and behavioral traits (Mori *et al.*, 2017; Connallon & Hall, 2018). Nonetheless, the extent to which sexually antagonistic selection can maintain polymorphism in a population is thought to be limited (Connallon & Clark, 2012). This is because theoretical studies have found that the necessary parameter conditions that give rise to balancing selection are often highly restrictive (Kidwell *et al.*, 1977; Pamilo, 1979; Hedrick, 1999; Curtsinger *et al.*, 1994; Patten *et al.*, 2010; Jordan & Charlesworth, 2012). Importantly, the effect of sexually antagonistic selection generally has been studied under strong simplifying assumptions such as constant population sizes and homogeneous environments (Kidwell *et al.*, 1977; Pamilo, 1979; Immler

*et al.*, 2012; Jordan & Charlesworth, 2012). Studies that have explored the effect of sexually antagonistic selection with more realistic assumptions, such as temporal fluctuations in selection (Connallon *et al.*, 2018) or demographic fluctuations (Connallon & Clark, 2012) have found that polymorphism can be maintained in a much wider set of conditions than classical studies predict. These results suggest that environmental fluctuations are essential to fully understand the effects of sexually antagonistic selection.

The contribution of environmental fluctuations to genetic diversity remains a debated issue in evolutionary biology. Classic theoretical models predict that temporal fluctuations in environmental conditions are unlikely to maintain a genetic polymorphism in haploid populations (Dempster, 1955; Hedrick, 1974; 1986). However, other studies have found that fluctuating selection can maintain genetic variance when populations experience density dependence (Dean, 2005), on sex-linked traits (Reinhold, 2000), or in populations where generations overlap (Ellner & Hairston Jr, 1994; Ellner & Sasaki, 1996). Similarly, temporal changes in population sizes have been shown to mitigate the effect of genetic drift in small populations (Pemberton *et al.*, 1996) and in annual plant systems (Nunney, 2002). Importantly, progress requires more than just identifying if environmental fluctuations can maintain genetic diversity in a population, but to quantify how exactly they contribute to its maintenance (Ellner *et al.*, 2016).

Temporal variability in the environment has been shown to promote diversity maintenance in ecological contexts (Levins, 1979; Armstrong & McGehee, 1980; Chesson, 2000a; Barabás *et al.*, 2018). Note that from an ecological perspective, polymorphism of sexually antagonistic alleles is equivalent to the coexistence of species, and the fixation of either

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one of the alleles in a population is equivalent to competitive exclusion. Allelic poly-

morphism, thus, can be examined through the same lens as the coexistence of competing

species. (Ellner & Hairston Jr, 1994; Ellner & Sasaki, 1996; Dean, 2005; Schreiber, 2010).

The benefit of analyzing evolutionary dynamics through this lens is that the main theo-

retical framework used to examine how competing species coexist, often called Modern

Coexistence Theory (Chesson, 2000b; 1994; Barabás *et al.*, 2018), allows the quantifica-

tion of how environmental fluctuations contribute to coexistence. Despite that the use of

Modern Coexistence Theory often requires complex mathematical analysis of the mod-

els describing the systems dynamics and restrictive assumptions to make them tractable

(Barabás *et al.*, 2018), recent computation approaches allow the quantification of the rel-

ative importance of environmental fluctuations to coexistence using simulations (Ellner

*et al.*, 2016; 2019; Shoemaker *et al.*, 2020).

Here, we seek to explicitly quantify how temporal environmental fluctuations con-

tribute to the maintenance of polymorphism under sexually antagonistic selection by us-

ing simulations. We examined how fluctuations in selection values, fluctuations in pop-

ulation sizes, and their interactions can further or hinder polymorphism. In particular,

we examined i) Can fluctuations in population sizes and selection values allow sexually

antagonistic alleles to coexist when differences in their fitness would typically not allow

them to? and ii) What are the relative contributions of different types of fluctuations that

allow two sexually antagonistic alleles to be maintained in a population? Our study pro-

vides the tools to analyze sexual antagonism from a novel perspective and contributes to

answering long-lasting questions regarding the effect of non-constant environments on

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genetic diversity.

# 3  Methods

We first present a model that describes the evolutionary dynamics of sexually antago-

nistic alleles. We then show how we simulated different scenarios of alleles invading a

population, where we allowed population sizes, selection, both, or neither to vary. Fi-

nally, we detail how we examined the relative contribution of each type of fluctuation to

the maintenance of polymorphism.

## Population dynamics of sexually antagonistic alleles

Our model examined evolution at a single, biallelic locus. We examined the dynammics

of two sexually antagonistic alleles, $j$ and $k$, that affect fitness in the haploid state. The

frequencies of each allele in each sex at the beginning of a life-cycle at time $t$ are given by:

$$p_{jm,t} = \frac{n_{jm,t}}{N_{m,t}} \tag{1}$$

$$p_{jf,t} = \frac{n_{jf,t}}{N_{f,t}} \tag{2}$$

$$p_{km,t} = \frac{N_{m,t} - n_{jm,t}}{N_{m,t}} \tag{3}$$

$$p_{kf,t} = \frac{N_{f,t} - n_{jf,t}}{N_{f,t}} \tag{4}$$

where $N_{m,t}$ and $N_{f,t}$ are the total numbers of males and females in the population at time

$t$, $n_{jf,t}$ is the number of females $f$ with allele $j$, and $n_{jm,t}$ is the number of males $m$ with

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allele $j$ at time $t$, respectively.

The individuals in the population mate at random before selection occurs, and there-fore the frequency of offspring with allele $j$ after mating, $p'_{j,t}$ can be expressed as:

$$p'_{j,t} = \frac{n_{jf}}{N_f}\frac{n_{jm}}{N_m} + \frac{1}{2}\frac{n_{jf}}{N_f}\frac{(N_m - n_{jm})}{N_m} + \frac{1}{2}\frac{(N_f - n_{jf})}{N_f}\frac{n_{jm}}{N_m} , \tag{5}$$

which upon rearranging and simplifying gives:

$$p'_{j,t} = \frac{N_{m,t}n_{jf,t} + N_{f,t}n_{jm,t}}{2N_f N_m} . \tag{6}$$

Selection acts upon these offspring in order to determine the allelic frequencies in females and males in the next generation, $t + 1$. As an example, the frequency of females with allele $j$ after selection is given by:

$$p_{jf,t+1} = \frac{n_{jf,t+1}}{N_{f,t+1}} = \frac{p'_{j,t}w_{jf}}{p'_{t,j}w_{jf} + (1 - p'_{t,j})w_{kf}} \tag{7}$$

The logarithmic per capita growth rate of allele $j$ in females is therefore given by the number of females carrying allele $j$ after selection divided by the original number of fe-males carrying allele $j$:

$$r_{jf,t} = \ln\left(\frac{n_{jf,t+1}}{n_{jf,t}}\right) \tag{8}$$

An equivalent expression for the logarithmic per capita growth rate of allele $j$ in males $m$ can be obtained by exchanging $f$ for $m$ across the various subscripts in Eqn. 7.

Polymorphism in a sexual population, however, is ultimately influenced by growth and establishment of an allele across both sexes. Therefore, the growth rate of allele $j$ across the entire population of females *and* males is given by:

$$r_{j,t} = \ln \left( \frac{n_{jf,t+1} + n_{jm,t+1}}{n_{jf,t} + n_{jf,t}} \right) \tag{9}$$

An equivalent expression describes $r_{k,t}$, the growth rate of allele $k$.

Our model further assumed allele $j$ always has a high fitness in females ($w_{jf} = 1$) but variable fitness in males ($w_{jm} < 1$); and allele $k$ has a high fitness in males ($w_{km} = 1$) but variable fitness in females ($w_{kf} < 1$). The selection against allele $j$ in males is therefore $S_m = 1 - w_{jm}$, and the selection against allele $k$ in females is $S_f = 1 - w_{kf}$. When population sizes and selection values are constant, selection mantains both alleles in the population, under the condition that:

$$\frac{S_m}{1 + S_m} < S_f < \frac{S_m}{1 - S_m} \tag{10}$$

(Kidwell *et al.*, 1977; Pamilo, 1979; Patten *et al.*, 2010; Connallon *et al.*, 2018). Thus, the maintenance of polymorphism of sexually antagonistic alleles is solely determined by the values of $S_m$ and $S_f$. Note that in our model, the values $S_m$ and $S_f$ are bounded from 0 to 1. Therefore the parameter space of sexually antagonistic selection is within the range $0 < S_m, S_f < 1$. Classic theoretical models predict that, in constant environments, polymorphism is maintained in $\approx 0.38$ of the parameter space (Kidwell *et al.*, 1977; Pamilo, 1979; Connallon *et al.*, 2018). Nonetheless it is unrealistic to assume population sizes and

selection are constat through time. Temporal changes in population densities are ubiqui-

tous in nature (Connallon & Clark, 2012; Reinhold, 2000). Similarly, the effect of sexual

selection has been show to vary through space and time (Kasumovic *et al.*, 2008). If fluctu-

ations in population sizes or selection values have an effect on the coexistence of sexually

antagonistic alleles, it would be reflected in increases or decreases of the proportion of the

parameter space of selection where polymorphism is maintained.

# References

Armstrong, R.A. & McGehee, R. (1980). Competitive exclusion. *The American Naturalist*, 115, 151–170.

Arnqvist, G. & Rowe, L. (2013). *Sexual conflict*. Princeton University Press.

Barabás, G., D'Andrea, R. & Stump, S.M. (2018). Chesson's coexistence theory. *Ecological Monographs*, 88, 277–303.

Chesson, P. (1994). Multispecies competition in variable environments. *Theoretical population biology*, 45, 227–276.

Chesson, P. (2000a). General theory of competitive coexistence in spatially-varying environments. *Theoretical Population Biology*, 58, 211–237.

Chesson, P. (2000b). Mechanisms of maintenance of species diversity. *Annual review of Ecology and Systematics*, 31, 343–366.

Connallon, T. & Clark, A.G. (2012). A general population genetic framework for antagonistic selection that accounts for demography and recurrent mutation. *Genetics*, 190, 1477–1489.

Connallon, T. & Clark, A.G. (2014). Balancing selection in species with separate sexes: insights from fisher's geometric model. *Genetics*, 197, 991–1006.

Connallon, T. & Hall, M.D. (2018). Environmental changes and sexually antagonistic selection. *eLS*, pp. 1–7.

Connallon, T., Sharma, S. & Olito, C. (2018). Evolutionary Consequences of Sex-Specific Selection in Variable Environments: Four Simple Models Reveal Diverse Evolutionary Outcomes. *The American Naturalist*, 193, 93–105.

Curtsinger, J.W., Service, P.M. & Prout, T. (1994). Antagonistic pleiotropy, reversal of dominance, and genetic polymorphism. *The American Naturalist*, 144, 210–228.

Dean, A.M. (2005). Protecting haploid polymorphisms in temporally variable environments. *Genetics*, 169, 1147–1156.

Dempster, E.R. (1955). Maintenance of genetic heterogeneity. In: *Cold Spring Harbor Symposia on Quantitative Biology*. Cold Spring Harbor Laboratory Press, vol. 20, pp. 25–32.

Ellner, S. & Hairston Jr, N.G. (1994). Role of overlapping generations in maintaining genetic variation in a fluctuating environment. *The American Naturalist*, 143, 403–417.

Ellner, S. & Sasaki, A. (1996). Patterns of genetic polymorphism maintained by fluctuating selection with overlapping generations. *theoretical population biology*, 50, 31–65.

Ellner, S.P., Snyder, R.E. & Adler, P.B. (2016). How to quantify the temporal storage effect using simulations instead of math. *Ecology letters*, 19, 1333–1342.

Ellner, S.P., Snyder, R.E., Adler, P.B. & Hooker, G. (2019). An expanded modern coexistence theory for empirical applications. *Ecology Letters*, 22, 3–18.

Gavrilets, S. (2014). Is sexual conflict an "engine of speciation"? *Cold Spring Harbor perspectives in biology*, 6, a017723.

Hedrick, P.W. (1974). Genetic variation in a heterogeneous environment. i. temporal heterogeneity and the absolute dominance model. *Genetics*, 78, 757–770.

Hedrick, P.W. (1986). Genetic polymorphism in heterogeneous environments: a decade later. *Annual review of ecology and systematics*, 17, 535–566.

Hedrick, P.W. (1999). Antagonistic pleiotropy and genetic polymorphism: a perspective. *Heredity*, 82, 126–133.

Hedrick, P.W. (2007). Balancing selection. *Current Biology*, 17, R230–R231.

Immler, S., Arnqvist, G. & Otto, S.P. (2012). Ploidally antagonistic selection maintains stable genetic polymorphism. *Evolution: International Journal of Organic Evolution*, 66, 55–65.

Jordan, C.Y. & Charlesworth, D. (2012). The potential for sexually antagonistic polymorphism in different genome regions. *Evolution: International Journal of Organic Evolution*, 66, 505–516.

Kasumovic, M.M., Bruce, M.J., Andrade, M.C. & Herberstein, M.E. (2008). Spatial and temporal demographic variation drives within-season fluctuations in sexual selection. *Evolution: International Journal of Organic Evolution*, 62, 2316–2325.

Kidwell, J., Clegg, M., Stewart, F. & Prout, T. (1977). Regions of stable equilibria for models of differential selection in the two sexes under random mating. *Genetics*, 85, 171–183.

Lande, R. (1980). Sexual dimorphism, sexual selection, and adaptation in polygenic characters. *Evolution*, pp. 292–305.

Levins, R. (1979). Coexistence in a variable environment. *The American Naturalist*, 114, 765–783.

Mitchell-Olds, T., Willis, J.H. & Goldstein, D.B. (2007). Which evolutionary processes influence natural genetic variation for phenotypic traits? *Nature Reviews Genetics*, 8, 845–856.

Mori, E., Mazza, G. & Lovari, S. (2017). Sexual dimorphism. *Encyclopedia of Animal Cognition and Behavior (J. Vonk, and T. Shakelford, Eds). Springer International Publishing, Switzerland*, pp. 1–7.

Nunney, L. (2002). The effective size of annual plant populations: the interaction of a seed bank with fluctuating population size in maintaining genetic variation. *The American Naturalist*, 160, 195–204.

Pamilo, P. (1979). Genic variation at sex-linked loci: Quantification of regular selection models. *Hereditas*, 91, 129–133.

Patten, M.M., Haig, D. & Ubeda, F. (2010). Fitness variation due to sexual antagonism and linkage disequilibrium. *Evolution: International Journal of Organic Evolution*, 64, 3638–3642.

Pemberton, J., Smith, J., Coulson, T.N., Marshall, T.C., Slate, J., Paterson, S., Albon, S., Clutton-Brock, T.H. & Sneath, P.H.A. (1996). The maintenance of genetic polymorphism

in small island populations: large mammals in the hebrides. *Philosophical Transactions of the Royal Society of London. Series B: Biological Sciences*, 351, 745–752.

Reinhold, K. (2000). Maintenance of a genetic polymorphism by fluctuating selection on sex-limited traits. *Journal of Evolutionary Biology*, 13, 1009–1014.

Schreiber, S.J. (2010). Interactive effects of temporal correlations, spatial heterogeneity and dispersal on population persistence. *Proceedings of the Royal Society B: Biological Sciences*, 277, 1907–1914.

Shoemaker, L.G., Barner, A.K., Bittleston, L.S. & Teufel, A.I. (2020). Quantifying the relative importance of variation in predation and the environment for species coexistence. *Ecology letters*, 23, 939–950.

Walsh, B. & Lynch, M. (2018). *Evolution and Selection of Quantitative Traits*. OUP Oxford.