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Original Article

Polygenic response of sex chromosomes to sexual antagonism

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Abstract

Sexual antagonism occurs when males and females differ in their phenotypic fitness optima but are constrained in their evolution to these optima because of their shared genome. The sex chromosomes, which have distinct evolutionary "interests" relative to the autosomes, are theorized to play an important role in sexually antagonistic conflict. However, the evolutionary responses of sex chromosomes and autosomes have usually been considered independently, that is, via contrasting the response of a gene located on either an X chromosome or an autosome. Here, we study the coevolutionary response of the X chromosome and autosomes to sexually antagonistic selection acting on a polygenic phenotype. We model a phenotype initially under stabilizing selection around a single optimum, followed by a sudden divergence of the male and female optima. We find that, in the absence of dosage compensation, the X chromosome promotes evolution toward the female optimum, inducing coevolutionary male-biased responses on the autosomes. Dosage compensation obscures the female-biased interests of the X, causing it to contribute equally to male and female phenotypic change. We further demonstrate that fluctuations in an adaptive landscape can generate prolonged intragenomic conflict and accentuate the differential responses of the X and autosomes to this conflict.

Keywords: sexual antagonism, population genetics, sex chromosomes

Introduction

Sexually antagonistic selection arises when males and females have different fitness optima for a shared phenotype, but are hindered in evolving to these different optima because they share the majority of their genome. This form of intragenomic conflict is predicted to be common in any species with separate sexes, as males and females within a species will often experience different selection pressures due to their distinct life histories and reproductive strategies (Chapman et al., 2003; Bonduriansky & Chenoweth, 2009; Flintham et al., 2023; Mank, 2017a; Rice & Chippindale, 2001; Ruzicka et al., 2020; van Doorn, 2009). The fitness costs that sexually antagonistic conflict imposes on a population may eventually be resolved through a variety of evolutionary mechanisms (Connallon & Clark, 2010, 2011; Mank, 2017b; Wright et al., 2018) that lead to sexual dimorphism—quantitative or qualitative differences between males and females within a species.

While most of the genome is autosomal, and thus inherited symmetrically between the sexes, the sex chromosomes are an important exception to this symmetry. The X and Z chromosomes in heterogametic species spend time in both sexes, but, due to their sex-biased inheritance, have distinct evolutionary "interests" in this conflict compared with the autosomes. Understanding how sexual antagonism manifests and is resolved on the sex chromosomes has therefore been a major focus of theoretical (Frank & Patten, 2020; Fry, 2010; Haig, 2006; Hitchcock & Gardner, 2020; Rice, 1984) and empirical (Gibson et al., 2002; Ruzicka & Connallon, 2020, 2022; Vicoso & Charlesworth, 2006) investigation.

While there has been considerable theory describing the dynamics of sexually antagonistic selection, this theory has usually assumed that the locus (or loci) under sexually antagonistic selection is either autosomal or X-linked, that is, the gene controlling the phenotype is entirely aligned with the evolutionary "interests" of the X or the autosomes. However, because many phenotypes are polygenic—controlled by many loci scattered throughout the genome—they will often in fact be controlled by loci on both the X chromosome and autosomes; in these scenarios, the X chromosome and autosomes must coevolve in order to resolve this intragenomic conflict (Frank & Crespi, 2011). The X and Z chromosomes often comprise a significant portion of an organism's genome, potentially resulting in a substantial influence of these chromosomes on the evolution of polygenic phenotypes.

The major focus of our work is therefore to understand the dynamics of this coevolution between the sex chromosomes and autosomes under a realistic model of sexually antagonistic selection on a polygenic phenotype. In order to study these dynamics, we consider an explicitly phenotype-based model, in which the selective costs and benefits of individual alleles arise organically from a model of selection on the phenotype. This approach is facilitated by the recent development of whole-genome evolutionary simulation software

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(Haller & Messer, 2019), which enables us to simultaneously study the phenotypic and genotypic response to sexually antagonistic selection across the sex chromosomes and autosomes.

In the model we study, we assume that the phenotype in question is under stabilizing selection. There is considerable evidence that stabilizing selection is a common form of selection on phenotypes (Estes & Arnold, 2007; Sanjak et al., 2018; Simons et al., 2018; Sella & Barton, 2019), including phenotypes that have been shown to be involved in sexually antagonistic conflict in a number of species (Abbott et al., 2010; Mank, 2017a; Prasad et al., 2007; Sanjak et al., 2018; Stulp et al., 2012). We examine a scenario in which males and females initially experience stabilizing selection around a fitness optimum for the phenotype, but then the male and female fitness optima suddenly diverge. This divergence induces opposing directional selection on the phenotype in the two sexes (Lande, 1976, 1980). While the general dynamics of adaptation to a new optimum are well studied (Hayward & Sella, 2022; Jain & Stephan, 2017; Lande, 1976, 1980; Thornton, 2019), the unique role of the sex chromosomes in adaptation to a new sexually dimorphic optimum—and, importantly, the dynamics of their coevolution with the autosomes in this process—remains largely unexplored.

Overall, our goal is to investigate how the sex chromosomes and autosomes may synergistically interact to facilitate the evolution of sexual dimorphism in a polygenic phenotype, while analyzing the differences in the genetic and phenotypic response across these genomic regions. Our work, taking place in an explicitly polygenic framework, may therefore also shed light on the expected genetic signatures of this intragenomic conflict across the sex chromosomes and autosomes—an area of much recent empirical interest (Abbott et al., 2023; Mank, 2017a; Ruzicka et al., 2020).

Methods

Model overview

We study the response of a polygenic phenotype, initially under stabilizing selection around a common optimal value in both sexes, to an instantaneous change in the male and female fitness optima. For simplicity, we model only the genetic component of the phenotype, assuming no environmental effects on the phenotype; this allows us to more precisely identify the genetic response to sexually antagonistic selection, which would otherwise be obscured by environmentally based phenotypic variation. We first examine an additive genetic model, in which the phenotype of an individual is determined by summing the allelic effect sizes across all loci across both copies of the individual's genome. Under these assumptions, an individual's phenotype corresponds to their additive genetic value. We allow mutations to occur at the loci underlying the phenotype, which generate new alleles that have an equal probability of increasing or decreasing the phenotypic value. We assume that the male and female effect sizes of each new allele are correlated, such that the direction of the phenotypic effect of a new mutation will often, though not always, be concordant in the two sexes (Figure 1). This corresponds to a phenotype with a shared genetic basis between the sexes but also some level of sexual differentiation—a common situation for a variety of morphological and developmental phenotypes across taxa (Poissant et al., 2010; Kassam & McRae, 2016).

We simulate an instantaneous shift in fitness optimum in both males and females, so that the male optimum moves to an increased value, while the female optimum moves to a decreased value. This induces sexually antagonistic conflict, requiring males and females to evolve in opposite directions, against the underlying mutational genetic correlation of the phenotype. As a contrast, we also consider a scenario where the male and female fitness optima suddenly shift in the same

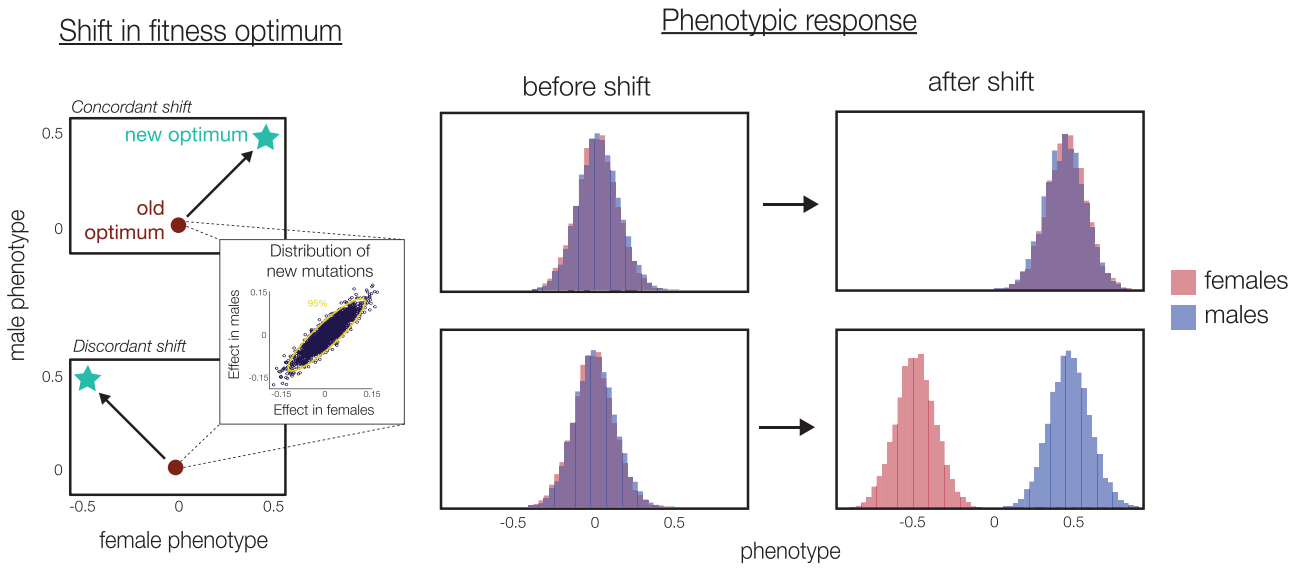

Figure 1. Divergence of male and female optima generates sexual antagonism. Illustrated are a concordant shift of the male–female optimum (top), in the same direction as the underlying male–female correlation of mutational effects on the phenotype (inset), and a discordant shift of the male–female optimum (bottom), orthogonal to the direction of the mutational correlation (inset). In both scenarios, the mean phenotype evolves toward the new male–female optimum. However, in the case of the discordant shift (bottom), movement to the new optimum involves opposing directional selection on the male and female phenotypes, that is, sexual antagonism. At the end of this process, once the population has reached the new male–female optimum, the male and female phenotypic distributions have diverged and sexual dimorphism in the phenotype has been established.

direction, so that the resulting phenotypic changes are aligned with the underlying genetic correlation.

Simulation setup

The population is composed of 10,000 diploid individuals (5,000 male and 5,000 female throughout) and evolves according to a Wright–Fisher process with random mating. We implement stabilizing selection as a Gaussian fitness function with standard deviation $\omega = 1$. This standard deviation, ω, which is the width of the stabilizing selection function, is inversely proportional to the strength of stabilizing selection acting on the phenotype. Initially, the male and female fitness optima are identical: $O_{\sigma} = O_{\varphi} = 0$. After 100,000 generations, these optima shift such that $O_{\sigma} = +0.5$ and $O_{\varphi} = -0.5$. Under the configuration of mutational effect sizes we adopt, these correspond to a shift of approximately $2.5V_{P0}$ where V_{P0} is the phenotypic variance at the time of the shift. We then observe the population for 100,000 additional generations. The strength of stabilizing selection remains constant throughout.

The phenotype is controlled by 1,000 loci (the total genome length, L, is therefore 1,000), a number chosen to mimic a polygenic phenotype while maintaining simulation efficiency. Unless otherwise stated, these loci freely recombine with each other, and there is no intralocus recombination. We implement a per-locus mutation rate of $u = 10^{-5}$, so that the mutation rate per gamete per generation is $U = Lu = 0.01$. Unless otherwise stated, we assume that the effects of these mutations on the phenotype in males and females, e_m and e_f, are drawn from a bivariate normal distribution with variance 0.01 and an intersex correlation of 0.9. We also consider a scenario with reduced effect sizes, drawn from a bivariate normal distribution with variance 0.001. We parameterize e_m and e_f to describe the homozygous effect of an allele. The effect of an individual allele is therefore $0.5e_m$ in males and $0.5e_f$ in females in simulations in which additive effects are assumed or he_m and he_f in simulations in which the dominance coefficient (h) varies. In simulations in which dominance varies, dominance coefficients were drawn from a uniform distribution between 0 and 1. We assume that the dominance coefficient of an allele is the same in males and females. At generation 0, we seed the population with 100 mutations, with effects drawn from the distribution described above and with frequencies chosen from a uniform distribution between 0 and 1.

After 100,000 ($10N$) generations, the fitness optima for males and females instantaneously diverge. We record the frequency and effect sizes of alleles segregating in the population at the time of the shift, along with their genomic location, and track the frequencies of these alleles across subsequent generations at different time points. Unless otherwise stated, we report the frequency of mutations that have appeared during the course of the simulation (i.e., derived alleles). We also record the average male and female phenotypic values at multiple time points before and after the shift in optimum.

All simulations were run across 10 replicates in SLiM 3.3 or 4.1 (Haller & Messer, 2019). All analyses were conducted in R, and regression lines were calculated using the "lm" function in the "stat" package (R Core Team, 2022).

Single inheritance mode simulations

We initially study, in isolation, an entirely autosomal genome and an entirely X-linked genome, to clarify the evolutionary interests of these genomic regions. We have chosen to simulate an X chromosome rather than a Z chromosome, but all of our results equally apply to the Z chromosome (albeit with the sexes reversed).

In these simulations, we assume that our 1,000 freely recombining loci are all inherited according to the pattern of an autosome or an X chromosome. That is, in the case of an X, females will be diploid and males will be haploid, and males inherit all alleles from their mothers. We do not consider a sex-specific (Y) chromosome (see Discussion).

In our X chromosome simulations, we consider both the scenario where the X does not experience dosage compensation and the scenario where it does. Without dosage compensation, the effect on the male phenotype of an allele on the X is $0.5e_m$ (regardless of the dominance of the allele in females).

Many species have diverse dosage compensation mechanisms to maintain the X–autosome expression ratio in the face of different X copy number in each sex. Dosage compensation can occur through a variety of mechanisms, and its degree can also vary across the X chromosome itself (Mank, 2013; Gu & Walters, 2017). Here, we have chosen to implement dosage compensation by doubling the effect size of alleles on the X chromosome in males (Kent et al., 2005), such that under dosage compensation, an X-linked allele's effect on the male phenotype is e_m (a proxy for the upregulation of the entire X chromosome). This is analogous to the dosage compensation mechanism observed in species like *Drosophila melanogaster*, where the expression of the X chromosome in males is doubled (Conrad & Akhtar, 2012; Lucchesi & Kuroda, 2015). This model also provides a good fit to X chromosome genetic variation for polygenic phenotypes in humans (Sidorenko et al., 2019).

Full genome simulations

In these simulations, we consider a genome containing both sex chromosomes and autosomes. We simulate 1,000 loci along a *Drosophila melanogaster*-like genome, using the linkage map produced by Comeron et al. (2012). Unless otherwise stated, we allow for autosomal recombination in males (unlike in *Drosophila*), which we assume to be identical to the autosomal recombination map of females. In the *Drosophila melanogaster*-like genome, the X chromosome comprises ~17% of the length of a haploid genome, relative to the autosomes' ~83%. We do not simulate a Y chromosome (but see Discussion). We assume that allelic effects at diploid loci are additive.

In the simulations, we separately tracked the additive genetic value for the phenotype derived from the X chromosome and autosomes, by summing up either the male or female effect sizes of all X-linked and all autosomal alleles carried by each individual.

Moving optimum

We simulated a dynamic adaptive landscape in which the male and female fitness optima are continually changing. We assumed that the male–female optimum shifts every 500 generations by an absolute (Euclidean) distance of $\lambda = 0.5$. We consider three scenarios for the direction of this shift in the male–female optimum.

In the first scenario, the direction of the optimum shift is random, with its angle A drawn from a uniform distribution

between 0 and 360 degrees. The new male and female optima are then $O^{♀}_{t+1} = O^{♀}_{t} + \lambda \cos A$ and $O^{♂}_{t+1} = O^{♂}_{t} + \lambda \sin A$. In the second scenario, we simulate a fluctuating male–female optimum that switches between a sexually antagonistic optimum of $O^{♀} = -0.5$ and $O^{♂} = 0.5$ and the original optimum of $O^{♀} = 0$ and $O^{♂} = 0$ every 500 generations. In the third scenario, we simulate a fluctuating male optimum only, such that the male–female optimum shifts between $O^{♀} = 0$ and $O^{♂} = 0.5$ and the original optimum of $O^{♀} = 0$ and $O^{♂} = 0$ every 500 generations. In all three scenarios, we tracked the angle at which the mean male–female phenotype moved every generation for 50,000 generations following the first optimum shift, along with the angle at which the mean additive genetic value of X-linked and autosomal loci moved every generation. In these simulations, we assumed a *Drosophila melanogaster*-like genome as described above.

Results

The response of the sex chromosomes and autosomes to sexually antagonistic selection

The sex chromosomes and autosomes, in isolation of each other, take different phenotypic paths to a new fitness optimum

We first study the phenotypic response of an entirely autosomal and an entirely X-linked genome to the divergence of the male and female fitness optima (Figure 1). This shift induces opposing directional selection in males and females, driving the initial evolution of sexual dimorphism in the phenotype. Note that, while it is primarily to generate intuition that we initially study these special cases, they do in fact apply to haplodiploid species (for the X) and species with environmental sex determination (for the autosomes).

First, consider the case of an entirely autosomal polygenic phenotype. Because all individuals inherit a set of autosomes from their mother and their father, autosomes spend an equal amount of time in males and females, and will therefore respond equally to selection in males and females. This means that, assuming selection is acting equally strongly in males and females, the autosomal phenotype will take a straight path to the new optimum in male–female phenotype space (Figure 2).

We now turn to the phenotypic response of an X chromosome, in isolation, to the onset of sexually antagonistic selection. In contrast to the autosomes, the X chromosome, due to its unique transmission pattern, spends twice as much time in females as in males. As a result, in the absence of dosage compensation, an X-linked phenotype will respond twice as strongly to selection in females than in males. This leads to a curved phenotypic path (Figure 2), with initial rapid movement toward the female optimum followed by subsequent movement toward the male optimum.

We see a somewhat similar trajectory, in the absence of dosage compensation, for an X-linked phenotype even in the case of a concordant shift in the male–female optimum, although the curvature of the phenotypic path is more extreme in the case of a sexually antagonistic shift (Supplementary Figure S1).

In contrast, dosage compensation of the X chromosome increases the phenotypic variance of males, thereby increasing the rate at which the X moves toward the male optimum. This approximately cancels out the effect of the X spending twice as much time in females, so that a polygenic phenotype specified by a dosage-compensated X will take a path to the optimum similar to one specified by the autosomes (Figure 2; see also Charlesworth et al., 1987).

The response of correlated phenotypes to directional selection over the generations can be described via the multivariate breeder's equation (Lande, 1980; Walsh & Blows, 2009), which can be modified to describe the response to selection of an X-linked phenotype in males and females (Fernando & Grossman, 1990; Kent et al., 2005; Lande, 1980; Yang et al., 2011) (Supplementary Appendix). While this approach relies on assumptions of constant additive genetic variance and covariance across time, we find that these multivariate breeder's equations, appropriately parameterized, provide an excellent approximation of the phenotypic response of a polygenic phenotype specified entirely by autosomes or an X chromosome (Figure 2; Supplementary Appendix)

Thus far, we have chosen to model a simultaneous shift in the male and female fitness optima. Another common scenario thought to induce sexually antagonistic selection is a change in the male optimum (e.g., induced by sexual selection and a change in the female mate preference). When the male optimum alone suddenly shifts, we see that the initial response, regardless of genomic region, is for the population to move in a correlated direction (Supplementary Figure S2). Importantly, this displacement then places the population in a position almost identical to that modeled in the main text—in which males and females experience opposing directional selection to reach their new fitness optima. This suggests that the scenario of sexual antagonism that we study can likely be induced by a number of different changes in the adaptive landscape.

Under sexually antagonistic phenotypic selection, alleles may be divided into three categories based on their directional effects on the phenotype. First, those that decrease the phenotype in females and increase the phenotype in males. After the shift in optimum, these alleles are beneficial in both sexes, as they move both males and females closer to their respective fitness optima. There are also alleles that increase the phenotype in females and decrease it in males—these are deleterious in both sexes. The final category of alleles—those which increase or decrease the phenotype in both sexes—would traditionally be considered sexually antagonistic: They will be selected for in one sex and against in the other (Zhu et al., 2023).

We can examine the genetic response of an autosomal polygenic phenotype using this categorization. The divergence of the male and female phenotype is caused by an increase in the frequency of alleles in the first category described above, and a decrease in frequency of alleles in the second category (Figure 2). We do not observe consistent changes in the frequency of alleles in the third category. These results are robust to decreasing the average effect size of individual alleles (Supplementary Figure S3).

In contrast, when we examine the genetic response of an entirely X-linked phenotype, we see that the curved phenotypic path of the X chromosome is achieved by the increase in frequency of alleles that are aligned with the optimum shift in males and females, but also by those that decrease the phenotype in both sexes, that is, sexually antagonistic alleles that are beneficial in females and costly in males (Figure 2). This pattern is consistent with previous analytical work, which has suggested that the X chromosome is likely to have female-biased "interests" in the case of mainly additive alleles underlying a polygenic phenotype (Frank & Patten, 2020; Fry,

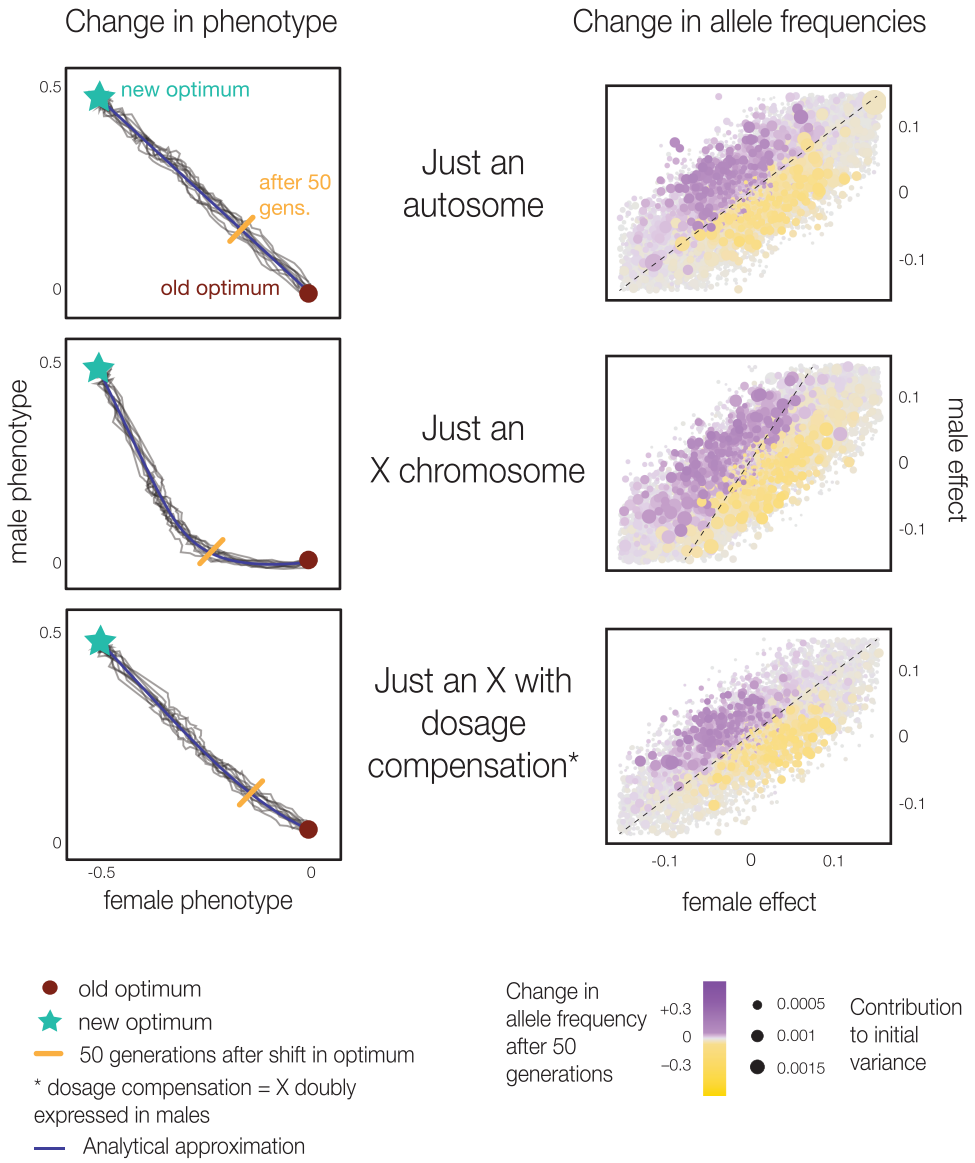

Figure 2. Autosomal and X-linked polygenic phenotypes take distinct paths to a new sexually antagonistic optimum. The left panels display the movement in male–female phenotype space of a polygenic phenotype specified entirely by an autosome (top), an X chromosome without dosage compensation (middle), and a dosage-compensated X (bottom), following a discordant shift in the male–female fitness optimum. Black lines indicate the trajectories observed across 500 generations in each of 10 replicate simulations, while the solid indigo line shows the path predicted by the multivariate breeder's equation modified for each case (Supplementary Appendix). The gold bar indicates the mean phenotype 50 generations after the shift in optimum. Right panels show, for all alleles that were segregating at the time of the optimum shift, their changes in frequency across the subsequent 50 generations (color of bubbles) as a function of their effects in females (x-axis) and males (y-axis) and a proxy for their contribution to phenotypic variance at the time of the optimum shift (size of bubbles): $\frac{1}{2}(\alpha_{\varphi}^2 + \alpha_{\sigma}^2)p(1-p)$ where p is the frequency of the allele. The dotted lines are the boundaries between alleles that are expected to be selectively favored versus disfavored, such that alleles along the line should be selectively neutral. In the top and bottom panels, these dotted lines have slope 1, representing the equal weighting of male and female fitness for autosomes and for a dosage-compensated X chromosome; in the middle panel, the slope is 2, reflecting the female-biased fitness weighting of a non-dosage-compensated X chromosome.

2010; Rice, 1984). Another way to describe this pattern is that the marginal effect of an X-linked allele is greater in females owing to the unique transmission of this chromosome, and therefore, the X chromosome is more strongly selecting on the female phenotypic effects of alleles than their male phenotypic effects (Supplementary Figure S4).

Finally, in the case of a dosage-compensated X, because the increased selection pressure in males cancels the underlying bias of the X toward female fitness, the genetic response—reflecting the phenotypic response—resembles the autosomal case.

The effect of dominance

A potential complicating factor for the different responses of the X and autosomes to sexually antagonistic selection is the possibility of alleles with variable dominance. The X chromosome is haploid in males, exposing the effects of recessive alleles in males that would be hidden in heterozygotes on an autosome. We therefore also examined a scenario in which the dominance of alleles affecting the phenotype varied. For simplicity, we assumed that the dominance coefficient of each allele was the same in males and females. Note that here we define dominance in terms of an allele's effect on the

phenotype, not in terms of its effect on fitness, the usual context in which dominance has been considered in the sexual antagonism literature (Frank & Patten, 2020; Rice, 1984).

We see very little difference in the relative contributions of dominant versus recessive alleles to phenotypic change on the X chromosome, compared to the autosomes, despite the fact that recessive alleles should be more "visible" to selection on the X due to their hemizygous expression in haploid males (Supplementary Figures S5 and S6; Charlesworth et al., 1987). These results can be understood in light of the analyses of Orr and Betancourt (2001), who consider the relative rate of adaptation via beneficial mutations across X-linked and autosomal loci. Their one-locus results demonstrate that the probabilities of fixation of previously deleterious newly beneficial alleles are essentially independent of dominance when adaptation occurs from the standing variation. This is because recessive deleterious alleles persist at higher copy number under mutation-selection balance than dominant deleterious alleles, but each recessive allele is also less strongly selected when it becomes beneficial (Haldane's sieve).

By this logic, despite the difference in dominance patterns induced by X-linked versus autosomal transmission, dominance will not substantially affect the probability of fixation of alleles across the two cases. While we consider an explicitly polygenic phenotype in which fixation of alleles is rare during short-term adaptation, in contrast to Orr and Betancourt's (2001) single-locus model of selective sweeps from standing variation, the intuition about the lack of impact of dominance in the two models is similar. In our model, beneficial alleles, with phenotypic effects aligned to the shift in optimum, will generally have been selected against due to underdominance induced by stabilizing selection prior to the shift in optimum, and adaptation also primarily occurs via the increase in frequency of alleles from the standing genetic variation (Orr and Betancourt, 2001). We observe a negative relationship between the dominance of an allele and its frequency prior to the shift in optimum (Supplementary Figure S7), consistent with the view that dominant alleles are at lower frequency and that this trade-off drives the lack of difference in the use of dominant versus recessive alleles on the X chromosome compared with the autosomes in our model (Supplementary Figure S6).

Coevolution of the X chromosome and autosomes

Thus far, we have considered the evolutionary dynamics of sex chromosomes and autosomes in isolation. This has built intuition to understand the distinct evolutionary "interests" of the autosomes and the sex chromosomes under sexually antagonistic selection in a polygenic framework. In taxa with heterogametic sex determination, however, sex chromosomes and autosomes coexist within the same genome (Bachtrog et al., 2014). Our major aim is therefore to examine the coevolutionary dynamics induced by sexually antagonistic selection acting on a polygenic phenotype controlled by both autosomes and sex chromosomes and to understand the compromise struck between the distinct evolutionary interests of these different genomic regions.

The details of the dynamics of sexually antagonistic selection in a genome containing both sex chromosomes and autosomes will of course depend on the relative proportions of the genome that they comprise, as well as their relative gene content, recombination rates, etc., which vary extensively across taxa. For simplicity, in our analyses, we have chosen to simulate a genome based on the karyotype and recombination patterns of *Drosophila melanogaster*, although we allow autosomal recombination in males (our results are qualitatively robust to there being no autosomal recombination in males [Supplementary Figure S8]).

If we consider the fate of a polygenic phenotype controlled by loci distributed across a *Drosophila*-like genome, we find that the overall path to the new sexually antagonistic optimum closely resembles that of an entirely autosomal phenotype (Figure 3). This is not unexpected, as even in the case of a *Drosophila*-like genome, with relatively few autosomes and a large X chromosome, the majority of loci underlying the phenotype are autosomal, so that the response of autosomal loci dominates the overall phenotypic response to sexually antagonistic selection.

We can also examine the specific contributions of the X chromosome and autosomes to this overall phenotypic response. We initially examine the case of no dosage compensation. In this case, the X chromosome responds very strongly to selection in females, rapidly pushing the phenotype toward the female optimum and not the male optimum (Figure 3). Countervailing this effect of the X chromosome, the autosomes evolve to contribute more to phenotypic movement to the male optimum than to the female optimum (Figure 3). These dynamics are consistent with previous theoretical work on the potential for coevolution between genomic regions in response to sexual antagonism (Ågren et al., 2019; Patten, 2018; Wade & Drown, 2016; Wade & Fogarty, 2021).

Essentially, the X chromosome within this genome strongly prioritizes movement to the female optimum, regardless of the effect on male fitness, in the generations immediately following the shift in optimum. In our simulations of an entirely X-linked phenotype, we observed that such a phenotype will eventually respond to selection in males and move toward the male optimum, creating the "hockey-stick" pattern seen in our simulations of an entirely X-chromosomal genome (Figure 2). However, in the case of a genome containing both a sex chromosome and autosomes, the autosomes provide the predominant contribution to movement toward the male optimum, so that the X chromosome remains largely occupied with movement to the female optimum, as reflected in its strong female-biased change in additive genetic values (Figure 3).

To understand these patterns in more detail, we can examine the frequency change of individual alleles across the X chromosome and autosomes. We find, as expected, that the X chromosome shows a pronounced pattern of selection for alleles with phenotypic effects that move females closer to their optimum, but no similar pattern of selection for male phenotypic effects, while the autosomes show evidence for selection on both male and female phenotypic effects (Figure 4).

The distinct contribution of X-linked compared with autosomal loci to phenotypic change in males and females in the case of no dosage compensation is unique to sexually antagonistic selection. When the male and female optima shift in a concordant direction, there is a slight difference in the contributions of X-linked loci to phenotypic change in males and females, but this effect is much reduced in magnitude relative to the case of a sexually antagonistic shift in the male and female optima (Supplementary Figure S9).

We now consider the case of dosage compensation, with the X up-regulated in males. In this case, we observe a very

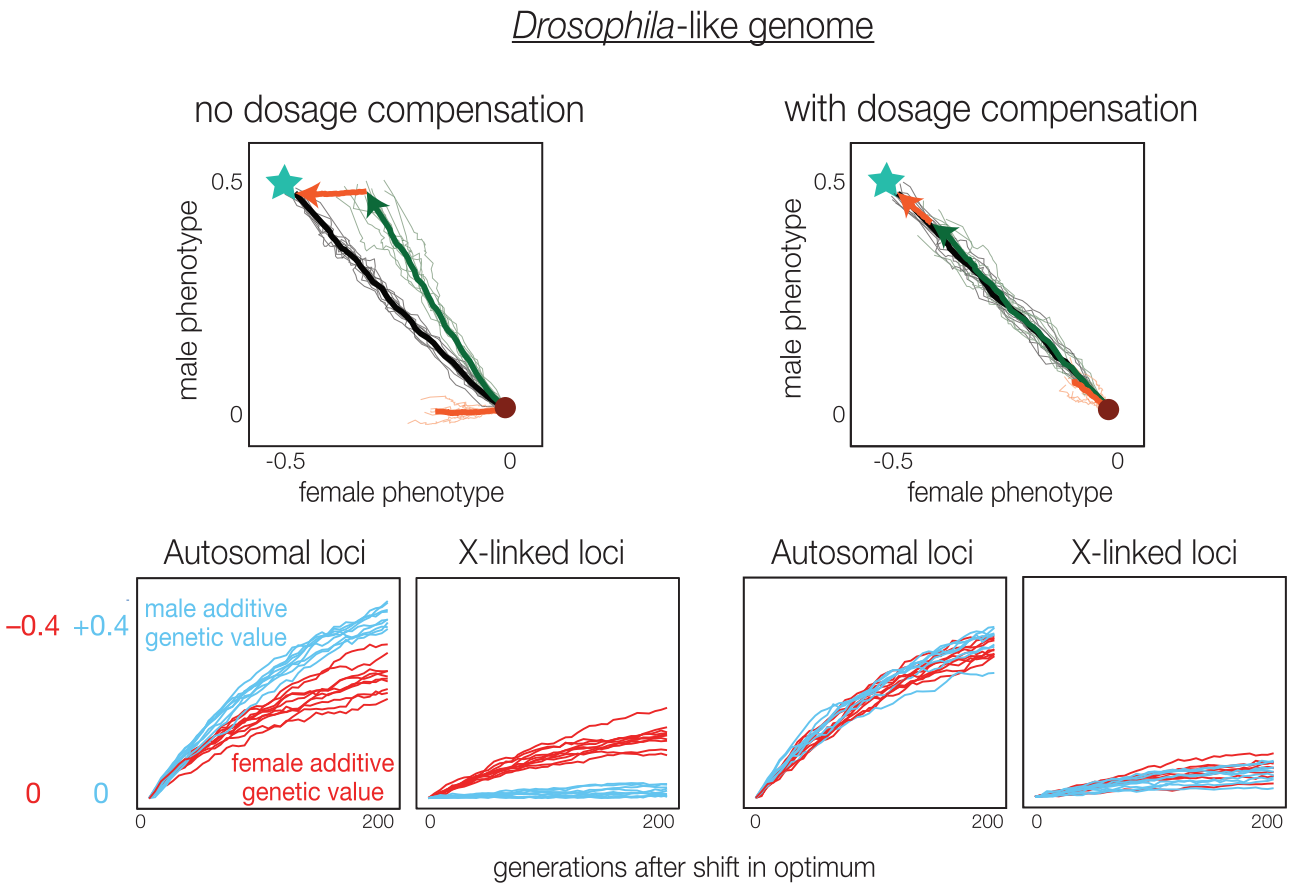

Figure 3. Phenotypic response to sexually antagonistic selection of X-linked and autosomal loci within the same genome. We simulate the response of a phenotype controlled by loci distributed across a *D. melanogaster*-like genome, both where the X chromosome does not (left) and does (right) experience dosage compensation. The top panels show the overall path that the mean phenotype takes across the male–female phenotype landscape (black), which is similar in both cases. Under no dosage compensation; however, the X chromosome contributes only to movement toward the female phenotypic optimum (orange path in left panel), while it contributes equally to movement toward the male and female optima when dosage compensated (orange path in right panel). In the case of no dosage compensation, the autosomes contribute more to movement toward the male phenotypic optimum (green path), to compensate for the X's female-biased effect. Transparent lines show trajectories from individual simulations; bold lines show average trajectories across 10 replicates. To account for drift across chromosomes in their contributions to the trait during the initial burn-in period in our simulations, trajectories are normalized according to their starting values, so that all start at exactly $(0, 0)$ in the male–female phenotype space displayed here. The bottom panels track the additive genetic value of autosomes and X chromosomes after the shift in optimum, revealing the rapid evolution of a female-biased additive genetic value on the non-dosage-compensated X chromosome and compensatory evolution of a male-biased genetic value on the autosomes.

different pattern. Consistent with our previous simulations of a phenotype specified entirely by a dosage-compensated X chromosome, the X's contribution to male and female phenotypic changes is approximately equal in this case (Figure 3). With no need to balance out an unequal contribution of the X, the autosomes also contribute approximately equally to the male and female phenotypic change. This is also true in the case where the male and female optima shift concordantly (Supplementary Figure S9).

These results illustrate the importance of separately examining and developing intuition for the contribution of the sex chromosomes and autosomes. While the overall phenotypic movement resulting from genome-wide allele frequency shifts looks approximately symmetric with respect to the sexes in the absence of dosage compensation on the X, the contributions of the autosomes and X chromosome to this phenotypic change can be very distinct, reflecting both their own distinct evolutionary interests and the overarching coevolutionary compromise between the sex chromosomes and autosomes. It is furthermore clear from these results that details of the genomic architecture of the phenotype of interest, including the size of the sex chromosome and its enrichment for loci that causally affect the phenotype, will impact how the phenotype evolves in response to sexually antagonistic selection. These results also demonstrate that the presence or absence of dosage compensation can dramatically alter the role played by the X chromosome in sexual antagonism.

The distinct patterns of polygenic adaptation on sex chromosomes versus autosomes further suggest that sexually antagonistic selection could perhaps be detected via estimation of chromosome-specific contributions to mean genetic values, particularly in model organisms through crossing experiments. It is important to note, however, that it is the *change* in additive genetic contributions across the X and the autosomes, rather than their absolute values, which is the characteristic feature of sexual antagonism in our simulations; the X and autosomes may accumulate different additive genetic values even when males and females have the same fitness optimum, as long as the sum of their additive genetic values places the male and female phenotype at the

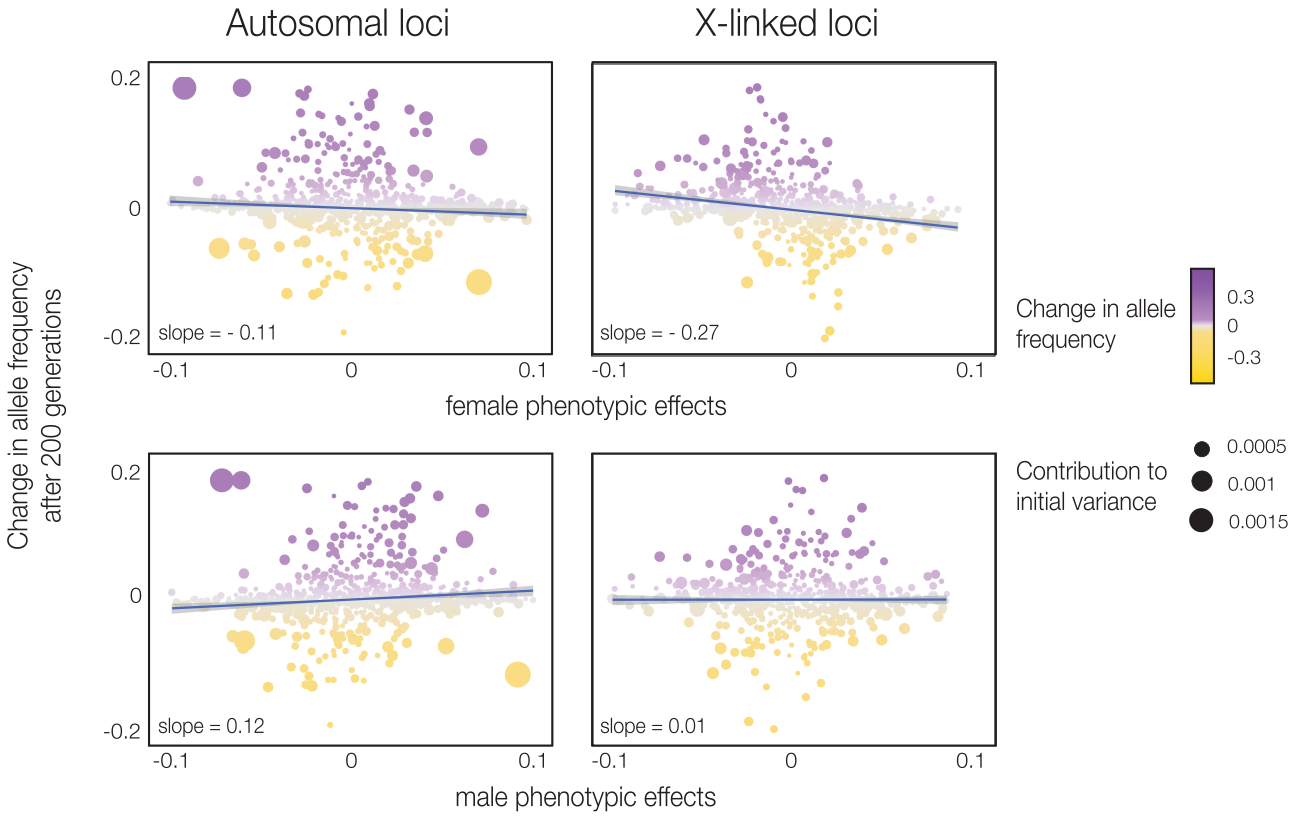

Figure 4. Female-biased genetic response of the X chromosome to sexually antagonistic selection, relative to autosomes within the same genome. Frequency changes of autosomal (left) and X-linked (right) alleles across 200 generations following a sexually antagonistic shift in male–female optima, plotted as a function of the alleles' phenotypic effects in females (top) and males (bottom). Simulations are based on a *D. melanogaster*-like genome without dosage compensation on the X, as in the left panels of Figure 3. In each case, we randomly sampled 1,000 alleles segregating on the X chromosome (right) and on the autosomes (left) at the time of the shift in optimum. Alleles segregating on the X chromosome show little evidence of selection based on their male phenotypic effects (weak correlation with change in frequency), but show strong evidence of selection based on their female phenotypic effects (strong correlation with change in frequency). In contrast, autosomal alleles show evidence of selection based on both male and female phenotypic effects. Note that because the new female optimum is lower than the initial optimum, while the new male optimum is higher, selection favors alleles with negative phenotypic effects in females (negative correlation of frequency change with effect size) and positive phenotypic effects in males (positive correlation).

optimum (Supplementary Figure S10). Studying the dynamics of sexual antagonism through chromosome-specific polygenic scores may therefore be especially amenable to experimental settings, in which the onset and strength of selection in males and females can be controlled and the additive genetic values of different genomic regions measured across time.

Evolutionary dynamics across the sex chromosomes and autosomes once the new male and female optima have been attained

We have described how a polygenic phenotype evolves toward the new sexually antagonistic fitness optimum, with a focus on understanding how the interaction between the sex chromosomes and autosomes generates this phenotypic response. Our simulations have shown that the coevolution of these genomic elements will enable a rapid approach to the new phenotypic optimum. While the overall outcome of sexually antagonistic selection is not dramatically changed by the coevolutionary dynamics of sex chromosomes and autosomes within a genome, the individual contributions of these genomic regions are very distinct at both the phenotypic and genomic levels, reflecting their divergent evolutionary "interests."

As the male and female phenotype approach the new optimum, however, the strength of directional selection inducing phenotypic evolution toward the new optimum decreases and selection instead begins to act to keep individuals at the new optimum, that is, stabilizing selection comes to dominate (Hayward & Sella, 2022; Thornton, 2019; Stephan & John, 2020). The short-term problem of sexual antagonism has then been "solved": Males and females have reached their new optima and show sexual dimorphism for the phenotype. Concomitantly, at the genetic level, alleles will no longer show the divergent directional selection in males and females that we associate with sexually antagonistic selection. Instead, the evolutionary dynamics at this stage will reflect the action of stabilizing selection, which acts to reduce variance in both the male and female phenotype.

Even after sexual antagonism has been resolved; however, the coexistence of an X chromosome and autosomes, with their unique transmission patterns, can change how stabilizing selection affects a population's evolution around diverged male and female fitness optima. Here, we highlight two key ways through which the action of stabilizing selection around sexually dimorphic fitness optima on a genome containing both an X chromosome and autosomes can impact (a) the allele frequency distribution across the genome and (b) the phenotypic distribution of males and females at equilibrium.

Correlational structure of allelic effects across the sex chromosomes and autosomes

How stabilizing selection affects the standing pool of alleles that underlie both the male and female phenotype is a key question that will shape any future evolutionary response to directional selection. Stabilizing selection can be thought of as inducing underdominant selection, such that alleles below 50% frequency are selected against, with a strength proportional to their squared effect size on the phenotype (Lande, 1976; Simons et al., 2018). However, because the autosomes and sex chromosomes spend different amounts of time, on average, in each sex, the relative impact of the female versus male effects of an allele on the strength of underdominant selection against that allele will correspondingly differ across these genomic regions.

Modifying the standard equations that describe allele frequency change under stabilizing selection (e.g., Simons et al., 2018) to incorporate distinct male and female phenotypes, we find the same pattern of underdominant selection, in which minor alleles with strong effects on either or both of the male or female phenotype are selected against because they increase phenotypic variance (Supplementary Appendix). In the case of autosomal loci, the effects of an allele on the male and female phenotype are equally weighted. However, in the case of non-dosage-compensated X-linked loci, the allele's effect on the female phenotype is "weighed" twice as strongly as the allele's effect on the male phenotype, due to the female-biased transmission of the X chromosome (Supplementary Appendix).

Under stabilizing selection, for both autosomal and X-linked loci, minor alleles with strong effects on both the male and female phenotype suffer stronger selection than ones that have a large effect in only one sex. This can be observed by examining the correlation of male and female phenotypic effects of alleles that segregate at different frequencies. Alleles segregating at low frequencies are likely to have arisen recently, and thus reflect the underlying correlation in the male and female effects of new mutations. Alleles at intermediate frequencies, in contrast, have been filtered through the sieve of stabilizing selection in both males and females and so will show a reduced intersex correlations, as alleles with strong effects in both sexes are particularly unlikely to increase in frequency under this selection regime. Our simulations confirm this intuition and show a decrease in the correlation between male and female effect sizes for minor alleles at higher frequencies on both the X chromosome and autosomes (Figure 5). This is in line with the idea that the quantitative trait genetic correlations (the G matrix) will be shaped by long-term selection (Arnold et al., 2008; Jones et al., 2003; Steppan et al., 2002). However, we do not observe noticeable differences in this correlation structure for the X-linked versus autosomal loci even in the absence of dosage compensation (Figure 5). This is likely because the majority of alleles with large effects on the female phenotype will generally also have correlated large effects on the male phenotype and will therefore tend to be selected against on both the autosomes and the X chromosomes; this leads to only a subtle difference in how selection shapes the correlation between male and female effect sizes predicted on the X chromosome compared with the autosomes.

These results suggest a novel approach through which the action of stabilizing selection on both males and females could be detected genome wide, and its strength potentially estimated: By studying the correlation of male and female effect sizes across the allele frequency spectrum (e.g., using GWAS data). This observation also may lead to the appearance of a more sex-specific genetic architecture because GWAS focuses on alleles with intermediate frequencies, which are more likely to have more sex-specific effects compared with rarer alleles.

The Bulmer effect across the sex chromosomes and autosomes

In species with degraded sex-specific chromosomes, the presence of one copy of the sex-biased X or Z chromosome in the heterogametic sex and two in the homogametic sex will induce differences in the phenotypic variance between the sexes. In addition, theories such as the "unguarded X" or "toxic Y" predict that the presence of a haploid X or a degenerate Y in males could also result in an increased genetic load in males (Brown et al., 2020; Connallon et al., 2022; Marais et al., 2018; Sultanova et al., 2023; Xirocostas et al., 2020). These effects of the haploid X chromosome on male fitness will naturally also apply in the scenario we have considered. In the context of stabilizing selection, we identify an additional mechanism through which sex chromosomes can cause differences in phenotypic variance, and hence, the genetic load between the sexes: the "Bulmer effect" acting across sex chromosomes and autosomes.

The Bulmer effect describes the negative covariance in phenotypic effects across alleles that is generated under stabilizing selection, which reduces the genetic contribution to phenotypic variance (Bulmer, 1971, 1974). By selecting against extreme phenotypes, stabilizing selection generates negative covariances—or negative linkage disequilibria—between alleles with the same directional effect on the phenotype (i.e., a phenotype-increasing allele is more likely to be transmitted alongside a compensatory phenotype-decreasing allele than alongside another, exacerbatory phenotype-increasing allele). These negative covariances in allelic effects are generated by selection but broken up by recombination in subsequent generations, eventually reaching a stable equilibrium value (assuming the strength of stabilizing selection remains constant).

Previous consideration of the Bulmer effect has focused on the negative covariance generated among autosomal loci (Bulmer, 1971, 1974). However, sex chromosomes generate an interesting asymmetry between the sexes in their inherited negative covariance in allelic effects. In species with a degenerate Y chromosome, a female will inherit an X chromosome and an autosomal set of chromosomes from her father. Assuming ongoing stabilizing selection in both sexes, this X-autosome set will have experienced stabilizing selection in the same (paternal) genome, generating negative covariance between all loci—autosomal and X-linked—based on their phenotypic effects in males. She will also inherit an X-autosome set from her mother, which will also carry negative covariance genome-wide generated based on alleles' phenotypic effects in females. In contrast, male offspring inherit only a single X-autosome set, from their mothers, which will carry negative covariance based on alleles' female phenotypic effects; from their fathers, males receive only autosomes and the negative covariances they contain based on selection on males.

Essentially, females enjoy the benefit of two coadapted X-autosome dyads, one of which has been "tuned" based on

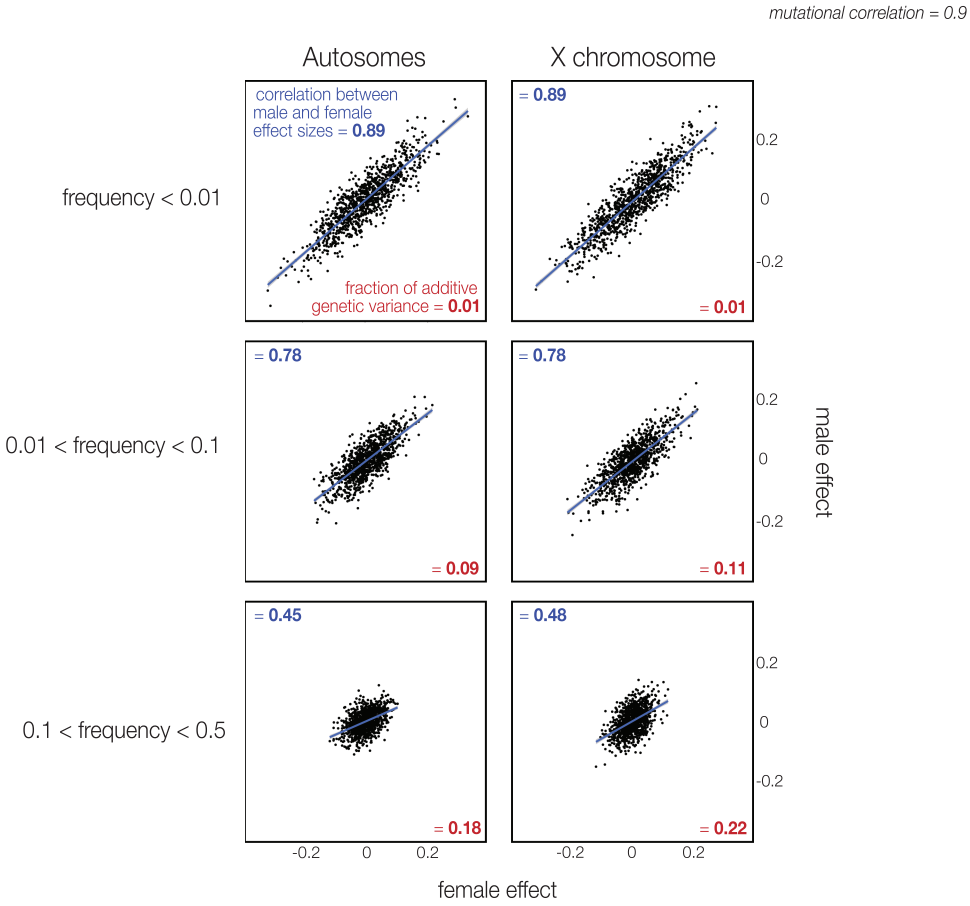

Figure 5. The correlation of the male and female effect sizes of segregating alleles differs across the allele frequency spectrum under stabilizing selection. 5*N* generations after the initial, discordant shift in optimum, we randomly sampled 1,000 segregating autosomal (left) or X-linked (right) alleles, assuming no dosage compensation, from each of three frequency bins, roughly describing minor alleles at low ($p < 0.01$), moderate ($0.01 < p < 0.1$), and high frequencies ($0.1 < p < 0.5$). Alleles in the low-frequency bin show a strong correlation in male–female effect sizes, reflecting an analogous correlation in the underlying mutational distribution. Alleles in the higher frequency bins show a reduced correlation because stabilizing selection tends to remove alleles with strong effects in both sexes. The samples of 1,000 alleles from the moderate and high-frequency bins also explain a far greater proportion of the total additive genetic variance $\frac{1}{2}(\alpha_{\varphi}^2 + \alpha_{\delta}^2)p(1-p)$ summed across alleles) than the sample of 1,000 alleles from the low-frequency bin.

selection in her own sex, while males, in constrast, inherit only one coadapted X–autosome dyad, which has been tuned based on selection in the opposite sex. Males therefore inherit alleles with less negative covariance than females, and therefore exhibit a higher phenotypic variance.

Using the framework of Bulmer (1971), we can calculate the expected equilibrium values for the negative covariance in males and females in this case, and extend these calculations to account for correlated allelic effects between the sexes (Supplementary Appendix). The relative importance of the Bulmer effect acting between the sex chromosomes and autosomes will depend on details of the sex chromosome system and recombination rates. As an example, we apply our calculations to an organism with *D. melanogaster*-like chromosome sizes. We assume a focal phenotype under stabilizing selection and controlled by loci evenly dispersed across the X chromosome and autosomes and that autosomal loci freely recombine in both sexes (as in our previous simulations, we assume the Y chromosome is degenerate, but see Supplementary Appendix).

We observe, as predicted, more negative covariances in females than in males (Figure 6). The overall reduction in phenotypic variance due to negative allelic covariance (the Bulmer effect) is relatively small (around 3% in males and 4% in females) (Figure 6) even with a large *D. melanogaster*-like X chromosome. However, the difference between males and females in their inherited covariance is approximately 30% of the total reduction in male phenotypic variance due to the Bulmer effect (Figure 6, assuming equal initial variance). This suggests that the sex chromosomes can play a strong role in the sex-specific distribution of phenotypic variance.

There is empirical evidence for greater genetic load in the heterogametic sex across taxa (Pipoly et al., 2015; Sultanova et al., 2023; Xirocostas et al., 2020), with our results adding to the confluence of mechanisms that could explain this pattern (Brown et al., 2020; Connallon et al., 2022; Pipoly et al., 2015; Marais et al., 2018; Xirocostas et al., 2020). The rapidly growing availability of data on sex-determining mechanisms across diverse species offers new opportunities to disentangle these mechanisms in a robust phylogenetic context (Bachtrog et al., 2014; Tree of Sex Consortium, 2014), and perhaps to characterize the impact of asymmetric Bulmer effects on differences in genetic load between the sexes, especially given recent evidence that alternative mechanisms may not fully explain these differences (Connallon et al., 2022).

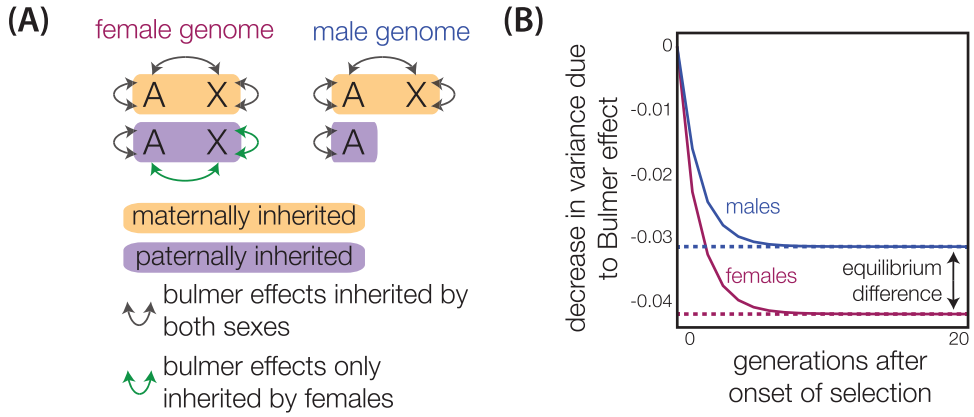

Figure 6. The Bulmer effect across sex chromosomes and autosomes results in higher phenotypic variance in males than in females. (A) Asymmetric inheritance across the genome of the negative covariances induced by stabilizing selection. Because females inherit an X chromosome from their fathers, they inherit negative covariances in phenotypic effects across the X chromosome and autosomes, generated by selection on males in the previous generation. Males, who do not inherit an X chromosome from their fathers, do not inherit these negative X–autosome covariances (see Supplementary Appendix for a discussion of the case of a nondegraded Y chromosome). (B) In simulations of a *D. melanogaster*-like genome, the reduction in phenotypic variance due to the Bulmer effect rapidly equilibrates in both sexes, but the overall negative covariance in females is greater than that in males, leaving phenotypic variance higher in males. To isolate this asymmetric impact of the Bulmer effect on males and females, we have assumed that males and females start with the same phenotypic variance at the onset of selection; results for the case in which males have a reduced initial variance owing to their hemizygosity for the X are shown in Supplementary Figure S11.

Maintaining sexually antagonistic selection across the sex chromosomes and autosomes

Across all the scenarios we have considered, we have observed that a polygenic phenotype under sexually antagonistic selection will rapidly adapt to the new male and female optima, despite a strong male–female genetic correlation, via coevolution between the X chromosome and autosomes. As sexually antagonistic selection can be broadly defined as opposing directional selection on males and females, differences in the signature of sexually antagonistic conflict across the X chromosome and autosomes will therefore also likely dissipate when the population nears the new optimum. In essence, when the population has reached the new male and female fitness optima, the problem of sexual antagonism has been resolved by the divergence of male and female phenotypic values, that is, the evolution of sexual dimorphism.

However, although we observed rapid resolution of sexual antagonism in our simulations, extensive empirical evidence suggests ongoing sexually antagonistic selection in a wide variety of species (Bonduriansky & Chenoweth, 2009; Mank, 2017a; Ruzicka et al., 2020). This suggests that the directional phase of the dynamics we have described may be more extended than we have observed in the models presented thus far.

There are three potential categories of evolutionary constraints that could extend the period of directional selection, thereby increasing the probability of detecting ongoing sexually antagonistic selection, and the different evolutionary responses across the sex chromosomes and autosomes generated by sexually antagonistic selection. The first category involves limits on mutational input. We have considered a realistic scenario in which alleles have strongly, but imperfectly correlated phenotypic effects in males and females. If this correlation were stronger, however, movement in an anticorrelated direction toward a new sexually antagonistic optimum would be correspondingly slower (indeed, if the correlation were perfect, with all alleles having identical phenotypic effects in males and females, there could be no anticorrelated movement and therefore no resolution to sexual antagonism).

The second category of constraints that could prolong the directional phase of sexually antagonistic selection involve additional pleiotropic limitations on selection. If the alleles underlying our focal phenotype, for example, also pleiotropically influenced another phenotype whose male and female optima remained the same, this would exert a considerable restraint on the ability of the focal phenotype to reach a new optimum.

The third category of constraints involves changes in environment. We have modeled the evolution of a population to a single new sexually antagonistic optimum. However, in reality, populations experience continual shifts in their adaptive landscape, with male and female fitness optima potentially shifting repeatedly due to environmental changes or interspecific interactions. In such dynamic adaptive landscapes, a population will continuously chase after different fitness peaks over time.

Changing fitness peaks could result in sustained sexually antagonistic selection and prolong the coevolution generated by sexually antagonistic selection across the sex chromosomes and autosomes. To explore this possibility in more depth, we simulated a fluctuating adaptive landscape, in which the male and female fitness optima for a phenotype continually change. In the first scenario we consider, the male–female fitness landscape jumps regularly to a new optimum a fixed distance away from the previous one, but the angle at which the jump occurs is random. Under these conditions, we find that, despite the direction of each shift in the male-female optimum being random, the population spends the majority of time evolving in an anticorrelated direction (Figure 7). This is because phenotypic adaptation in the same direction as the genetic correlation between males and females is very rapid, as standing genetic variation is plentiful along this axis; the immediate phenotypic response to a random shift in the male-female optimum is therefore generally in a correlated direction. In contrast, movement in an anticorrelated direction is comparatively slow

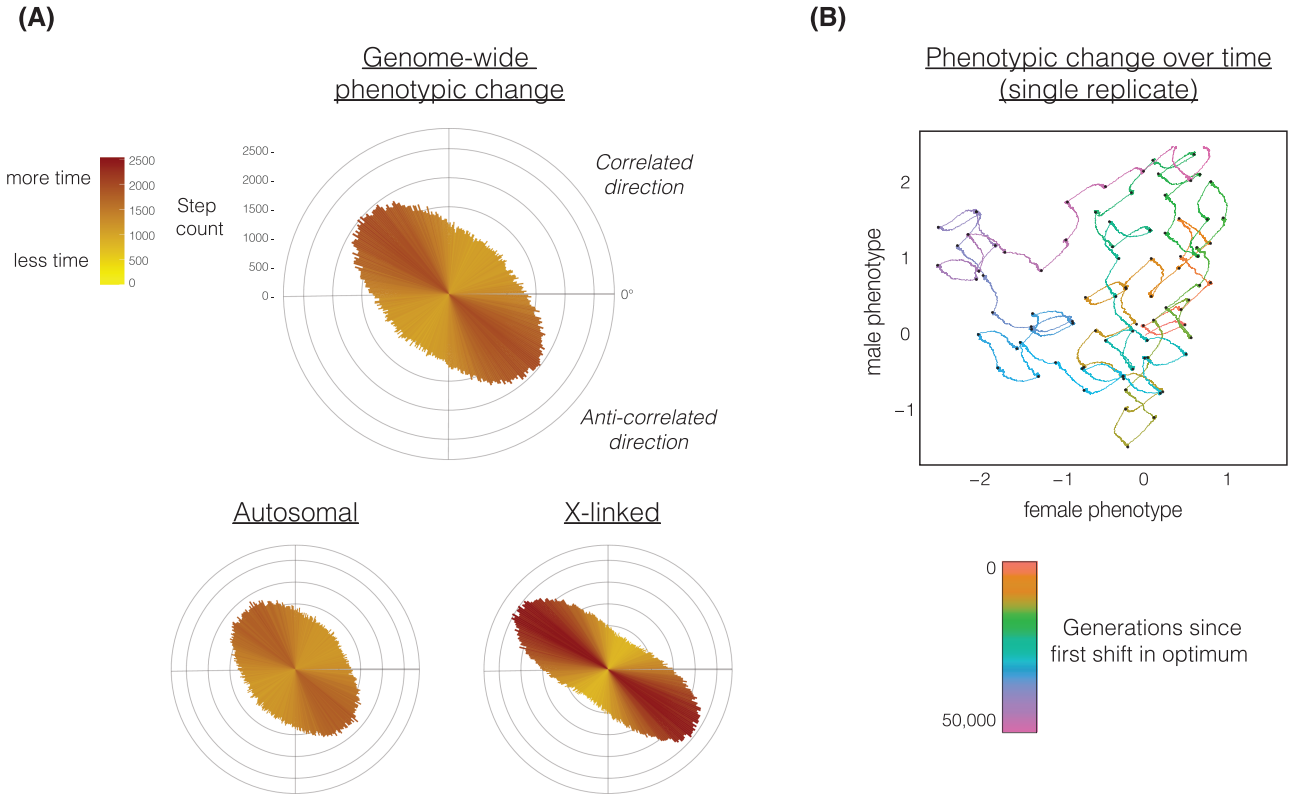

Figure 7. Random fluctuations of the adaptive landscape can generate ongoing sexually antagonistic selection. We simulate a population with a *D. melanogaster*-like genome structure, as before. The male–female fitness optimum changes every 500 generations, moving a constant distance each time in male–female phenotype space but at a random angle. (A) Histogram of the number of generations in which the population moves in various directions in male–female phenotype space (pooled across replicate simulations of 50,000 generations). Upward-right (~45°) and downward-left (~225°) movements follow the axis of the underlying male–female genetic correlation of mutations, while downward-right (~315°) and upward-left (~135°) movements are orthogonal to this underlying mutational correlation, and induce sexually antagonistic selection. We generate this histogram based on the mean population phenotype (top), the mean additive genetic value on the autosomes (bottom left), and the mean additive genetic value on the X chromosome (bottom right). (B) A representative path taken by the mean phenotype across male–female phenotype space in response to continual shifts in the fitness optimum (black dots).

because less mutational variation is available along this axis. Consistent with this reasoning, the effect is enhanced if the underlying correlation in male and female phenotypic effects is increased (Supplementary Figure S12). Therefore, although the population covers, on average, the same amount of ground in each direction, the duration of time it spends moving in an anticorrelated direction—and thus, experiencing sexually antagonistic selection—is longer.

Our simulations of a single sexually antagonistic shift in optimum identified the distinct contributions of the X chromosome and autosomes in facilitating phenotypic evolution to the new optimum. We can perform a similar decomposition to understand the overall contributions of the X chromosome and autosomes to this ongoing movement across an adaptive landscape, finding that, as predicted by our simulations of a single optimum shift, a non-dosage-compensated X chromosome spends most of its time evolving to promote female phenotypic change, while the autosomes, in a compensatory response, spend more time contributing to evolution in the male phenotype.

We go on to examine additional scenarios of fluctuating adaptive landscapes, in which the environment is predictably fluctuating between two male–female optima (e.g., due to seasonal variation in selective pressures)(Bergland et al., 2014) or a scenario in which only the male optimum is changing between two points on the adaptive landscape (e.g., due to the cycling of different female mate preferences)(Iwasa & Pomiankowski, 1995). Surprisingly, we find that regardless of the exact nature of the shifts in the adaptive landscape, we observe the same general pattern: A non-dosage-compensated X chromosome is primarily "occupied" with the evolution of the female phenotype, while the autosomes in turn are slightly biased toward promoting the evolution of the male phenotype (although this pattern is especially strong in the case of a shifting male optimum) (Supplementary Figures S13 and S14. In other words, it would seem that the coevolutionary patterns between the X and the autosomes, we have observed will occur whenever sexually antagonism is induced, regardless of the details of the underlying fitness landscape. The sexually antagonistic selection induced by changing fitness landscapes may even have the effect of "baking in" the differences in additive genetic values across these genomic regions, thereby increasing the probability that these differences can be detected using population genomic data.

Discussion

We have developed a model to study how a polygenic phenotype controlled by both sex chromosomes and autosomes will respond to sexually antagonistic selection. We confirm that

polygenic phenotypes will rapidly adapt to different male and female fitness optima, even in the face of a strong underlying genetic correlation, via coevolution between the X chromosome and autosomes—but that the details of these coevolutionary dynamics are sensitive to the presence of dosage compensation on the X chromosome. We have then studied the coevolutionary dynamics between the X chromosome and autosomes once the polygenic phenotype has reached its new male–female fitness optimum, uncovering a subtle role for the Bulmer effect in generating differences in the equilibrium phenotypic variance of males and females. Finally, we have examined how shifting adaptive landscapes can induce prolonged sexually antagonistic selection and demonstrated that the unique coevolutionary compromise between the X chromosome and autosomes will manifest across a wide range of adaptive scenarios. While we have phrased our results in the language of male heterogamety and an X chromosome, our results apply equally well to female heterogamety and a Z chromosome, *mutatis mutandis*. Our conclusions therefore apply to a broad multitude of taxa with diverse sex-determining mechanisms.

Extensions and limitations of the model

Our analyses have attempted to shed light on the basic dynamics of a polygenic phenotype under sexually antagonistic selection. However, in building our models, we have made assumptions about the evolutionary dynamics at play which may not hold broadly in natural populations or across species.

We have assumed a relatively simple population model, excluding demographic complications such as population structure and nonrandom mating, which can impact the dynamics of sexually antagonistic selection and the selective dynamics across the sex chromosomes and autosomes (Albert & Otto, 2005; Arnqvist, 2011; Flintham et al., 2021; Muralidhar, 2019; Tazzyman & Abbott, 2015). Sexual selection, in particular, and a change in male fitness optima due to female mate preferences, is often considered a key underlying cause of sexual antagonism, and understanding the coincident dynamics of nonrandom mating and sexual antagonism in the context of polygenic phenotypes could be a particularly fruitful avenue of future research. It would also be interesting to examine how demographic processes arising from resource limitation and competition may intersect with sexual antagonism to promote phenotypic divergence between males and females, and the role of the sex chromosomes in this divergence. Theoretical analyses of the speciation process have found that disruptive selection from resource competition can drive the divergent evolution of niche specification between males and females within a species (Bolnick & Doebeli, 2003; De Lisle, 2019; Slatkin, 1984). Given the prevalence across taxa of sexually dimorphic niche partitioning, it may be useful to consider how the dynamics of sexually antagonistic selection that we have outlined here can interact with ecological or demographic constraints to promote sexual dimorphism, particularly in light of new experimental evidence for this phenomenon (De Lisle, 2023).

We have assumed that the underlying mutational distribution of male and female effects stays constant throughout the adaptive process and that this mutational distribution is identical across the sex chromosomes and autosomes. In our model, this mutational distribution represents the extent of the shared underlying genetic architecture of the phenotype, and thus the constraint on the ability of the phenotype to evolve toward separate male and female optima (Lande, 1980; Walsh & Blows, 2009). The stronger the correlation between male and female effect sizes, the stronger the intragenomic conflict generated by divergence of male and female fitness optima. While we have treated this correlation as a constant parameter, the underlying mutational distribution of effect sizes may itself evolve over time. We predict that, given continual random shifts in the male and female optima as we have simulated above, selection would act to reduce the mutational correlation in male and female effect sizes, allowing the population to adapt more efficiently in any direction. In contrast, if the optimum tends to shift systematically in a correlated or anticorrelated direction, that is, nonrandomly, an increase or decrease in the underlying mutational correlation would be favored. This is consistent with previous theoretical and empirical results that suggest that the underlying distribution of mutational effects on quantitative phenotypes (the M matrix), which in turn shapes the correlated genetic architecture of those phenotypes (the G matrix), can itself evolve in response to a dynamic adaptive landscape (do Ó & Whitlock, 2023; Svensson & Berger, 2019; Svensson, 2022). While these evolutionary changes to the distribution of effect sizes are likely to occur on slower time scales than adaptation to new male–female fitness optima, they may be relevant for the long-term impact of sexual antagonism and its resulting selective signature across the genome (Arnold et al., 2008; do Ó & Whitlock, 2023; Mank, 2017b; Svensson, 2022).

The effect of dosage compensation on the evolutionary response to sexual antagonism

Dosage compensation clearly plays a critical role in modulating the evolutionary interests of the sex chromosomes to sexual antagonism. With no dosage compensation, the X chromosome is skewed toward female-biased evolution; under a model of dosage compensation where male effect sizes are doubled, many of the dynamics of the X chromosome follow very similar lines to the autosomes. While in a number of genetic model systems (*Drosophila*, mice, *Caenorhabditis elegans*) dosage compensation is relatively complete across the X chromosome, there is increasing evidence that dosage may not be compensated chromosome wide in many taxa, with variation in degree along the sex chromosomes (Gu & Walters, 2017; Mank, 2013) (e.g., bird taxa generally show incomplete dosage compensation). Our results for dosage compensation versus no dosage compensation may therefore be thought of as two ends of a continuum, with taxa in which dosage compensation is not complete expected to show intermediate versions of our results.

We have also assumed a particular relationship between the phenotypic effect of an allele and its response to dosage compensation. In our models of the X chromosome without dosage compensation, we assume the phenotypic effect of an allele on the X chromosome in males is $0.5e_m$, while in the case with dosage compensation, the phenotypic effect of that allele is e_m; that is, we assume a linear relationship between the phenotypic effect of an allele and the overall expression and copy number of the X chromosome. While there is evidence for such a relationship for polygenic phenotypes in humans (Sidorenko et al., 2019), it is a simplification of the complex array of mutations affecting polygenic phenotypes and their relationship to gene expression; there are also categories of alleles (e.g., alleles containing knockout mutations at protein-coding genes) for which this relationship is unlikely to

hold. Future work incorporating more explicit models of gene expression may provide greater insight into precisely how dosage compensation can affect the evolutionary dynamics of sexual antagonism on the sex chromosomes.

Sexual antagonism and sex-specific chromosomes

We have ignored the sex-specific (Y or W) chromosome in our analyses because, in many taxa, it is highly degenerative and gene poor. However, a large Y (or W) chromosome may exist in species in which the sex chromosome system has recently evolved or turned over and could substantially influence a polygenic phenotype under sexually antagonistic selection. Two possible scenarios are of interest here with respect to the dynamics of sexually antagonistic selection. First, in species with recombination along much of the lengths of the X and Y chromosomes, they will behave approximately autosomally in genetic transmission and so their response to sexually antagonistic selection will closely resemble that of the autosomes.

Alternatively, in species where all (or the majority) of the Y does not experience recombination (e.g., in *Drosophila*-like species, in which males are achiasmic or species in which male crossovers are restricted to the extreme terminal regions of the chromosomes (e.g., Berset-Brändli et al., 2008), most alleles on a newly evolved Y chromosome will not be exchanged with X chromosome alleles. Therefore, Y-linked alleles will contribute to a male-specific evolutionary trajectory in which their evolutionary "interests" are distinct from those of the autosomes and the X chromosome.

As these alleles exist only in males, they cannot be said to experience sexually antagonistic selection per se; however, the Y could still play an important role in sexually antagonistic selection across the genome. We would expect Y-linked loci to evolve solely in response to selection in males, and thus rapidly to evolve an additive genetic value that pushes the phenotype toward the male optimum. In our X-autosome simulations, we found that the autosomes contribute more to movement to the male optimum to compensate for the female bias of the X chromosome's response (Figure 3). The presence of a large Y would lessen this pressure on the autosomes to compensate for the X—indeed, the autosomes might even contribute predominantly to movement to the female optimum to compensate for the very strong male bias of the Y.

Conclusions

In conclusion, we have demonstrated that the coevolutionary dynamics between the sex chromosomes and autosomes not only determine the immediate phenotypic response to sexually antagonistic selection but also generate lasting differences in the genetic underpinnings of the trait across these genomic regions. Given the prevalence of species with heterogametic sex determination, these results have clear implications for the dynamics of sexual antagonism and the eventual evolution of sexual dimorphism within populations. The polygenic response of sex chromosomes can also have implications for how transitions in sex-determining mechanisms play out in an explicitly polygenic context, which is particularly of interest given the recent debate on the role of sexual antagonism in the formation and degradation of sex chromosomes (Ironside, 2010; Lenormand & Roze, 2022). The different patterns of polygenic adaptation we have observed across the sex chromosomes and the autosomes may also have implications for crosses between populations, or hybridization events between species, that have experienced different historical selection pressures. If one population has experienced stronger sexually antagonistic selection than the other, hybrids may suffer disproportionately due to mismatched phenotypic contributions from the sex chromosomes. This might provide yet another mechanism—among the many already proposed—for why the sex chromosomes play a particularly important role in hybrid fitness (Charlesworth et al., 1987; Orr, 1997; Payseur et al., 2018; Presgraves, 2008; Veller et al., 2023).

Supplementary material

Supplementary material is available online at *Evolution*.

Data availability

Simulation code is available at https://github.com/Pavitra451/polygenic_outcomes_sexual_antagonism.

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Conflict of interest: The authors declare no conflicts of interest.

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