Haploid Selection, Sex Ratio Bias, and Transitions Between sex-determination systems

Michael F Scott∗[1], Matthew M Osmond∗[2], and Sarah P Otto[2]

∗ These authors contributed equally to this work

[1] Department of Botany, University of British Columbia, #3529 - 6270 University Boulevard, Vancouver, BC, Canada V6T 1Z4

[2] Department of Zoology, University of British Columbia, #4200 - 6270 University Boulevard, Vancouver, BC, Canada V6T 1Z4

email: mfscott@biodiversity.ubc.ca, mmosmond@zoology.ubc.ca

Contributions:

Abstract

Sex-determination systems are remarkably dynamic; many taxa display shifts in the location of sex-determining loci or the evolution of entirely new sex-determining systems. Predominant theories for why we observe such transitions generally conclude that novel sex-determining systems are favoured by selection if they equalise the sex ratio or increase linkage with a sexually-antagonistic locus. We use population genetic models to extend these theories in two ways: (1) We explicitly consider how selection on very tightly sex-linked loci influences the spread of novel sex-determiners. We find that tightly sex-linked genetic variation can favour the spread of new sex-determination systems in which the heterogametic sex changes (XY to ZW or ZW to XY) and the new sex-determining region is less closely linked (or unlinked) to the sex-linked locus under selection; a result that is not found with loose sex-linkage. (2) We also consider selection upon haploid genotypes either during gametic competition (e.g., pollen/sperm competition) or meiosis (i.e., non-Mendelian segregation); selective processes that typically occur in one sex or the other. With haploid selection, we again find that transitions between male and female heterogamety can occur even if the new sex-determining region is less closely linked to the locus under selection. Haploid selection in the heterogametic sex can also cause sex ratio biases, which may increase or decrease with the spread of new sex chromosomes. Thus, transitions between sex-determination systems cannot be simply predicted by selection to equalise the sex-ratio. Overall, our models reveal that transitions between sex-determination systems, particularly transitions where the heterogametic sex changes, can be driven by loci in unexpected genomic locations that experience selection during diploid and/or haploid phases, which might be reflected by the lability with which sex-determination systems evolve.

Introduction

Animals and angiosperms exhibit extremely diverse sex-determination systems (reviewed in Bull 1983, Charlesworth and Mank 2010, Beukeboom and Perrin 2014, Bachtrog et al. 2014). Among species with genetic sex determination of diploid sexes, some taxa have heterogametic males (XY) and homogametic females (XX), including mammals and most dioecious plants (Ming et al. 2011); whereas other taxa have homogametic males (ZZ) and heterogametic females (ZW), including Lepidoptera and birds. Within several taxa, the chromosome that harbours the master sex-determining region changes. For example, transitions of the master sex-determining gene between chromosomes or the evolution of new master sex-determining genes have occurred in Salmonids (Li et al. 2011, Yano et al. 2012), Diptera (Vicoso and Bachtrog 2015), and *Oryzias* (Myosho et al. 2012). In addition, many gonochoric clades with genetic sex determination exhibit transitions between male (XY) and female (ZW) heterogamety, including snakes (Gamble et al. 2017, Current Biology), lizards (Ezaz et al. 2009), eight of 26 teleost fish families (Mank et al. 2006), true fruit flies (Tephritids, Vicoso and Bachtrog 2015), amphibians (Hillis and Green 1990), the angiosperm genus *Silene* (Slancarova et al. 2013), the angiosperm family *Salicaceae* (Pucholt et al. 2015, 2017), and Coleoptera and Hemiptera (Beukeboom and Perrin 2014, plate 2). Indeed, in some cases, both male and female heterogametic sex-determination systems can be found in the same species, as exhibited by some cichlid species (Ser et al. 2010) and *Rana rugosa* (Ogata et al. 2007) (Miura 2007). In addition, multiple transitions have occurred between genetic and environmental sex-determination systems, e.g., in reptiles and fishes (Conover and Heins 1987, Mank et al. 2006, Pokorná and Kratochvíl 2009, Ezaz et al. 2009, Pen et al. 2010, Holleley et al. 2015).

Predominant theories accounting for the spread of new sex-determination systems by selection involve fitness differences between sexes (e.g., sexually antagonistic selection) or sex-ratio selection. van Doorn and Kirkpatrick (2007; 2010) show that new sex-determining loci can be favoured if they arise in closer linkage with a locus that experiences sexual antagonism. Tighter linkage allows a

stronger favourable association to build up between a male-beneficial allele, and a neo-Y chromosome, for example. Such associations can favour a new master sex-determining gene on a new chromosome (van Doorn and Kirkpatrick 2007) and can also favour a transition between male and female heterogamety (e.g., a ZW to XY transition, van Doorn and Kirkpatrick 2010). However, any sexually-antagonistic loci that are more closely linked to the ancestral sex-determination locus will develop similar, favourable associations and hinder the spread of a new sex-determination system.

The sex ratio is directly affected by the sex-determination system, and it has therefore been suggested that sex-ratio selection is a dominant force in the evolution of sex determination (e.g., Bull 1983, p 66-67; Beukeboom and Perrin 2014, Chapter 7). 'Fisherian' sex-ratio selection favours a 1:1 zygotic sex ratio when assuming that males and females are equally costly to produce (Fisher 1930, Charnov 1982). This follows from the fact that, for an autosomal locus, half of the genetic material is inherited from a male and half from a female (West 2009). Thus, if the population sex ratio is biased towards one sex, the average per-individual contribution of genetic material to the next generation from the opposite sex is greater. Therefore, a mutant that increases investment in the rarer sex will spread via the higher per-individual contributions made by that sex. In the case of sex-chromosome evolution, Kozielska et al. (2010) consider systems in which the ancestral sex chromosomes experience meiotic drive (e.g., where driving X or Y chromosomes are inherited disproportionately often), which causes sex ratios to become biased (Hamilton 1967). They find that new, unlinked sex-determining loci (masculinizing or feminizing mutations, i.e., neo-Y or neo-W loci) can then spread, which restore an even sex ratio.

Here we use mathematical models to find the conditions under which new sex-determination systems spread when individuals experience selection at both diploid and haploid stages. Even in animal and plant species that have much larger and more conspicuous diploid phases than haploid phases, many loci experience significant haploid selection through gamete competition and/or meiotic

drive (Mulcahy et al. 1996, Joseph and Kirkpatrick 2004). We use the term 'meiotic drive' to refer to the biased (non-Mendelian) segregation of genotypes during gamete production (from one parent) and the term 'gametic competition' to refer to selection upon haploid genotypes within a gamete/gametophyte pool (potentially from multiple parents); the term 'haploid selection' encompasses both processes. Genetic mapping experiments, which are typically designed to minimize selection in diploids, have revealed segregation distortion in various species, including mice, Drosophila, Rice, Maize, Wheat, Barley, Cotton... In some of these cases, biased segregation has been attributed to meiotic drive and/or gametic selection (Leppala et al. 2013, Didion et al. 2015, 2016 Xu et al 2013 (rice), Fishman...).

Meiotic drive generally occurs either during the production of male or female gametes only (Úbeda and Haig 2005, Lindholm et al. 2016). Because there are typically many more pollen/sperm than required for fertilization, gametic competition is also typically sex specific, occurring primarily among male gametes. Gametic competition may be particularly common in plants, in which 60-70% of all genes are expressed in the male gametophyte and these genes exhibit stronger signatures of selection than random genes (Borg et al. 2009, Arunkumar et al. 2013, Gossmann et al. 2014). In addition, artificial selection pressures applied to male gametophytes are known to cause a response to selection (e.g., Hormaza and Herrero 1996, Ravikumar et al. 2003, Hedhly et al. 2004, Clarke et al. 2004). A smaller proportion of genes are thought to be expressed and selected during competition in animal sperm, although precise estimates are uncertain (Zheng et al. 2001, Joseph and Kirkpatrick 2004, Vibranovski et al. 2010). Recent studies have demonstrated that sperm competition can alter haploid allele frequencies and increase offspring fitness (Immler et al. 2014) (Alavioon et al. 2017).

There are various ways in which a period of haploid selection could influence transitions between sex-determination systems. If we assume that haploid selection at any particular locus predominantly occurs in one sex (e.g., meiotic drive during spermatogenesis), then such loci experience a form of sex-specific selection. In this respect, we might expect that haploid selection would affect transitions

between sex-determination systems in a similar manner to sex-specific diploid selection (as explored by van Doorn and Kirkpatrick 2007; 2010). That is, new masculinizing mutations (neo-Y chromosomes) could be favoured via associations with alleles that are beneficial in the male haploid stage. On the other hand, sex ratios can also become biased by linkage between the sex-determining region and a locus that harbours genetic variation in haploid fitness. For example, there are several known cases of sex-ratio bias caused by sex-linked meiotic drive alleles (Burt and Trivers 2006, Chapter 3) or selection among X- and Y-bearing pollen (Lloyd 1974, Conn and Blum 1981, Stehlik and Barrett 2005; 2006, Field et al. 2012; 2013). It is not immediately clear how the spread of new sex-determination systems would be influenced by the combination of sex-ratio biases and associations between haploid selected loci and sex-determining regions.

We find that sex-ratio biases caused by haploid selection can exert Fisherian sex-ratio selection upon novel sex-determiners but that their spread is also determined by selection on genetically-associated alleles. Consequently, it is possible for selection on linked alleles to drive turnover between sex-determining systems despite causing transitory or even permanent increases in sex-ratio bias. Another significant feature of our model is that we consider selection loci that are under selection and also in very tight linkage with the ancestral sex-determining region. Even in the absence of haploid selection, we show that transitions between male and female heterogamety can then evolve despite the fact that the neo-sex-determining locus is less closely linked to a locus under selection and therefore disrupts favourable ancestral associations between sex and the alleles selected in that sex.

Model

Change all $\alpha^{♀}$ to $(1 + \alpha^{♀}_{\Delta})$.

switch between χ and ρ in all places because χ is used for double recombination events.

Change ζ to represent zygotic sex ratio of males, consistent with q and figures.

We consider transitions between ancestral and novel sex-determining systems using a three-locus model, each locus having two alleles. Locus **X** is the ancestral sex-determining region, with alleles X and Y (or Z and W). Locus **A** is a locus under selection, with alleles A and a. Locus **M** is a novel sex-determining region, at which the null allele (M) is initially fixed in the population such that sex of zygotes is determined by the genotype at the ancestral sex-determining region, **X**; XX genotypes become females and XY become males (or ZW become females and ZZ become males). To evaluate the evolution of new sex-determination systems, we consider the invasion, fixation, maintenance, and/or loss of novel sex-determining alleles (m) at the **M** locus. We assume that the **M** locus is epistatically dominant over the **X** locus such that zygotes with at least one m allele develop as females with probability k and as males with probability $1 - k$, regardless of the **X** locus genotype. With $k = 0$, the m allele is a masculinizer (i.e., a neo-Y) and with $k = 1$ the m allele is a feminizer (i.e., a neo-W). With intermediate k, we can interpret m as an environmental sex determination (ESD) allele, such that zygotes develop as females in a proportion (k) of the environments they experience.

In each generation, we census the genotype frequencies in male and female gametes/gametophytes (hereafter gametes) before gametic competition. A full description of our model, including recursion equations, is given in the Appendix. First, competition occurs among male gametes (sperm/pollen competition) and among female gametes (egg/ovule competition) separately. Selection during gametic competition depends on the **A** locus genotype, relative fitnesses are given by $w_A^{♀}$ and $w_a^{♀}$ ($♀ \in \{♀, ♂\}$; see table 1). We assume that all gametes compete for fertilization during gametic competition, which assumes a polygamous mating system. Gametic competition in monogamous mating systems is, however, equivalent to meiotic drive in our model (described below), as both only alter the frequency of gametes produced by heterozygotes. After gametic competition, random mating occurs between male and female gametes. The resulting zygotes develop as males or females, depending on their genotypes at the **X** and **M** loci. Diploid males and

females then experience selection, with relative fitnesses $w^{\mathfrak{F}}_{AA}$, $w^{\mathfrak{F}}_{Aa}$, and $w^{\mathfrak{F}}_{aa}$. The next generation of gametes is produced by meiosis, during which recombination and sex-specific meiotic drive can occur. Recombination (i.e., an odd number of cross-overs) occurs between loci **X** and **A** with probability r, between loci **A** and **M** with probability R, and between loci **X** and **M** with probability χ. Any linear order of the loci can be modelled with appropriate choices of r, R, and χ (see Table S.1). Individuals that are heterozygous at the **A** locus may experience meiotic drive; a gamete produced by Aa heterozgotes of sex $\mathfrak{F}$ bear allele A with probability $\alpha^{\mathfrak{F}}$. Thus, the **A** locus can experience sex-specific gametic competition, diploid selection, and/or meiotic drive.

Table 1: Relative fitness of different genotypes in sex $\mathfrak{F} \in \{\mathfrak{P}, \mathfrak{O}\}$

Genotype	Relative fitness during gametic competition
A	$w^{\mathfrak{F}}_{A} = 1 + t^{\mathfrak{F}}$
a	$w^{\mathfrak{F}}_{a} = 1$
Genotype	**Relative fitness during diploid selection**
AA	$w^{\mathfrak{F}}_{AA} = 1 + s^{\mathfrak{F}}$
Aa	$w^{\mathfrak{F}}_{Aa} = 1 + h^{\mathfrak{F}} s^{\mathfrak{F}}$
aa	$w^{\mathfrak{F}}_{aa} = 1$
Genotype	**Transmission during meiosis in Aa heterozygotes**
A	$\alpha^{\mathfrak{F}} = 1/2 + \alpha^{\mathfrak{F}}_{\Delta}/2$
a	$1 - \alpha^{\mathfrak{F}} = 1/2 - \alpha^{\mathfrak{F}}_{\Delta}/2$

Results

The model outlined above describes both ancestrally-XY and ancestrally-ZW sex-determination systems if we relabel the two sexes as being ancestrally 'heterogametic' or ancestrally 'homogametic'. Without loss of generality, we primarily refer to the ancestrally heterogametic sex as male and the ancestrally homoga-

metic sex as female. That is, we describe an ancestral XY sex-determination system but our model is equally applicable to an ancestral ZW sex-determination system (relabelling the ancestrally-heterogametic sex as female and the ancestrally-homogametic sex as male).

Generic invasion by a neo-Y or neo-W

The evolution of a new sex-determination system requires that a rare mutant allele at the novel sex-determining locus, m, increases in frequency when rare. The spread of a rare mutant m at the **M** locus is determined by the leading eigenvalue, λ, of the system of eight equations describing the frequency of eggs and sperm carrying the m allele in the next generation (equations S.1). This system simplifies substantially in a number of cases of interest. Dominant neo-Y (when $k = 0$) or neo-W alleles (when $k = 1$) are only found in male diploids (neo-Y) or female diploids (neo-W) such that their growth rate ultimately depends only on the change in frequency of m-bearing gametes produced by males or by females, respectively. Furthermore, if the m allele is fully epistatically dominant over the ancestral sex-determining system, phenotypes are not affected by the genotype at the ancestral sex-determining region (**X** locus). Thus, the invasion of rare dominant neo-Y or neo-W alleles is determined by the largest eigenvalue that solves a quadratic characteristic polynomial, Mention the possibility that the other roots yield the leading eigenvalue somewhere. $\lambda^2 + b\lambda + c = 0$. Here, $b = -(\lambda_{mA} + \lambda_{ma}) + (\rho_{mA} + \rho_{ma})$ and $c = (\lambda_{mA} - \rho_{mA})(\lambda_{ma} - \rho_{ma}) - \rho_{mA}\rho_{ma}$, where λ_{mi} is the multiplicative growth rate of mutant haplotypes on background $i \in \{A, a\}$, without accounting for loss due to recombination, and ρ_{mi} is the rate at which mutant haplotypes on background $i \in \{A, a\}$ recombine onto the other **A** locus background in heterozygotes (see Table 2). The λ_{mi} and ρ_{mi}, and thus the spread of the mutant m allele, depend on the frequency of alleles at the **A** and **X** loci in the ancestral population. In the ancestral population, it is convenient to follow the frequency of the A allele among female gametes (eggs), $p_X^{\female}$, and among X-bearing, $p_X^{\male}$, and among Y-bearing, $p_Y^{\male}$, male gametes (sperm/pollen). We also track the fraction of male gametes that are

Y-bearing, q, which may deviate from $1/2$ due to meiotic drive in males.

Table 2: Parameters determining invasion of mutant neo-Y and neo-W alleles into an ancestrally XY system

neo-Y ($k = 0$)
$\lambda_{mA} = \{2(1-\zeta)\}^{-1}\left[p_X^{\varphi} w_A^{\varphi} w_A^{\sigma} w_{AA}^{\sigma} + 2(1-p_X^{\varphi}) w_a^{\varphi} w_A^{\sigma} w_{Aa}^{\sigma} \alpha^{\sigma}\right] / \left(\bar{w}_H^{\varphi} \bar{w}_H^{\sigma} \bar{w}^{\sigma}\right)$
$\lambda_{ma} = \{2(1-\zeta)\}^{-1}\left[(1-p_X^{\varphi}) w_a^{\varphi} w_a^{\sigma} w_{aa}^{\sigma} + 2p_X^{\varphi} w_A^{\varphi} w_a^{\sigma} w_{Aa}^{\sigma} (1-\alpha^{\sigma})\right] / \left(\bar{w}_H^{\varphi} \bar{w}_H^{\sigma} \bar{w}^{\sigma}\right)$
$\rho_{mA} = R\,\{2(1-\zeta)\}^{-1}\left[2(1-p_X^{\varphi}) w_a^{\varphi} w_A^{\sigma} w_{Aa}^{\sigma} \alpha^{\sigma}\right] / \left(\bar{w}_H^{\varphi} \bar{w}_H^{\sigma} \bar{w}^{\sigma}\right)$
$\rho_{ma} = R\,\{2(1-\zeta)\}^{-1}\left[2p_X^{\varphi} w_A^{\varphi} w_a^{\sigma} w_{Aa}^{\sigma} (1-\alpha^{\sigma})\right] / \left(\bar{w}_H^{\varphi} \bar{w}_H^{\sigma} \bar{w}^{\sigma}\right)$
neo-W ($k = 1$)
$\lambda_{mA} = (2\zeta)^{-1}\left[\bar{p}^{\sigma} w_A^{\sigma} w_A^{\varphi} w_{AA}^{\varphi} + 2(1-\bar{p}^{\sigma}) w_a^{\sigma} w_A^{\varphi} w_{Aa}^{\varphi} \alpha^{\varphi}\right] / \left(\bar{w}_H^{\varphi} \bar{w}_H^{\sigma} \bar{w}^{\varphi}\right)$
$\lambda_{ma} = (2\zeta)^{-1}\left[(1-\bar{p}^{\sigma}) w_a^{\sigma} w_a^{\varphi} w_{aa}^{\varphi} + 2\bar{p}^{\sigma} w_A^{\sigma} w_a^{\varphi} w_{Aa}^{\varphi} (1-\alpha^{\varphi})\right] / \left(\bar{w}_H^{\varphi} \bar{w}_H^{\sigma} \bar{w}^{\varphi}\right)$
$\rho_{mA} = R\,(2\zeta)^{-1}\left[2(1-\bar{p}^{\sigma}) w_a^{\sigma} w_A^{\varphi} w_{Aa}^{\varphi} \alpha^{\varphi}\right] / \left(\bar{w}_H^{\varphi} \bar{w}_H^{\sigma} \bar{w}^{\varphi}\right)$
$\rho_{ma} = R\,(2\zeta)^{-1}\left[2\bar{p}^{\sigma} w_A^{\sigma} w_a^{\varphi} w_{Aa}^{\varphi} (1-\alpha^{\varphi})\right] / \left(\bar{w}_H^{\varphi} \bar{w}_H^{\sigma} \bar{w}^{\varphi}\right)$

$\bar{p}^{\sigma} = (1-q)p_X^{\sigma} + q p_Y^{\sigma}$ is the average frequency of the A allele among X- and Y-bearing male gametes.
ζ is the zygotic sex ratio (fraction female)
$\bar{w}^{\varphi}$ is the mean fitness of diploids of sex φ, see Table S.2
$\bar{w}_H^{\varphi}$ is the mean fitness of haploids from sex φ, see Table S.2

We are particularly concerned with the conditions under which a rare neo-sex-determining allele increases in frequency, which occurs when the largest eigenvalue, λ, is greater than one. If the average change in frequency of the two haplotypes that carry the m allele (Am and am) is positive, invasion will always occur, i.e., if $(\lambda_{mA} + \lambda_{ma})/2 > 1$ then $\lambda > 1$. If neither haplotype increases in frequency ($\lambda_{mA}, \lambda_{ma} < 1$), the m allele will not invade. Otherwise, the new sex-determining allele increases in frequency on one **A** background and declines on the other, and invasion requires

$$\rho_{ma}\left(\lambda_{mA} - 1\right) + \rho_{mA}\left(\lambda_{ma} - 1\right) > 0. \tag{1}$$

For example, if we assume that only the mA haplotype has a positive growth rate

($\lambda_{ma} < 1 < \lambda_{mA}$), the second term on the left-hand side of (1) is negative and invasion requires that the growth rate of mA haplotypes and the rate at which they are produced by recombination is sufficiently large relative to that of ma haplotypes. In other words, invasion requires that the average growth rate of the two haplotypes, weighted by the rates they are created by recombination, is positive.

Table 2 illustrates a number of key points about the invasion of neo-Y and neo-W mutations. First, Fisherian sex-ratio selection will favour the spread of a neo-Y if the ancestral zygotic sex ratio is biased towards females, $\zeta > 1/2$ (i.e., $\zeta > 1/2$ causes the first factor of the λ_{mi} to be greater than one for a neo-Y and vice versa for a neo-W). However, the spread of a neo-Y (neo-W) also depends on the male (female) fitness of associated alleles (terms in square brackets). Second, invasion by a neo-Y (neo-W) allele does not directly depend on the fitness of female (male) diploids (for a given set of equilibrium allele frequencies). This is because a dominant neo-Y (neo-W) is always found in males (females), and therefore the frequency of the neo-Y (neo-W) allele, m, only changes in males (females). Finally, invasions by a neo-Y and a neo-W are qualitatively different. This is because a gamete with the ancestral- or neo-Y always pairs with a female gamete containing an X, and both develop into males. By contrast, a gamete with a neo-W can pair with an X or Y male gamete, developing into a female, while female gametes without the neo-W can become female (when paired with X) or male (when paired with Y). Consequently, the types of females produced differ in the frequency of A alleles they obtain from mating.

In order to explicitly determine the conditions under which a rare neo-sex-determining allele spreads, we must calculate the equilibrium frequency of the A allele in the ancestral population (i.e., $\hat{p}_X^{\female}$, $\hat{p}_X^{\male}$, and $\hat{p}_Y^{\male}$). Since only the **A** locus experiences selection directly, any deterministic evolution requires that there is a polymorphism at the **A** locus. Polymorphisms can be maintained by mutation-selection balance or transiently present during the spread of beneficial alleles. However, polymorphisms maintained by selection can maintain alleles at higher allele frequencies for longer periods. Here, we focus of polymorphisms maintained by se-

lection, where the A allele reaches a stable intermediate equilibrium frequency under the ancestral sex-determination system before the neo-sex-determining allele (m) arises. We can analytically calculate the allele frequency of the A allele using two alternative simplifying assumptions: (1) the **A** locus is within (or tightly linked to) the non-recombining region around the ancestral SDR ($r \approx 0$) or (2) selection is weak relative to recombination ($s^{\male}$, $t^{\male}$, $\alpha_{\Delta}^{\male}$ of order $\epsilon << 1$).

Change to $\hat{p}$ throughout as we assume that allele frequencies change slowly such that lambda is unaffected

Tight linkage with the ancestral sex-determining region

The ancestral equilibrium allele frequencies and their stability conditions are given in the appendix. When there is complete linkage between the ancestral sex-determining region and the **A** locus ($r = 0$), either the A allele or the a allele must be fixed on the Y. Because the labelling of alleles is arbitrary, we will assume that the a locus is fixed on the Y ($p_Y^{\male} = 0$), without loss of generality. If there are two alleles maintained at the **A** locus, the X can either be fixed for the A allele ($\hat{p}_X^{\female} = \hat{p}_X^{\male} = 1$) or polymorphic ($0<\hat{p}_X^{\female}, \hat{p}_X^{\male}<1$).

A neo-Y will never invade an ancestral XY system that already has tight linkage with the locus under selection ($r = 0$, for details see supplementary *Mathematica* file). A neo-Y haplotype with the same allele as the ancestral Y is neutral ($\lambda_{ma} = 1$) and does not change in frequency. The other neo-Y haplotype will not spread ($\lambda_{mA} < 1$) given that the initial equilibrium is stable. Therefore, a neo-Y mutation cannot spread ($\lambda \leq 1$) in an ancestral XY system that is at equilibrium with all selected loci within the non-recombining region around the SDR. In essence, through tight linkage with the **A** locus, the ancestral Y becomes strongly specialized on the allele that has the highest fitness across male haploid and diploid phases. Given that the ancestral Y is at this equilibrium, it is not possible for a neo-Y to create males that have higher fitness than the ancestral Y.

Neo-W alleles, on the other hand, can invade an ancestral XY system under some conditions (the full invasion conditions are given in the appendix; equations

S.6 and S.7). That is, selection on loci within the non-recombining region of the SDR can favour the invasion of a less closely linked neo-W, see Figure 1. This result is unexpected given the results of van Doorn and Kirkpatrick (2010), who did not explicitly calculate equilibrium allele frequencies under tight linkage and generally concluded that heterogametic transitions occur when neo-sex-determining alleles are in tighter linkage with loci under sex-specific diploid selection. To develop an understanding (intuition) for how this happens, we focus on cases where there is no haploid selection and discuss the effects of haploid selection in the appendix.

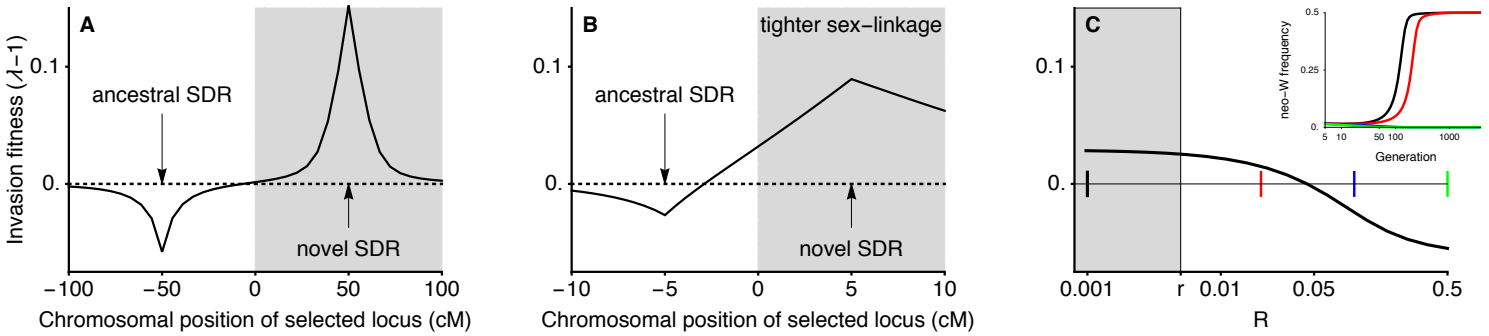

Figure 1: Transitions between XY and ZW systems can occur even when the neo-SDR is more loosely linked to a locus under sexually-antagonistic selection (here, without haploid selection $t^{\male} = \alpha_{\Delta}^{\male} = 0$). In panel A, linkage is loose enough relative to selection that the weak selection analytical results hold, and a neo-W can only invade when it is more tightly linked with the selected locus ($R < r$; shaded region). In panel B, linkage is tight enough relative to selection that the weak selection analytical results do not hold, and a neo-W can only invade even when it is less tightly linked with the selected locus ($r < R$; unshaded region). In panel C we vary the recombination rate between the neo-W and the selected locus (R) for a fixed recombination rate between the ancestral-SDR and the selected locus ($r = 0.005$). Coloured markers show recombination rates for which the temporal dynamics of invasion are plotted in the inset, demonstrating that neo-W alleles can fix (reach frequency 0.5 among female gametes) if they are more (black) or less (red) closely linked to a locus experiencing sexually-antagonistic selection. A very loosely linked neo-W does not spread in this case (blue and green lines overlap and go to 0). Indeed, we show that neo-W invasion fitness is negative when $R = 1/2$ and $s^{\female}s^{\male} < 0, 0 < h^{\female} < 1$) in the supplementary *Mathematica* file. Fitness parameters are shown by an asterisk in Figure 2: $w_{AA}^{\female} = 1.05$, $w_{aa}^{\male} = 1.2$, $w_{aa}^{\female} = w_{AA}^{\male} = 0.85$, $w_{Aa}^{\female} = 1$. consider removing panel A, which is repeated in Figure 3.

If we categorise the a allele as being ancestrally 'male-beneficial' via the fact that it is fixed on the Y, then $\lambda_{mA} > 1$ indicates that the neo-W spreads when found with the ancestrally 'female-beneficial' allele. Broadly, this is possible because

the ancestral X chromosome is not able to perfectly specialise on the 'female-beneficial' allele due to the fact that X's are sometimes found in males. For example, when the a allele is favoured in males, a polymorphism of A and a alleles can be maintained on the X despite directional selection in favour of the A allele in females ($s^{\varphi} > 0$, $0 < h^{\varphi} < 1$). Indeed, Figure 2A indicates that λ_{mA} tends to be larger than one with sexually-antagonistic selection where the a allele is strongly favoured in males (w_{aa} much larger than w_{Aa}). In this case, W-A haplotypes will only create females with high fitness (AA or Aa genotypes) and therefore have higher fitness than ancestral females, which sometimes also produce aa females. When only one neo-W haplotype can has a positive growth rate (see Figure 2), a neo-W can invade as long as equation (1) is satisfied, which may require that the recombination rate, R, is small enough. Nevertheless, because we assume here that r is small, these results indicate that a more loosely linked sex-determining region can spread. Therefore, tightly sex-linked loci that experience sexually-antagonistic selection can drive heterogametic transitions in which the neo-SDR is less closely linked to the locus under selection (Figure 1).

Given that the a allele can be considered ancestrally 'male-beneficial' because it is fixed on the Y, it is surprising that neo-W-a haplotypes can sometimes be favoured by selection in females ($\lambda_{ma} > 1$). Again, this occurs because ancestral X's also experience selection in males, in which they will always be paired with a Y-a. Hence, if there is overdominance in males, X-A Y-a males have high fitness and the A allele is favoured by selection on the X in males. Therefore, the X can be polymorphic or even fixed for the A allele despite favouring the a allele during selection in females (e.g., see outlined region in Figure 2B and Lloyd and Webb 1977, Otto 2014). In such cases, neo-W-a haplotypes can spread because they create more Aa and aa females when pairing with an X from males and because they bring Y-a haplotypes into females, in which case females are always aa. As discussed in the appendix, this scenario where neo-W's associated with a are favoured can also occur with haploid selection, even without overdominance (e.g., when a is female-beneficial and favoured by haploid selection in male gametes).

Both W-A and W-a haplotypes can spread, as is the case when AA individuals have low fitness in females yet the A is polymorphic or fixed on the X due to overdominance in males (Figure 2B and 2C). Both neo-W-A and neo-W-a haplotypes then produce fewer unfit AA females. This is true for the neo-W-A haplotype because it can pair with a $Y-a$ haplotype and still be female. Wherever both haplotypes have positive growth rates, invasion by a neo-W is expected regardless of its linkage with the selected locus (i.e., even unlinked neo-W alleles can invade, see Figures S.1 and S.2 for examples).

What can we discuss about haploid selection here. Perhaps the fact that overdominance is not required for $\lambda_{Ma} > 1$ when there is haploid selection? We also don't yet discuss the fact that polymorphic equilibria (mixed systems) can be stable.

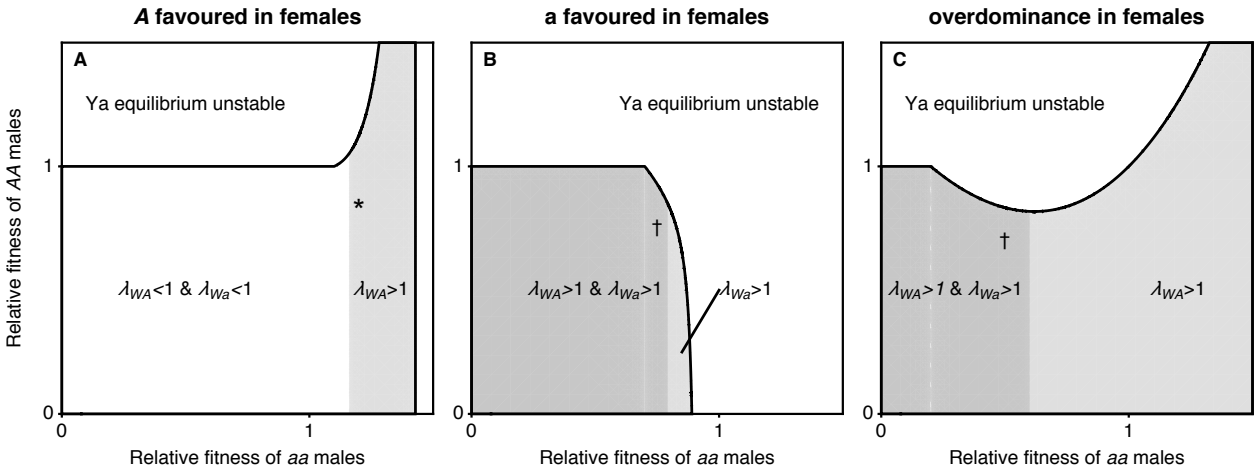

Figure 2: When the ancestral-XY locus is tightly linked to a locus under selection ($r = 0$), one or both neo-W haplotypes can spread. We vary the fitness of male homozygotes relative to heterozygotes ($w^{\male}_{Aa} = 1$) and only consider stable equilibria at which both **A** locus alleles are maintained and the a allele is initially fixed on the Y, region outlined. Here, selection in females can favour the A allele (panel A, $w^{\female}_{aa} = 0.85$, $w^{\female}_{AA} = 1.05$), favour the a allele (panel B, $w^{\female}_{aa} = 1.05$, $w^{\female}_{AA} = 0.85$), or be overdominant (panel C, $w^{\female}_{aa} = w^{\female}_{AA} = 0.6$). If λ_{wA} or λ_{wa} is greater than one, then a rare neo-W can spread for, at least, some values of $R > r$. For the parameter values marked with an asterisk, example invasion dynamics are shown in Figure 1C. Where both λ_{wA} and λ_{wa} are greater than one, a neo-W will spread when rare, regardless of linkage with the selected locus (for any R). Figure S.1 shows two examples using the parameters marked with a dagger. Here, there is no haploid selection $t^{\male} = \alpha^{\male}_{\Delta} = 0$.

Loose linkage with the ancestral sex-determining region

Assuming that selection is weak relative to all recombination rates (r, R and χ), we denote the leading eigenvalues describing the invasion of a neo-Y ($k = 0$) and a neo-W ($k = 1$) into an ancestrally XY system by $\lambda_{Y',XY}$ and $\lambda_{W',XY}$, respectively. To leading order in selection, these are:

$$\lambda_{Y',XY} = 1 + V_A S_A^2 \frac{(r - R)}{rR} + O\left(\epsilon^3\right) \tag{2}$$

and

$$\lambda_{W',XY} = \lambda_{Y',XY} + \left(2\alpha_\Delta^{\male} - 2\alpha_\Delta^{\female} + t^{\male} - t^{\female}\right)\left(\hat{p}_Y^{\male} - \hat{p}_X^{\male}\right)/2 + O\left(\epsilon^3\right) \tag{3}$$

where $V_A = \bar{p}(1 - \bar{p})$ is the variance in the frequency of A and $S_A = (D^{\male} + \alpha_\Delta^{\male} + t^{\male}) - (D^{\female} + \alpha_\Delta^{\female} + t^{\female})$ describes sex differences in selection for the A versus a across diploid selection, meiosis, and gametic competition. The diploid selection term, $D^{\mathfrak{g}} = \left(\bar{p}s^{\mathfrak{g}} + (1-\bar{p})h^{\mathfrak{g}}s^{\mathfrak{g}}\right) - \left(\bar{p}h^{\mathfrak{g}}s^{\mathfrak{g}} + (1-\bar{p})\right)$, is the difference in fitness between A and a alleles in diploids of sex $\mathfrak{g} \in \{\female, \male\}$, where $\bar{p}$ is the leading-order probability of mating with an A-bearing gamete from the opposite sex (see Appendix).

The neo-sex-determining allele, m, will spread if $\lambda_{m,XY} > 1$. Equation (2) demonstrates that under weak selection a neo-Y will invade an XY system if and only if it is more closely linked to the selected locus than the ancestral sex-determining region (i.e., if $R < r$; note that $V_A S_A^2$ is strictly positive as long as $\mathbf{A}$ is polymorphic). This echoes our tight linkage results above where a neo-Y could never invade if $r \approx 0$ and is consistent with the results of van Doorn and Kirkpatrick (2007), who considered diploid selection only and also found that homogametic transitions (XY to XY or ZW to ZW) can only occur when the neo-sex-determining locus is more closely linked to a locus under sexually-antagonistic selection.

With weak selection and no haploid selection ($t^{\mathfrak{g}} = \alpha_\Delta^{\mathfrak{g}} = 0$), the spread of a neo-W is equivalent to the spread of a neo-Y ($\lambda_{W',XY} = \lambda_{Y',XY}$), such that heterogametic transitions (XY to ZW or ZW to XY) can also occur only if the neo-

sex-determining region is more closely linked to a locus under selection ($R < r$), as found by van Doorn and Kirkpatrick (2010). With haploid selection, however, the additional term in equation (3) can be positive, which can allow, for example, neo-W invasion ($\lambda_{W',XY} > 1$) even when the neo-sex-determining region is less closely linked to the selected locus ($R > r$).

Equation (3) shows that, with weak selection, neo-W alleles can invade an XY system for a large number of selective regimes. To clarify the parameter space under which $\lambda_{W',XY} > 1$, we consider several special cases. Firstly, if the **A** locus is unlinked to the ancestral sex-determining region ($r = 1/2$), a more closely linked neo-W ($R < 1/2$) can always invade because there is then no association between A alleles and sex chromosomes in males, $\left(\hat{p}_Y^{\male} - \hat{p}_X^{\male}\right) = 0$, see equation (S.5). The second term in equation (3) then disappears and invasion depends only on the sign of $(r-R)$. Indeed, invasion typically occurs when the neo-W is more closely linked to the selected locus than the ancestral sex-determining region, under a variety of selective regimes (Figure 3). Secondly, we can simplify the discussion of cases where invasion occurs despite looser sex-linkage, $R > r$, by focussing on the special case where $R = 1/2$ and $r < 1/2$ (e.g., the selected locus is on the ancestral sex chromosome and the novel sex-determining locus arises on an autosome). In table 3 we give the conditions where invasion occurs when we further assume that haploid selection only occurs in one sex (e.g., during male meiosis only) and dominance coefficients are equal in the two sexes, $h^{\female} = h^{\male}$. When there is no gametic competition and meiotic drive is in one sex only, an unlinked neo-W can invade as long as the same allele is favoured during diploid selection in males and females ($s^{\female}s^{\male} > 0$, see Figure 3B and Figure 4B). When there is no meiotic drive and gametic competition occurs in one sex only, an unlinked neo-W can invade as long as the same allele is favoured in male and female diploid selection and there are sex differences in selection of one type (e.g., $s^{\female}(s^{\male} - s^{\female}) > 0$, see Figure 3C). These special cases indicate that neo-W invasion can occur for a relatively large fraction of the parameter space, even if the neo-W uncouples the sex-determining locus from a locus under selection.

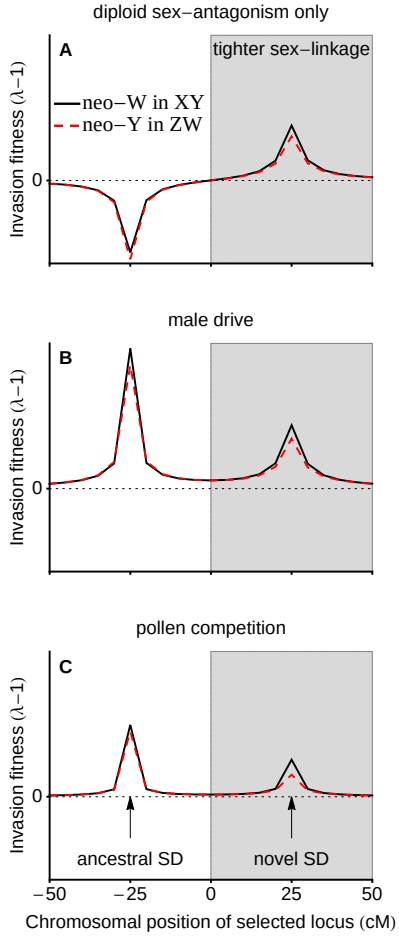

Figure 3: A neo-W can invade an XY system under a large number of selective regimes. In panel A, there is no haploid selection ($t^{\male} = \alpha_{\Delta}^{\male} = 0$) and selection in diploids is sexually antagonistic ($s^{\male} = -s^{\female} = 1/10$, $h^{\male} = 1 - h^{\female} = 3/10$), in which case the neo-sex-determining allele can only invade if it is more closely linked to the selected locus ($R < r$, gray region; but see Figure 1B for the case of very tight linkage). In panel B, male drive ($\alpha_{\Delta}^{\male} = -1/20$, $t^{\male} = \alpha_{\Delta}^{\female} = 0$) opposes selection in diploids (no sex-differences: $s^{\male} = 1/10$, $h^{\male} = 7/10$), in which case the neo-sex-determining allele can invade regardless of linkage. In panel C, gametic competition in males ($t^{\male} = -1/10$, $t^{\female} = \alpha_{\Delta}^{\male} = 0$) opposes selection in diploids (sex-differences: $s^{\male} = 1/20$, $s^{\female} = 3/20$, $h^{\male} = 7/10$), in which case the neo-sex-determining allele can once again invade regardless of linkage. We use Haldane's map function (Equation 3 in Haldane 1919) to convert from map distance (centiMorgans, cM) to the probability of recombination (an odd number of cross-over events). Check the mismatch between red and black lines here: probably because of adding or subtracting from 1.

Previous research suggests that when the ancestral sex-determining locus is linked to a locus that experiences haploid selection (e.g., meiotic drive), a new, unlinked sex-determining locus invades in order to restore equal sex ratios (Koziel-

Table 3: Invasion conditions for unlinked neo-W ($R = 1/2$, $r < 1/2$) into ancestral XY with one form of haploid selection

Scenario	Assumptions	neo-W spreads ($\lambda_{W',XY} > 1$) if
male drive only	$h^{\male} = h^{\female}$, $t^{\female} = t^{\male} = \alpha_{\Delta}^{\female} = 0$	$s^{\female}s^{\male} > 0$
female drive only	$h^{\male} = h^{\female}$, $t^{\female} = t^{\male} = \alpha_{\Delta}^{\male} = 0$	$s^{\female}s^{\male} > 0$
sperm competition only	$h^{\male} = h^{\female}$, $t^{\female} = \alpha_{\Delta}^{\female} = \alpha_{\Delta}^{\male} = 0$	$s^{\female}(s^{\male} - s^{\female}) > 0$
egg competition only	$h^{\male} = h^{\female}$, $t^{\male} = \alpha_{\Delta}^{\female} = \alpha_{\Delta}^{\male} = 0$	$s^{\male}(s^{\female} - s^{\male}) > 0$

ska et al. 2010). Consider, for example, the case where the **A** locus is linked to the ancestral-SDR ($r < 1/2$) and experiences meiotic drive in males only (e.g., during spermatogenesis but not during oogenesis, $\alpha_{\Delta}^{\male} \neq 0$, $\alpha_{\Delta}^{\female} = 0$), without gametic competition ($t^{\female} = t^{\male} = 0$). In this case, the zygotic sex ratio can be initially biased only if the ancestral sex-determining system is XY (Figure 4B). We might therefore expect a difference in the potential for XY to ZW and ZW to XY transitions. However, to leading order with selection weak relative to recombination, we find that sex ratio selection favours the spread of a neo-W (through the first terms in table 2) by an amount that is equal in magnitude to the fitness effects of alleles associated with new sex-determining alleles (second terms in table 2). Thus, invasion by a neo-W into an XY system and invasion by a neo-Y into a ZW system occur under the same conditions ($\lambda_{Y',XY} = \lambda_{W',ZW}$ and $\lambda_{Y',ZW} = \lambda_{W',XY}$, at least to order ϵ^2). For example, in Figure 4B neo-W alleles invade an ancestrally XY system where females are initially rare because the ancestral-Y is associated with a male meiotic drive allele. However, Figure 4A shows that a neo-Y can invade an ancestrally ZW system under the same conditions. In fact, where $R < 1/2$ the neo-Y becomes associated with the male meiotic drive allele such that the zygotic sex ratio evolves to become biased towards males.

The green curves in Figure 4 demonstrate a case where transitions between male and female heterogametey occur even though the new sex-determining region is unlinked to a locus that experiences haploid and diploid selection. We use this example to discuss why heterogametic transitions can occur when $R = 1/2$ and $r < 1/2$, as in Table 3. In Figure 4B, an unlinked neo-W can spread because the zygotic

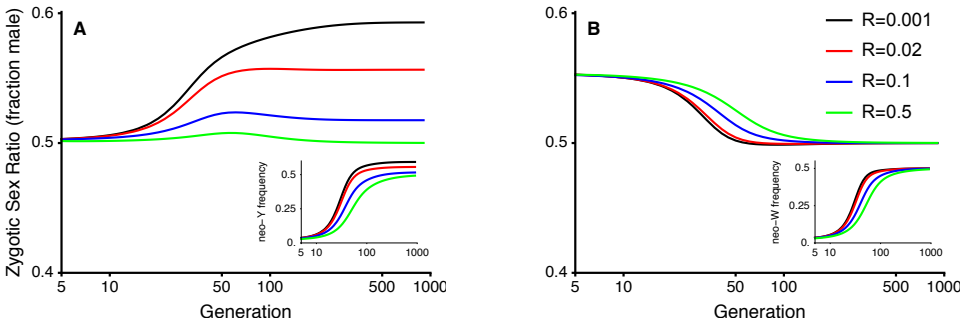

Figure 4: Fisherian sex-ratio selection alone is not a good predictor of turnover between sex-determining systems. In this figure, selection is ploidally antagonistic with haploid selection favouring the a allele during male meiosis ($s^{\varphi} = s^{\sigma} = 0.2$, $h^{\varphi} = h^{\sigma} = 0.7$, $t^{\varphi} = t^{\sigma} = \alpha^{\sigma}_{\Delta} = 0$). In panel A, male drive in an ancestral ZW system has no affect on the zygotic sex ratio, yet a neo-Y can invade and replace the ancestral sex-determination system (inset shows neo-Y frequency among male gametes, the ancestral W also goes to fixation during this transition). When $R < 1/2$, the neo-Y becomes associated with the allele favoured by drive, causing the zygotic sex ratio to become biased, hence the frequency of neo-Y among male gametes can be higher than 0.5 (inset). In panel B, male drive in an ancestral XY system causes a male bias, allowing a neo-W to invade and replace the ancestral sex-determination system (inset shows neo-W frequency among female gametes, the ancestral Y also goes to fixation), which balances the zygotic sex ratio. Parameters: $s^{\varphi} = s^{\sigma} = 0.2$, $h^{\varphi} = h^{\sigma} = 0.7$, $t^{\varphi} = t^{\sigma} = \alpha^{\sigma}_{\Delta} = 0$, $\alpha^{\sigma}_{\Delta} = -0.2$, $r = 0.02$.

sex ratio is ancestrally male biased. However, in Figure 4A, an unlinked neo-Y spreads despite the fact that the ancestral zygotic sex ratio is even. In this case, the the male meiotic drive allele, a, is initially more common among ancestral-Z-bearing eggs than ancestral-W-bearing eggs because the Z is found in males more often than the W and $r < 1/2$ (equation S.5). Polymorphism at the **A** locus is maintained by counter-selection against the a allele in diploids and therefore ancestral-ZZ males have generally low diploid fitness. A freely recombining neo-Y ($R = 1/2$) is not directly favoured or dis-favoured by male meiotic drive because it is equally likely to be segregate with the A or a allele when found in a heterozygote. The neo-Y spreads because it produces males with high diploid fitness through matings with ancestral-W-bearing female gametes, which are more likely to carry the A allele. Thus, a key factor in explaining why heterogametic transitions can occur when $R > r$ is that that the neo-SDR determines sex in the diploid phase but then recombination occurs before any subsequent haploid selection.

Environmental sex determination

We next consider the case where the new sex-determining mutation, m, causes sex to be determined probabilistically or by heterogeneous environmental conditions (environmental sex determination, ESD), with individuals carrying allele m developing as females with probability k. Here, we do not assume that the environmental conditions that determine sex also differentially affect the fitness of males versus females. Such correlations can favour environmental sex-determination systems that allow each sex to be produced in the environment in which it has highest fitness; in the absence of these correlations, previous theory would predict that ESD is favoured when it produces more equal sex ratios than the ancestral system (see reviews by Charnov 1982, Bull 1983, West 2009).

The characteristic polynomial determining the eigenvalues (equations S.1) does not factor for ESD mutants as it does for $k = 0$ or $k = 1$. We therefore focus on weak selection here. Assuming weak selection, the spread of the new sex-determining region is given by

$$\begin{aligned}\lambda_{ESD',XY} =& 1 + (1-2k)^2 V_A {S_A}^2 \frac{r-R}{rR} \\ &+ \frac{k(\hat{p}_Y^{\male} - \hat{p}_X^{\male})}{2}\left(k\left(2\alpha_\Delta^{\male} - 2\alpha_\Delta^{\female} + t^{\male} - t^{\female}\right) - 4(1-k)S_A\right) + O\left(\epsilon^3\right),\end{aligned} \tag{4}$$

which reduces to $\lambda_{Y',XY}$ when $k = 0$ and $\lambda_{W',XY}$ when $k = 1$.

Of particular interest are ESD mutations that cause half of their carriers to develop as females and half as males ($k = 1/2$, creating equal sex ratios), the spread of which is given by

$$\lambda_{ESD',XY} = 1 + \frac{1}{2}\frac{(\lambda_{Y',XY|R=1/2} - 1) + (\lambda_{W',XY|R=1/2} - 1)}{2} + O\left(\epsilon^3\right), \tag{5}$$

where $\lambda_{Y',XY|R=1/2}$ and $\lambda_{W',XY|R=1/2}$ represent $\lambda_{Y',XY}$ and $\lambda_{W',XY}$ when evaluated at $R = 1/2$ (equations 2 and 3). That is, recombination between the selected locus

and the novel sex-determining locus, R, doesn't enter into the $k = 1/2$ results. This is because sex is essentially randomized each generation, preventing associations from building up between allele A and sex. Equation (5) shows that the neo-ESD gets half of the fitness of a feminizing mutation (neo-W) and half of the fitness of a masculinizing mutation (neo-Y), but only has an effect one half of the time (the other half of the time it produces the same sex as the ancestral system would have, to leading order). As discussed above, $\lambda_{Y',XY|R=1/2}$ is necessarily less than one, but $\lambda_{W',XY|R=1/2}$ can be greater than one if there is haploid selection. That is, when there is haploid selection, ESD mutations can invade an ancestrally-XY system because they generate females that are either rare or have high fitness, in the same manner as a neo-W.

Significantly, equation (5) is the same whether ESD is invading an ancestrally XY or ZW system (because $\lambda_{Y',XY} = \lambda_{W',ZW}$ and $\lambda_{W',XY} = \lambda_{Y',ZW}$). Thus, because the sex ratio is only biased by male haploid selection when the ancestral sex-determination system is XY, Fisherian sex-ratio selection alone does not explain the invasion of ESD under weak selection. Specifically, with male haploid selection, the neo-ESD is equally likely to invade when it equalizes the zygotic sex ratio (through $\lambda_{W',XY}$) and when it doesn't (through $\lambda_{Y',ZW}$). In addition, we note that ESD may not invade, even if the sex ratio is initially biased (e.g., with drive in males only, $r < 1/2$, $h^{♀} = h^{♂}$, and $s^{♀}s^{♂} < 0$, such that $\lambda_{W',XY} < 1$, see Table 3).

Discussion

Two predominant theories explaining the remarkably high frequency of transitions between sex-determination systems are sexually-antagonistic selection and sex-ratio selection (reviewed in Blaser et al. 2012) (van Doorn, 2014, sexual development). The former predicts that neo-sex-determining alleles can invade when they arise in closer linkage with a sexually-antagonistic locus (van Doorn and Kirkpatrick 2007; 2010). The latter predicts that new sex-determining systems are generally favoured if they result in more equal sex-ratios than the ancestral sys-

tem. Firstly, we show that selection (including sexually-antagonistic selection) on loci within or near the non-recombining region of the ancestral sex-determining region can favour heterogametic transitions (XY to ZW or ZW to XY) to new sex-determining systems that have looser linkage (e.g., see Figure 1). Secondly, assuming that selection is weak relative to recombination, we show that new sex-determining alleles are typically favoured if they are more closely linked to a locus under haploid selection, which is the only condition favouring homogametic transitions (XY to XY or ZW to ZW). In addition, with haploid selection and weak selection, heterogametic transitions (XY to ZW or ZW to XY) can occur even when the new sex-determining region is less closely linked to the locus under selection (e.g., see Figure 4).

Sex-ratio biases caused by haploid selection can facilitate heterogametic transitions between sex-determining systems. For instance, alleles favoured by haploid selection in males often become associated with the Y, which leads to a male sex-ratio bias. This male bias increases the potential for a neo-W to invade (Table 2), which can equalize the sex-ratio (e.g., see Figure 4B, for related examples see Kozielska et al. 2010, Úbeda et al. 2015). However, sex-ratio selection can be overwhelmed by additional selective effects (e.g., when a linked allele is beneficial for male diploids but detrimental for female diploids; Table 3), preventing the neo-W from invading. Indeed, transitions between sex-determining systems can even lead to stronger sex-ratio biases. For example, where a neo-Y invades and is linked with a locus that experiences haploid selection in male gametes, the sex ratio evolves to become biased (e.g., see Figure 4A and step 1 in Úbeda et al. 2015). Furthermore, with weak selection, we find that there is no difference in conditions allowing XY to ZW and ZW to XY transitions, indicating that sex chromosome transitions are not predominantly predicted by their effect on the sex-ratio (i.e., the sex-ratio bias created by male haploid selection facilitates the spread of a neo-W into an XY system the same way that male haploid selection drives the spread of a neo-Y into a ZW system with a 1:1 sex ratio). Thus, haploid selection can favour heterogametic transitions both via sex-ratio selection and via fitness effects of al-

leles that are associated with the neo-sex-determining allele, and these selection pressures are predicted to often be of roughly equal magnitude (unless linkage is tight).

We show that the spread of new sex determination systems can be driven by loci experiencing haploid selection. Because haploid selection can cause transitions that increase or decrease sex-linkage, haploid selection may lead to less stability, and greater potential for cycling, in sex-determination systems (e.g., the final state of the red line in Figure 4A is the starting state in Figure 4B). In particular, if haploid selection is strong but selective differences between male and female diploids are weak, we find that heterogametic transitions (XY to ZW or vice versa) are favoured more strongly than homogametic transitions (e.g., with $|D^{\male} - D^{\female}| << |\alpha_{\Delta}^{\male} - \alpha_{\Delta}^{\female} + t^{\male} - t^{\female}|$ we have $\lambda_{W',XY} > \lambda_{Y',XY}$; equations 3 and S.5). Turnovers driven by haploid selection may help to explain the relative rarity of heteromorphic sex chromosomes in plants, which are thought to experience more selection during their multicellular haploid stage. For example, among relatively few dioecious clades in which multiple species have well characterized sex chromosomes (Ming et al. 2011), heterogametic transitions have been inferred in *Silene* subsection *Otites* (Slancarova et al. 2013) and in *Salicaceae* (Pucholt et al. 2015, 2017). Furthermore, assuming that transitions from dioecy to hermaphroditism (equal parental investment in male and female gametes) are favoured in a similar manner to the ESD examined here (equal probability of zygotes developing as males or females), our results suggest that competition during the haploid stage could drive transitions between dioecy and hermaphroditism, which are frequent in plants (Käfer et al., 2017, Sabath et al., 2017).

In support of their role in sex chromosome turnover, genes expected to be under sexually-antagonistic selection (e.g., those causing bright male colouration) have been found on recently derived sex chromosomes (Lindholm and Breden 2002, Tripathi et al. 2009, Ser et al. 2010). Our results show that, if loci experiencing overdominance and/or sexually-antagonistic selection can be identified in close linkage with the ancestral sex-determining locus (rather than only

the novel sex-determining locus), then they could also be implicated in driving heterogametic transitions between sex-determination systems. As noted by van Doorn and Kirkpatrick (2010), it would be prudent to compare closely related clades in order to determine whether observed polymorphisms predate a transition in sex-determination or arose afterwards. In addition, we show haploid selection on loci around either the ancestral- or the novel-sex-determining regions could have had a role in driving sex chromosome turnover. A recent transcriptome analysis in *Rumex*, suggests a role for gametic competition in the evolution of sex-determination systems, showing that Y-linked genes are have higher expression in haploid pollen than autosomal genes (check this is accurate). Interestingly, haploid-expression is also more common on the autosome that is orthologous to the sex chromosomes in closely related species suggesting that new sex chromosomes may have been favoured through their association with haploid selected alleles on these chromosomes (Sandler et al., 2017, Personal Communication).

We assume that sex-determining alleles do not experience direct selection except via their associations with sex and selected alleles. However, in some cases, there may be significant degeneration around the sex-limited allele (Y or W) in the ancestral sex-determining region because recessive deleterious mutations and/or deletions accumulate around the Y or W sex-determining regions (Rice 1996, Charlesworth and Charlesworth 2000, Bachtrog 2006, Marais et al. 2008). During heterogametic transitions (XY to ZW or ZW to XY), but not homogametic transitions (XY to XY or ZW to ZW), any recessive deleterious alleles linked to the Y or W are revealed to selection in YY or WW individuals (Bachtrog et al. 2014). This phenomenon was studied by van Doorn and Kirkpatrick (2010), who found that degeneration can prevent fixation of a neo-W or a neo-Y allele, leading to a mixed sex-determination system where the ancestral and new sex-determining loci are both segregating. However, they noted that very rare recombination events around the ancestral sex-determining region can allow these heterogametic transitions to complete. Degeneration around the Y or W could explain why heterogametic transitions are not observed to be much more common than homogametic transitions

despite the fact that our models demonstrate that they are favoured under a wider range of conditions. For example, Vicoso and Bachtrog (2015) found a dozen sex chromosome configurations among Dipteran species but only one transition between male and female heterogametey.

Another simplification that we made is that meiotic drive involves only a single locus with two alleles. However, many meiotic drive systems involve an interaction with another locus at which alleles may 'suppress' the action of meiotic drive (Burt and Trivers 2006, Lindholm et al. 2016) Taylor,1999. Thus, the dynamics of meiotic drive alleles can be heavily dependent on the interaction between two loci and the recombination rate between them, which in turn can be affected by sex-linkage if there is reduced recombination between sex chromosomes (Hurst and Pomiankowski 1991). Furthermore, in some cases, a driving allele may act by killing any gametes that carry a 'target' allele at another locus, in which case there can be fertility effects which can affect the equilibrium frequency of a meiotic drive allele (Holman et al. 2015). In polygamous mating systems, the intensity of pollen/sperm competition can depend on the density of males available to donate pollen/sperm, which can itself depend on the sex ratio (Taylor and Jaenike 2002). In terms of our model, this implies that the strength of gametic competition (t^{σ}) may both determine and be determined by the sex ratio. How the evolution of new sex-determining mechanisms could be influenced by two-locus meiotic drive and/or by ecological feedbacks under different mating systems remains to be studied.

We have shown that tight sex-linkage and haploid selection can drive previously unexpected transitions between sex-determination systems. In particular, both can select for neo-sex-determining loci that are more loosely linked. In addition, haploid selection alone can cause transitions analogous to those caused by purely sexually-antagonistic selection, eliminating the need for differences in selection between male and female diploids. Perhaps counterintuitively, transitions involving haploid selection can be driven by sex-ratio selection or cause sex-ratio biases to evolve. We therefore argue that haploid selection should be considered

as a pivotal factor in the evolution of sex-determination systems. Overall, our results suggest several new scenarios under which new sex-determination systems are favoured, which could help to explain why the evolution of sex-determination systems is so dynamic.

Discuss polymorphic mating systems somewhere? Say that haploid selection makes this particularly likely (I think there are examples with gametic competition and weak selection, whereas the vD&K, 2010 results suggest that it's not possible with weak selection and diploid selection alone)? This might be best as a section added to the appendix. When giving an example of polymorphic, make sure it's not just that variation was lost at the **A** locus. The following examples copied and pasted from from Vuilleumier et al. 2007 and vD&K, 2010, might be added to this section.

"Polygenic sex determination has been reported in many plants (e.g. Shannon & Holsinger 2007), fishes (Vandeputte et al. 2007; Ser et al. 2010; Liew et al. 2012), crustaceans (e.g. Battaglia 1958; Battaglia & Malesani 1959; Voordouw & Anholt 2002), bivalves (Haley 1977; Saavedra et al. 1997), gastropods (Yusa 2007a,b), and polychaetes (Bacci 1965, 1978; Premoli et al. 1996)." From Vuilleumier et al. 2007: "Polymorphism for sex-determining genes within or among populations has been reported in many species including houseflies, midges, woodlice, platyfish, cichlid fish, and frogs (Gordon, 1944; Kallman, 1970; Thompson, 1971; Macdonald, 1978; Bull, 1983; Rigaud et al., 1997; Caubet et al., 2000; Lande et al., 2001; Ogataet al., 2003; Lee et al., 2004; Mank et al., 2006)." Also check Kallman (1984) -from vD&K, 2010.

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Appendix

Recursion Equations

In each generation we census the genotype frequencies in male and female gametes/gametophytes (hereafter, gametes) between meiosis (and any meiotic drive) and gametic competition. At this stage we denote the frequencies of X- and Y-bearing gametes from males and females $x_i^{\male}$ and $y_i^{\male}$, where $\male \in \{\male, \female\}$ specifies the sex of the diploid that the gamete came from. $i \in \{1, 2, 3, 4\}$ specifies the genotype at the selected locus **A** and at the novel sex-determining locus **M** where $1 = MA$, $2 = Ma$, $3 = mA$, and $4 = ma$. The gamete frequencies from each sex sum to one, $\sum_i x_i^{\male} + y_i^{\male} = 1$.

Competition then occurs among gametes of the same sex (e.g., among eggs and among sperm separately) according to the genotype at the **A** locus ($w_1^{\male} = w_3^{\male} = w_A^{\male}$, $w_2^{\male} = w_4^{\male} = w_a^{\male}$, see Table 1). The genotype frequencies after gametic competition are $x_i^{\male,s} = w_i x_i^{\male} / \bar{w}_H^{\male}$ and $y_i^{\male,s} = w_i y_i^{\male} / \bar{w}_H^{\male}$, where $\bar{w}_H^{\male} = \sum_i w_i x_i^{\male} + w_i y_i^{\male}$ is the mean fitness of male ($\male = \male$) or female ($\male = \female$) gametes.

Random mating then occurs between gametes to produce diploid zygotes. The frequencies of XX zygotes are then denoted as xx_{ij}, XY zygotes as xy_{ij}, and YY zygotes as yy_{ij}, where **A** and **M** locus genotypes are given by $i, j \in \{1, 2, 3, 4\}$, as above. In XY zygotes, the haplotype inherited from an X-bearing gamete is given by i and the haplotype from a Y-bearing gamete is given by j. In XX and YY zygotes, individuals with diploid genotype ij are equivalent to those with diploid genotype ji; for simplicity, we use xx_{ij} and yy_{ij} with $i \neq j$ to denote the average of these frequencies, $xx_{ij} = (x_i^{\female,s} x_j^{\male,s} + x_j^{\female,s} x_i^{\male,s})/2$ and $yy_{ij} = (y_i^{\female,s} y_j^{\male,s} + y_j^{\female,s} y_i^{\male,s})/2$.

Denoting the **M** locus genotype by $b \in \{MM, Mm, mm\}$ and the **X** locus genotype by $c \in \{XX, XY, YY\}$, zygotes develop as females with probability k_{bc}. Therefore, the frequencies of XX females are given by $xx_{ij}^{\female} = k_{bc} xx_{ij}$, XY females are given by $xy_{ij}^{\female} = k_{bc} xy_{ij}$, and YY females are given by $yy_{ij}^{\female} = k_{bc} yy_{ij}$. Similarly, XX male frequencies are $xx_{ij}^{\male} = (1 - k_{bc}) xx_{ij}$, XY male frequencies are $xy_{ij}^{\male} = (1 - k_{bc}) xy_{ij}$, and YY males frequencies are $yy_{ij}^{\male} = (1 - k_{bc}) yy_{ij}$. This

notation allows both the ancestral and novel sex-determining regions to determine zygotic sex according to an XY system, a ZW system, or an environmental sex-determining system. In addition, we can consider any epistatic dominance relationship between the two sex-determining loci. Here, we assume that the ancestral sex-determining system (**X** locus) is XY ($k_{MMXX} = 1$ and $k_{MMXY} = k_{MMYY} = 0$) or ZW ($k_{MMZZ} = 0$ and $k_{MMZW} = k_{MMWW} = 1$) and epistatically recessive to a dominant novel sex-determining locus, **M** ($k_{Mmc} = k_{mmc} = k$).

Selection among diploids then occurs according to the diploid genotype at the **A** locus, $l \in \{AA, Aa, aa\}$, for an individual of type ij (see Table 1). The diploid frequencies after selection in sex φ are given by $xx_{ij}^{\varphi,s} = w_l^{\varphi} xx_{ij}/\bar{w}^{\varphi}$, $xy_{ij}^{\varphi,s} = w_l^{\varphi} xy_{ij}/\bar{w}^{\varphi}$, and $yy_{ij}^{\varphi,s} = w_l^{\varphi} yy_{ij}/\bar{w}^{\varphi}$, where $\bar{w}^{\varphi} = \sum_{i=1}^{4}\sum_{j=1}^{4} w_l^{\varphi} xx_{ij} + w_l^{\varphi} xy_{ij} + w_l^{\varphi} yy_{ij}$ is the mean fitness of individuals of sex φ.

Finally, these diploids undergo meiosis to produce the next generation of gametes. Recombination and sex-specific meiotic drive occur during meiosis. Here, we allow any relative locations for the SDR, **A**, and **M** loci by using three parameters to describe the recombination rates between them. R is the recombination rate between the **A** locus and the **M** locus, χ is the recombination rate between the **M** locus and the **X** locus, and r is the recombination rate between the **A** locus and the **X** locus. Table S.1 shows the value of χ in the absence of cross-over interference for each possible ordering of the loci. During meiosis in sex φ, meiotic drive occurs such that, in Aa heterozygotes, a fraction α^{φ} of gametes produced carry the A allele and $(1 - \alpha^{\varphi})$ carry the a allele.

Table S.1: χ substitutions for different loci orders (assuming no interference)

Order of loci	
SDR-A-M	$\chi = R(1-r) + r(1-R)$
SDR-M-A	$\chi = (r-R)/(1-2R)$
A-SDR-M	$\chi = (R-r)/(1-2r)$

Among gametes from sex φ, the frequencies of haplotypes (before gametic

competition) in the next generation are given by

$$
\begin{aligned}
x_1^{\male\prime} =& xx_{11}^{\male,s} + xx_{13}^{\male,s}/2 + (xx_{12}^{\male,s} + xx_{14}^{\male,s})\alpha^{\male} \\
& - R(xx_{14}^{\male,s} - xx_{23}^{\male,s})\alpha^{\male} \\
& + (xy_{11}^{\male,s} + xy_{13}^{\male,s})/2 + (xy_{12}^{\male,s} + xy_{14}^{\male,s})\alpha^{\male} \\
& - r(xy_{12}^{\male,s} - xy_{21}^{\male,s})\alpha^{\male} - \chi(xy_{13}^{\male,s} - xy_{31}^{\male,s})/2 \\
& + \big\{ -(R+r+\chi)xy_{14}^{\male,s} + (r+\chi-R)xy_{41}^{\male,s} \\
& + (R+r-\chi)xy_{23}^{\male,s} + (R+\chi-r)xy_{32}^{\male,s}\big\}\alpha^{\male}/2 \\
x_2^{\male\prime} =& xx_{22}^{\male,s} + xx_{24}^{\male,s}/2 + (xx_{12}^{\male,s} + xx_{23}^{\male,s})\alpha^{\male} \\
& - R(xx_{23}^{\male,s} - xx_{14}^{\male,s})\alpha^{\male} \\
& (xy_{22}^{\male,s} + xy_{24}^{\male,s})/2 + (xy_{21}^{\male,s} + xy_{23}^{\male,s})(1-\alpha^{\male}) \\
& - r(xy_{21}^{\male,s} - xy_{12}^{\male,s})(1-\alpha^{\male}) - \chi(xy_{24}^{\male,s} - xy_{42}^{\male,s})/2 \\
& + \big\{ -(R+r+\chi)xy_{23}^{\male,s} + (r+\chi-R)xy_{32}^{\male,s} \\
& + (R+r-\chi)xy_{14}^{\male,s} + (R+\chi-r)xy_{41}^{\male,s}\big\}(1-\alpha^{\male})/2 \\
x_3^{\male\prime} =& xx_{33}^{\male,s} + xx_{13}^{\male,s}/2 + (xx_{23}^{\male,s} + xx_{34}^{\male,s})\alpha^{\male} \\
& - R(xx_{23}^{\male,s} - xx_{14}^{\male,s})\alpha^{\male} \\
& (xy_{33}^{\male,s} + xy_{31}^{\male,s})/2 + (xy_{32}^{\male,s} + xy_{34}^{\male,s})\alpha^{\male} \\
& - r(xy_{34}^{\male,s} - xy_{43}^{\male,s})\alpha^{\male} - \chi(xy_{31}^{\male,s} - xy_{13}^{\male,s})/2 \\
& + \big\{ -(R+r+\chi)xy_{32}^{\male,s} + (r+\chi-R)xy_{23}^{\male,s} \\
& + (R+r-\chi)xy_{41}^{\male,s} + (R+\chi-r)xy_{14}^{\male,s}\big\}\alpha^{\male}/2
\end{aligned}
\tag{S.1a}
\tag{S.1b}
\tag{S.1c}
$$

$$
\begin{aligned}
x_4^{\male'} =& xx_{44}^{\male,s} + xx_{34}^{\male,s}/2 + (xx_{14}^{\male,s} + xx_{24}^{\male,s})\alpha^{\male} \\
& - R(xx_{14}^{\male,s} - xx_{23}^{\male,s})\alpha^{\male} \\
& (xy_{44}^{\male,s} + xy_{42}^{\male,s})/2 + (xy_{41}^{\male,s} + xy_{43}^{\male,s})(1-\alpha^{\male}) \\
& - r(xy_{43}^{\male,s} - xy_{34}^{\male,s})(1-\alpha^{\male}) - \chi(xy_{42}^{\male,s} - xy_{24}^{\male,s})/2 \\
& + \big\{ -(R+r+\chi)xy_{41}^{\male,s} + (r+\chi-R)xy_{14}^{\male,s} \\
& + (R+r-\chi)xy_{32}^{\male,s} + (R+\chi-r)xy_{23}^{\male,s} \big\}(1-\alpha^{\male})/2
\end{aligned}
\tag{S.1d}
$$

$$
\begin{aligned}
y_1^{\male'} =& yy_{11}^{\male,s} + yy_{13}^{\male,s}/2 + (yy_{12}^{\male,s} + yy_{14}^{\male,s})\alpha^{\male} \\
& - R(yy_{14}^{\male,s} - yy_{23}^{\male,s})\alpha^{\male} \\
& (xy_{11}^{\male,s} + xy_{31}^{\male,s})/2 + (xy_{21}^{\male,s} + xy_{41}^{\male,s})\alpha^{\male} \\
& - r(xy_{21}^{\male,s} - xy_{12}^{\male,s})\alpha^{\male} - \chi(xy_{31}^{\male,s} - xy_{13}^{\male,s})/2 \\
& + \big\{ -(R+r+\chi)xy_{41}^{\male,s} + (r+\chi-R)xy_{14}^{\male,s} \\
& + (R+r-\chi)xy_{32}^{\male,s} + (R+\chi-r)xy_{23}^{\male,s} \big\}\alpha^{\male}/2
\end{aligned}
\tag{S.1e}
$$

$$
\begin{aligned}
y_2^{\male'} =& yy_{22}^{\male,s} + yy_{24}^{\male,s}/2 + (yy_{12}^{\male,s} + yy_{23}^{\male,s})\alpha^{\male} \\
& - R(yy_{23}^{\male,s} - yy_{14}^{\male,s})\alpha^{\male} \\
& (xy_{22}^{\male,s} + xy_{42}^{\male,s})/2 + (xy_{12}^{\male,s} + xy_{32}^{\male,s})(1-\alpha^{\male}) \\
& - r(xy_{12}^{\male,s} - xy_{21}^{\male,s})(1-\alpha^{\male}) - \chi(xy_{42}^{\male,s} - xy_{24}^{\male,s})/2 \\
& + \big\{ -(R+r+\chi)xy_{32}^{\male,s} + (r+\chi-R)xy_{23}^{\male,s} \\
& + (R+r-\chi)xy_{41}^{\male,s} + (R+\chi-r)xy_{14}^{\male,s} \big\}(1-\alpha^{\male})/2
\end{aligned}
\tag{S.1f}
$$

$$
\begin{aligned}
y_3^{\male'} =& yy_{33}^{\male,s} + yy_{13}^{\male,s}/2 + (yy_{23}^{\male,s} + yy_{34}^{\male,s})\alpha^{\male} \\
& - R(yy_{23}^{\male,s} - yy_{14}^{\male,s})\alpha^{\male} \\
& (xy_{33}^{\male,s} + xy_{13}^{\male,s})/2 + (xy_{23}^{\male,s} + xy_{43}^{\male,s})\alpha^{\male} \\
& - r(xy_{43}^{\male,s} - xy_{34}^{\male,s})\alpha^{\male} - \chi(xy_{13}^{\male,s} - xy_{31}^{\male,s})/2 \\
& + \big\{ -(R+r+\chi)xy_{23}^{\male,s} + (r+\chi-R)xy_{32}^{\male,s} \\
& + (R+r-\chi)xy_{14}^{\male,s} + (R+\chi-r)xy_{41}^{\male,s} \big\}\alpha^{\male}/2
\end{aligned}
\tag{S.1g}
$$

$$
\begin{aligned}
y_4^{\female\prime} =& yy_{44}^{\female,s} + yy_{34}^{\female,s}/2 + (yy_{14}^{\female,s} + yy_{24}^{\female,s})\alpha^{\female} \\
& - R(yy_{14}^{\female,s} - yy_{23}^{\female,s})\alpha^{\female} \\
& (xy_{44}^{\female,s} + xy_{24}^{\female,s})/2 + (xy_{14}^{\female,s} + xy_{34}^{\female,s})(1-\alpha^{\female}) \\
& - r(xy_{34}^{\female,s} - xy_{43}^{\female,s})(1-\alpha^{\female}) - \chi(xy_{24}^{\female,s} - xy_{42}^{\female,s})/2 \\
& + \big\{ -(R+r+\chi)xy_{14}^{\female,s} + (r+\chi-R)xy_{41}^{\female,s} \\
& + (R+r-\chi)xy_{23}^{\female,s} + (R+\chi-r)xy_{32}^{\female,s} \big\}(1-\alpha^{\female})/2
\end{aligned}
\tag{S.1h}
$$

The full system is therefore described by 16 recurrence equations (three diallelic loci in two sexes, $2^3 \times 2 = 16$). However, not all diploid types are produced under certain sex-determination systems. For example, with the M allele fixed and an ancestral XY sex determination, there are XX males, XY females, or YY females ($x_3^{\female} = x_4^{\female} = y_4^{\female} = y_3^{\female} = y_i^{\male} = 0$). In this case, the system only involves six recursion equations, which we assume below to calculate the equilibria.

Resident equilibrium and stability

In the resident population (allele M fixed), we follow the frequency of A in X-bearing female gametes, $p_X^{\female}$, and X-bearing male gametes, $p_X^{\male}$, and Y-bearing male gametes, $p_Y^{\male}$. We also track the total frequency of Y among male gametes, q, which may deviate from $1/2$ due to meiotic drive in males. These four variables determine the frequencies of the six resident gamete types: $x_1^{\female} = p_X^{\female}$, $x_2^{\female} = 1 - p_X^{\female}$, $x_1^{\male} = (1-q)p_X^{\male}$, $x_2^{\male} = (1-q)(1-p_X^{\male})$, $y_1^{\male} = qp_Y^{\male}$, and $y_2^{\male} = q(1-p_Y^{\male})$. Mean fitnesses in the resident population are given in table S.2.

Various forms of selection can maintain a polymorphism at the **A** locus, including sexually antagonistic selection, overdominance, conflicts between diploid selection and selection upon haploid genotypes (ploidally antagonistic selection, Immler et al. 2012), or a combination of these selective regimes.

In particular special cases, e.g., no sex-differences in selection or meiotic drive ($s^{\male} = s^{\female}$, $h^{\male} = h^{\female}$, and $\alpha^{\male} = \alpha^{\female} = 1/2$), the equilibrium allele frequency and sta-

Table S.2: mean fitnesses in the resident population (M fixed, XY sex determination)

Sex & Life Cycle Stage	Mean Fitness
female gametes ($\bar{w}_H^{\female}$)	$p_X^{\female} w_A^{\female} + (1 - p_X^{\female}) w_a^{\female}$
male gametes ($\bar{w}_H^{\male}$)	$\bar{p}^{\male} w_A^{\male} + (1 - \bar{p}^{\male}) w_a^{\male}$
females ($\bar{w}^{\female}$)	$\{p_X^{\female} w_A^{\female} p_X^{\male} w_A^{\male} w_{AA}^{\female} +$ $(1 - p_X^{\female}) w_a^{\female} p_X^{\male} w_A^{\male} w_{Aa}^{\female} +$ $p_X^{\female} w_A^{\female} (1 - p_X^{\male}) w_a^{\male} w_{Aa}^{\female} +$ $(1 - p_X^{\female}) w_a^{\female} (1 - p_X^{\male}) w_a^{\male} w_{aa}^{\female}\} / \{\bar{w}_H^{\female} \bar{w}_H^{\male} \zeta\}$
males ($\bar{w}^{\male}$)	$\{p_X^{\female} w_A^{\female} p_Y^{\male} w_A^{\male} w_{AA}^{\male} +$ $(1 - p_X^{\female}) w_a^{\female} p_Y^{\male} w_A^{\male} w_{Aa}^{\male} +$ $p_X^{\female} w_A^{\female} (1 - p_Y^{\male}) w_a^{\male} w_{Aa}^{\male} +$ $(1 - p_X^{\female}) w_a^{\female} (1 - p_Y^{\male}) w_a^{\male} w_{aa}^{\male}\} / \{\bar{w}_H^{\female} \bar{w}_H^{\male} (1 - \zeta)\}$
zygotic sex ratio ζ	$\{(1 - q)(p_X^{\male} w_A^{\male} + (1 - p_X^{\male}) w_a^{\male})\} / \bar{w}_H^{\male}$

bility can be calculated analytically without assuming anything about the relative strengths of selection and recombination. However, here, we focus on two regimes (tight linkage and weak selection) in order to make fewer assumptions about fitnesses.

Recombination weak relative to selection (tight linkage between A and X)

We first calculate the equilibrium frequency of the Y and A alleles in the ancestral population when the recombination rate between the **X** and **A** loci is small (r of order ϵ). Selection at the **A** locus will not affect evolution at the novel sex-determining locus, **M**, if one allele is fixed on all backgrounds. We therefore focus on the five equilibria that maintain both A and a alleles, four of which are given to leading order by:

$$(A)\quad \hat{p}_Y^{\male} = 0,\ \hat{q} = \frac{1}{2} - \frac{(\alpha^{\male} - 1/2)w_{Aa}^{\male}\phi}{w_{Aa}^{\male}\phi + w_{aa}^{\male}\psi}, \tag{S.2a}$$

$$\hat{p}_X^{\female} = \frac{w_a^{\female}\phi}{w_a^{\female}\phi + w_A^{\female}\psi},\ \hat{p}_X^{\male} = \frac{2\alpha^{\male}w_{Aa}^{\male}\phi}{2\alpha^{\male}w_{Aa}^{\male}\phi + w_{AA}^{\male}\psi}$$

$$(A')\quad \hat{p}_Y^{\male} = 1,\ \hat{q} = \frac{1}{2} + \frac{(\alpha^{\male} - 1/2)w_{Aa}^{\male}\phi'}{w_{Aa}^{\male}\phi' + w_{AA}^{\male}\psi'}, \tag{S.2b}$$

$$\hat{p}_X^{\female} = 1 - \frac{w_A^{\female}\phi'}{w_A^{\female}\phi' + w_a^{\female}\psi'},\ \hat{p}_X^{\male} = 1 - \frac{2(1-\alpha^{\male})w_{Aa}^{\male}\phi'}{2(1-\alpha^{\male})w_{Aa}^{\male}\phi' + w_{aa}^{\male}\psi'}$$

$$(B)\quad \hat{p}_Y^{\male} = 0,\ \hat{p}_X^{\female} = 1,\ \hat{p}_X^{\male} = 1,\ \hat{q} = 1 - \alpha^{\male} \tag{S.2c}$$

$$(B')\quad \hat{p}_Y^{\male} = 1,\ \hat{p}_X^{\female} = 0,\ \hat{p}_X^{\male} = 0,\ \hat{q} = \alpha^{\male} \tag{S.2d}$$

$$\begin{aligned}
\phi =& \alpha^{\female}w_A^{\female}w_{Aa}^{\female}(w_a^{\male}w_{aa}^{\male} + 2\alpha^{\male}w_A^{\male}w_{Aa}^{\male}) - w_a^{\male}w_a^{\female}w_{aa}^{\male}w_{aa}^{\female}\\
\psi =& (1-\alpha^{\female})w_a^{\female}w_{Aa}^{\female}(w_a^{\male}w_{aa}^{\male} + 2\alpha^{\male}w_A^{\male}w_{Aa}^{\male}) - 2\alpha^{\male}w_A^{\male}w_A^{\female}w_{Aa}^{\male}w_{AA}^{\female}\\
\phi' =& (1-\alpha^{\female})w_a^{\female}w_{Aa}^{\female}(w_A^{\male}w_{AA}^{\male} + 2(1-\alpha^{\male})w_a^{\male}w_{Aa}^{\male}) - w_A^{\male}w_A^{\female}w_{AA}^{\male}w_{AA}^{\female}\\
\psi' =& \alpha^{\female}w_A^{\female}w_{Aa}^{\female}(w_A^{\male}w_{AA}^{\male} + 2(1-\alpha^{\male})w_a^{\male}w_{Aa}^{\male}) - 2(1-\alpha^{\male})w_a^{\male}w_a^{\female}w_{Aa}^{\male}w_{aa}^{\female}
\end{aligned}$$

A fifth equilibrium (C) also exists where A is present at an intermediate frequency on the Y chromosome ($0 < \hat{p}_Y^{\male} < 1$). However, equilibrium (C) is never locally stable when $r \approx 0$ and is therefore not considered further. Thus, the Y can either be fixed for the a allele (equilibria A and B) or the A allele (equilibria A' and B'). The X chromosome can then either be polymorphic (equilibria A and A') or fixed for the alternative allele (equilibria B and B'). Since equilibria (A) and (B) are equivalent to equilibria (A') and (B') with the labelling of A and a alleles interchanged, we discuss only equilibria (A) and (B), in which the Y is fixed for the a allele. If there is no haploid selection ($\alpha^{\female} = 1/2$, $w_A^{\female} = w_a^{\female} = 1$), these equilibria are equivalent to those found by Lloyd and Webb (1977) and Otto (2014).

We next calculate when (A) and (B) are locally stable for $r = 0$. According to the 'small parameter theory' (Karlin and McGregor 1972*a*;*b*), these stability

properties are unaffected by small amounts of recombination between the SDR and **A** locus, although equilibrium frequencies may be slightly altered. For the a allele to be stably fixed on the Y is stable if $\bar{w}^{\male}_{Ya} > \bar{w}^{\male}_{YA}$ where $\bar{w}^{\male}_{Ya} = w^{\male}_{a}(2p^{\female}_{X}(1-\alpha^{\male})w^{\female}_{A}w^{\male}_{Aa} + (1-p^{\female}_{X})w^{\female}_{a}w^{\male}_{aa})$ and $\bar{w}^{\male}_{YA} = w^{\male}_{A}(p^{\female}_{X}w^{\female}_{A}w^{\male}_{AA} + 2(1-p^{\female}_{X})\alpha^{\male}w^{\female}_{a}w^{\male}_{Aa})$. That is, Ya haplotypes must have higher fitness than YA haplotypes. Substituting in $p^{\female}_{X} = \hat{p}^{\female}_{X}$ from above, fixation of the a allele on the Y requires that $\gamma_i > 0$ where $\gamma_{(A)} = w^{\male}_{a}(2(1-\alpha^{\male})w^{\male}_{Aa}\phi + w^{\male}_{aa}\psi) - w^{\male}_{A}(w^{\male}_{AA}\phi + 2\alpha^{\male}w^{\male}_{Aa}\psi)$ for equilibrium (A) and $\gamma_{(B)} = 2(1-\alpha^{\male})w^{\male}_{a}w^{\male}_{Aa} - w^{\male}_{A}w^{\male}_{AA}$ for equilibrium (B). Stability of a polymorphism on the X chromosome (equilibrium A) further requires that $\phi > 0$ and $\psi > 0$. Fixation of the a allele on the X (equilibrium B) can be stable only if equilibrium (A) is not and requires $\psi < 0$ and $w^{\female}_{A}w^{\female}_{AA} > (1-\alpha^{\female})w^{\female}_{a}w^{\female}_{Aa}$.

check last condition and the stability condition below are correct

Selection weak relative to recombination (weak selection)

Here, we assume that selection and meiotic drive are weak relative to recombination (s^{σ}, t^{σ}, α^{σ}_{Δ} of order ϵ). The maintenance of a polymorphism at the **A** locus then requires that

$$\begin{aligned} & 0 < -((1-h^{\female})s^{\female} + (1-h^{\male})s^{\male} + t^{\female} + t^{\male} + \alpha^{\female}_{\Delta} + \alpha^{\male}_{\Delta}) \\ \text{and} \quad & 0 < (h^{\female}s^{\female} + h^{\male}s^{\male} + t^{\female} + t^{\male} + \alpha^{\female}_{\Delta} + \alpha^{\male}_{\Delta}). \end{aligned} \tag{S.3}$$

which indicates that a polymorphism can be maintained by various selective regimes.

Given that a polymorphism is maintained at the **A** locus by weak selection, the frequencies of A in each type of gamete are the same ($\hat{p}^{\female}_{X} = \hat{p}^{\male}_{X} = \hat{p}^{\male}_{Y} = \bar{p}$) and given, to leading order, by

$$\bar{p} = \frac{h^{\female}s^{\female} + h^{\male}s^{\male} + t^{\female} + t^{\male} + \alpha^{\female}_{\Delta} + \alpha^{\male}_{\Delta}}{(2h^{\female}-1)s^{\female} + (2h^{\male}-1)s^{\male}} + O(\epsilon). \tag{S.4}$$

Differences in frequency between gamete types are of $O(\epsilon)$:

$$\begin{aligned}
\hat{p}_X^{\male} - \hat{p}_X^{\female} &= V_A\left(D^{\male} - D^{\female} + \alpha_\Delta^{\male} - \alpha_\Delta^{\female}\right) + O(\epsilon^2) \\
\hat{p}_Y^{\male} - \hat{p}_X^{\female} &= V_A\left(D^{\male} - D^{\female} + \alpha_\Delta^{\male} - \alpha_\Delta^{\female} + (1-2r)(t^{\male} - t^{\female})\right)/2r + O(\epsilon^2) \\
\hat{p}_Y^{\male} - \hat{p}_X^{\male} &= V_A\left(D^{\male} - D^{\female} + \alpha_\Delta^{\male} - \alpha_\Delta^{\female} + t^{\male} - t^{\female}\right)(1-2r)/2r + O(\epsilon^2)
\end{aligned} \tag{S.5}$$

where $V_A = \bar{p}(1-\bar{p})$ is the variance in the frequency of A and $D^{\mathfrak{s}} = \left(\bar{p}s^{\mathfrak{s}} + (1-\bar{p})h^{\mathfrak{s}}s^{\mathfrak{s}}\right) - \left(\bar{p}h^{\mathfrak{s}}s^{\mathfrak{s}} + (1-\bar{p})\right)$ corresponds to the difference in fitness between A and a alleles in diploids of sex $\mathfrak{s} \in \{\female, \male\}$ ($\bar{p}$ is the leading-order probability of mating with an A-bearing gamete from the opposite sex). The frequency of Y among male gametes depends upon the difference in the frequency of the A allele between X- and Y-bearing male gametes and the strength of meiotic drive in favour of the A allele in males, $q = 1/2 + \alpha_\Delta^{\male}(\hat{p}_Y^{\male} - \hat{p}_X^{\male})/2 + O(\epsilon^3)$. Without gametic competition or drive ($\alpha_\Delta^{\mathfrak{s}} = t^{\mathfrak{s}} = 0$) our results reduce to those of van Doorn and Kirkpatrick (2007).

Invasion conditions

Cover the other parts of the characteristic polynomial here.

A rare neo-Y or neo-W will spread from a given ancestral equilibrium when the leading eigenvalue, λ, of the Jacobian matrix derived from the eight mutant recursion equations (given by S.1c,d,g,h), evaluated at the ancestral equilibrium, is greater than one. However, because a neo-Y (neo-W) is always in males (females) and is epistatically dominant to the ancestral sex-determining locus, we need only two recursion equations (e.g., tracking the change in the frequency of neo-Y-A and neo-Y-a gametes from males) and thus the leading eigenvalue is the largest solution to a quadratic characteristic polynomial $\lambda^2 + b\lambda + c = 0$ as described in the text (Table 2).

For tight linkage between the ancestral sex-determining locus and the selected locus we can calculate each of these terms exactly, while for weak selection we take a Taylor series of the leading eigenvalue. With weak selection, the leading

eigenvalue, λ, for any k, is given up to order ϵ^2 by equation (4).

Tight linkage between A and X (recombination weak relative to selection)

Here, we explore the conditions under which a neo-W invades an XY system assuming that the **A** locus is initially in tight linkage with the ancestral sex-determining region ($r \approx 0$). We disregard neo-Y mutations, which never spread given that the ancestral population is at a stable equilibrium (see supplementary *Mathematica* notebook for proof).

Starting with the simpler equilibrium (B), the terms of the characteristic polynomial are

$$\lambda_{mA} = (2\alpha^{\male} w_A^{\male})^{-1} \frac{w_A^{\female}}{w_A^{\female}} \frac{\left[w_A^{\male}\alpha^{\male} w_{AA}^{\female} + w_a^{\male}(1-\alpha^{\male}) w_{Aa}^{\female} 2\alpha^{\female}\right]}{w_A^{\female} w_{AA}^{\female}} \tag{S.6a}$$

$$\lambda_{ma} = (2\alpha^{\male} w_A^{\male})^{-1} \frac{w_a^{\female}}{w_A^{\female}} \frac{\left[w_A^{\male}\alpha^{\male} w_{Aa}^{\female} 2(1-\alpha^{\female}) + w_a^{\male}(1-\alpha^{\male}) w_{aa}^{\female}\right]}{w_A^{\female} w_{AA}^{\female}} \tag{S.6b}$$

$$\rho_{mA} = (2\alpha^{\male} w_A^{\male})^{-1} \frac{w_A^{\female}}{w_A^{\female}} \frac{R w_a^{\male}(1-\alpha^{\male}) w_{Aa}^{\female} \alpha^{\female}}{w_{AA}^{\female}} \tag{S.6c}$$

$$\rho_{ma} = (2\alpha^{\male} w_A^{\male})^{-1} \frac{w_a^{\female}}{w_A^{\female}} \frac{R w_A^{\male}\alpha^{\male} w_{Aa}^{\female}(1-\alpha^{\female})}{w_{AA}^{\female}} \tag{S.6d}$$

Haploid selection impacts the spread of neo-W haplotypes in three ways. Firstly, the zygotic sex ratio becomes male biased, $\zeta < 1/2$, when the a allele (which is fixed on the Y) is favoured during competition among male gametes or by meiotic drive in males. Specifically, at equilibrium (B), the sex ratio is $\zeta = \alpha^{\male} w_A^{\male} / \bar{w}_H^{\male}$ where $\bar{w}_H^{\male} = [(1-\alpha^{\male}) w_a^{\male} + \alpha^{\male} w_A^{\male}]$ has been canceled in equations (S.6) to leave the term $(2\alpha^{\male} w_A^{\male})^{-1}$. Male biased sex ratios facilitate the spread of a neo-W because neo-W alleles cause the zygotes that carry them to develop as the rarer, female, sex.

Secondly, haploid selection in females selects on neo-W haplotypes directly. At

equilibrium (B), the fitness of female gametes under the ancestral sex-determining system is w_A^{φ} such that the relative fitnesses of neo-W-A and neo-W-a haplotypes during female gametic competition are $w_A^{\varphi}/w_A^{\varphi}$ and $w_a^{\varphi}/w_A^{\varphi}$, see terms in equation (S.6). Meiotic drive in females will also change the proportion of gametes that carry the A versus a alleles, which will be produced by heterozygous females in proportions $(1+\alpha_\Delta^{\varphi})$ and $(1-\alpha_\Delta^{\varphi})$, respectively. These terms are only associated with heterozygous females, i.e., they are found alongside w_{Aa}^{φ}.

Thirdly, haploid selection in males affects the diploid genotypes of females by altering the allele frequencies in the male gametes that female gametes pair with. At equlibrium (B), neo-W female gametes will mate with X-A male gametes with probability $\alpha^{\sigma} w_A^{\sigma}/\bar{w}_H^{\sigma}$ and Y-a male gametes with probability $(1-\alpha^{\sigma}) w_a^{\sigma}/\bar{w}_H^{\sigma}$, where the $\bar{w}_H^{\sigma}$ terms have been canceled in (S.6). Thus, for example, neo-W-A haplotypes are found in AA female diploids with probability $\alpha^{\sigma} w_A^{\sigma}/\bar{w}_H^{\sigma}$ (first term in square brackets in equation S.6a) and in Aa female diploids with probability $(1-\alpha^{\sigma}) w_a^{\sigma}/\bar{w}_H^{\sigma}$ (see equation S.6c and second term in square brackets in equation S.6a).

The other terms in equations (S.6) are more easily interpreted if we assume that there is no haploid selection in either sex, in which case $\lambda_{mA} > 1$ when $w_{Aa}^{\varphi} > w_{AA}^{\varphi}$ and $\lambda_{ma} > 1$ when $(w_{Aa}^{\varphi} + w_{aa}^{\varphi})/2 > w_{AA}^{\varphi}$. These conditions cannot be met under purely sexually-antagonistic selection, where a is directionally favoured in males ($w_{AA}^{\sigma} > w_{Aa}^{\sigma} > w_{aa}^{\sigma}$) and A is directionally favoured in females ($w_{AA}^{\varphi} > w_{Aa}^{\varphi} > w_{aa}^{\varphi}$). Essentially, the X is already as specialized as possible for the female beneficial allele (XA is fixed), and the neo-W often makes daughters with the Y-a haplotype, increasing the flow of a alleles into females, which reduces the fitness of those females.

If selection doesn't uniformly favour A in females, however, neo-W-A haplotypes and/or neo-W-a haplotypes can spread ($\lambda_{mA} > 1$ and/or $\lambda_{ma} > 1$) at this equilibrium. A neo-W can spread alongside the A allele ($\lambda_{mA} > 1$), despite the fact that a neo-W brings Ya haplotypes into females, when $w_{Aa}^{\varphi} > w_{AA}^{\varphi}$. In this case the a allele is favoured by selection in females despite A being fixed on the

X. For this equilibrium to be stable, X-A must be sufficiently favoured in males to keep the frequency of XA at one (specifically, from the stability conditions, we must have $w^{\male}_{Aa}/((w^{\male}_{aa} + w^{\male}_{Aa})/2) > w^{\female}_{Aa}/w^{\female}_{AA}$).

Under this same condition, $w^{\female}_{Aa} > w^{\female}_{AA}$, the neo-W can also spread alongside the a allele ($\lambda_{ma} > 1$) if there is sufficiently strong underdominance in females ($w^{\female}_{aa} > w^{\female}_{Aa}$), such that $(w^{\female}_{Aa} + w^{\female}_{aa})/2 > w^{\female}_{AA}$. In this case, a is not favored in females near the equilibrium where females are AA (comparing Aa to AA genotypes) and yet the neo-W can spread with a because it produces female aa individuals by capturing Y-a haplotypes.

Similar equations can be derived for equilibrium (A) by subbing the equilibrium allele frequencies into Table 2.

$$\lambda_{mA} = \frac{a}{b}\left[w^{\female}_{AA}w^{\male}_{Aa}w^{\male}_{A}\alpha^{\male}\phi + 2w^{\female}_{Aa}\alpha^{\female}w^{\male}_{a}\frac{c}{d}\right]/w^{\female}_{a} \tag{S.7a}$$

$$\lambda_{ma} = \frac{a}{b}\left[2w^{\female}_{Aa}(1-\alpha^{\female})w^{\male}_{Aa}w^{\male}_{A}\alpha^{\male}\phi + w^{\female}_{aa}w^{\male}_{a}\frac{c}{d}\right]/w^{\female}_{A} \tag{S.7b}$$

$$\rho_{mA} = \frac{a}{b}R\left[2w^{\female}_{Aa}\alpha^{\female}w^{\male}_{a}\frac{c}{d}\right]/w^{\female}_{a} \tag{S.7c}$$

$$\rho_{ma} = \frac{a}{b}R\left[2w^{\female}_{Aa}(1-\alpha^{\female})w^{\male}_{Aa}w^{\male}_{A}\alpha^{\male}\phi\right]/w^{\female}_{A} \tag{S.7d}$$

where

$$a = w^{\female}_{a}\phi + w^{\female}_{A}\psi \tag{S.8a}$$

$$b = w^{\female}_{AA}\phi(2w^{\male}_{Aa}w^{\male}_{A}\alpha_{\male}\phi) + w^{\female}_{Aa}\psi(2w^{\male}_{Aa}w^{\male}_{A}\alpha_{\male}\phi + w^{\male}_{AA}w^{\male}_{a}\psi) + w^{\female}_{aa}\psi(w^{\male}_{AA}w^{\male}_{a}\psi) \tag{S.8b}$$

$$c = 2(w^{\male}_{Aa}\phi)^2(1-\alpha^{\male})\alpha_{\male} + w^{\male}_{Aa}\phi(w^{\male}_{AA}\psi + w^{\male}_{aa}\psi\alpha^{\male}) + w^{\male}_{aa}\psi w^{\male}_{AA}\psi \tag{S.8c}$$

$$d = 2w^{\male}_{Aa}\alpha^{\male}\phi + w^{\male}_{aa}\psi \tag{S.8d}$$

As with equilibrium (B), haploid selection again modifies invasion fitnesses by altering the sex-ratio and the diploid genotypes of females and directly select-

ing upon female gametes. The only difference is that resident XX females are no longer always homozygote AA and males are no longer always heterozygote Aa. Thus the effect of haploid selection in males is reduced, as is the difference in fitness between neo-W haplotypes and resident X haplotypes, as both can be on any diploid or haploid background.

The other terms are easier to interpret in the absence of haploid selection. For instance, without haploid selection, the neo-W-A haplotype spreads ($\lambda_{mA} > 1$) if and only if

$$2(w^{\female}_{Aa} - w^{\female}_{aa})w^{\male}_{AA}\psi^2 > (w^{\female}_{AA} - w^{\female}_{Aa})w^{\male}_{Aa}\phi(\phi - \psi) \tag{S.9}$$

where $\phi - \psi = w^{\female}_{AA}w^{\male}_{Aa} - w^{\female}_{aa}w^{\male}_{aa}$ and both ϕ and ψ are positive when equilibrium (A) is stable. In contrast to equilibrium (B), a neo-W haplotype can spread under purely sexually-antagonistic selection ($w^{\male}_{AA} > w^{\male}_{Aa} > w^{\male}_{aa}$ and $w^{\female}_{AA} > w^{\female}_{Aa} > w^{\female}_{aa}$). The neo-W-$A$ can spread as long as it becomes associated with females that bear more A alleles than observed at equilibrium (A).

Without haploid selection, the neo-W-a haplotype spreads ($\lambda_{ma} > 1$) if and only if

$$(w^{\female}_{aa} + w^{\female}_{Aa} - 2w^{\female}_{AA})w^{\male}_{Aa}\phi^2 + (w^{\female}_{aa} - w^{\female}_{Aa})(w^{\male}_{Aa} + 2w^{\male}_{AA})\phi\psi > 0 \tag{S.10}$$

This condition cannot be met with purely sexually antagonistic selection (as both terms on the left-hand side would then be negative), but it can be met under other circumstances. For example, with overdominance in males there is selection for increased A frequencies on X chromosomes in males, which are always paired with Y-a haplotypes. Directional selection for a in females can then maintain a polymorphism at the **A** locus on the X. This scenario selects for a modifier that increases recombination between the sex chromosomes (e.g., blue region of Figure 2d in Otto 2014) and facilitates the spread of neo-W-a haplotypes, which create more females bearing more a alleles than the ancestral X chromosome does.

Supplementary Figures

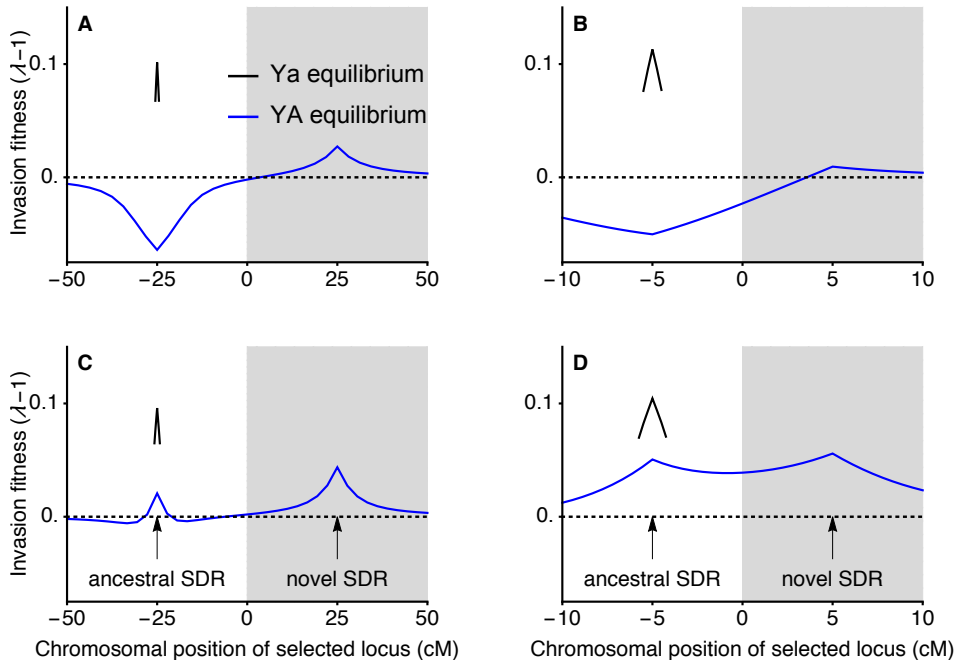

Figure S.1: Neo-W alleles can spread when loci under diploid selection are tightly linked to the ancestral sex determining locus ($r \approx 0$). In panels A and B, the a allele is favoured in females ($w^{\female}_{aa} = 1.05$, $w^{\female}_{Aa} = 1$, $w^{\female}_{AA} = 0.85$) and selection in males is overdominant ($w^{\male}_{aa} = w^{\male}_{AA} = 0.75$). In panels C and D, selection in males and females is overdominant ($w^{\female}_{aa} = w^{\female}_{AA} = 0.6$, $w^{\male}_{aa} = 0.5$, $w^{\male}_{AA} = 0.7$, $w^{\male}_{Aa} = 1$). These parameters are marked by a dagger in Figure 2, which shows that neo-W invasion is expected for any R when the a allele is nearly fixed on the Y (black lines). Equilibria where the A allele is more common among Y-bearing male gametes can also be stable for these parameters (blue lines). The weak selection approximation holds when all recombination rates are large relative to selection (around 0 in panels A and C), in which case neo-W alleles should spread if they are more tightly linked to the selected locus (positive invasion fitness in the grey region). However, when linkage is tight (panels C and D and when the selected locus is near the SDR), this prediction breaks down. Here, there is no haploid selection $t^{\male} = \alpha^{\male}_{\Delta} = 0$.

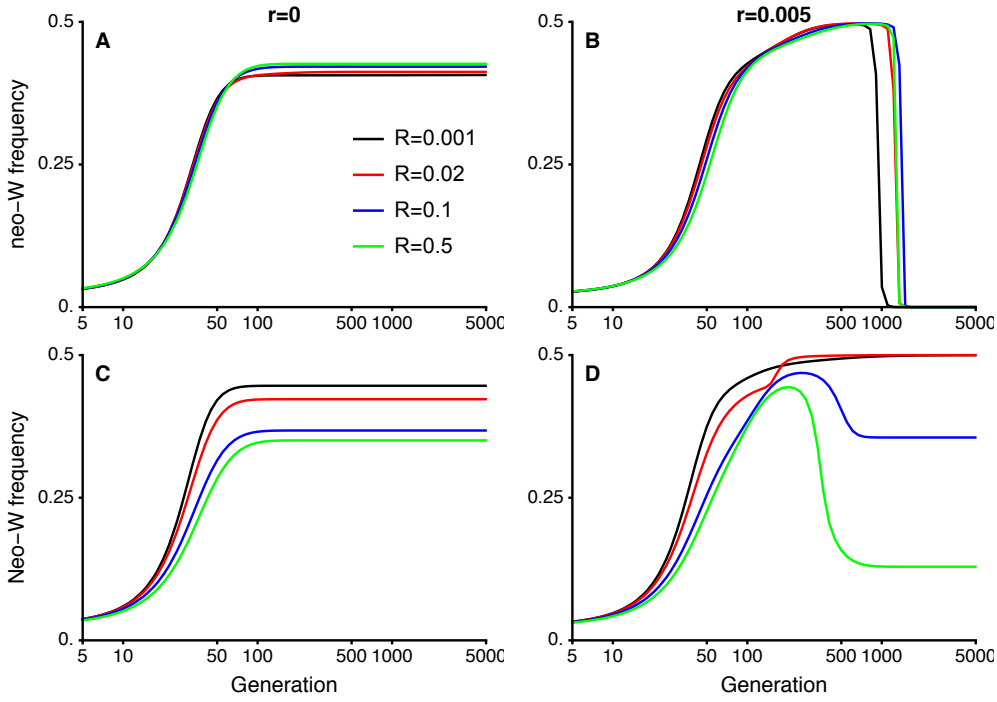

Figure S.2: Following invasion by a neo-W allele, there can be a complete transition to a new sex-determination system, maintenance of polymorphism at both ancestral-XY and neo-ZW sex determining regions, or loss of the new sex-determining allele. Here we plot the frequency of the neo-W allele among female gametes; as the neo-W reaches frequency 0.5, polymorphism at the ancestral XY locus is lost with Y becoming fixed such that sex is determined only be the ZW allele carried by a female gamete. Panels A, C and D show cases where a steady state is reached with the neo-W at a frequency below 0.5, in which case ancestral-X and Y alleles also both segregate. In all cases, we assume that the a allele is initially more common that the A allele on the Y (Ya is fixed when $r = 0$). When $r > 0$ (panels B and D), YA haplotypes created by recombination can become more common than Ya haplotypes as the neo-W spreads. In B, this leads to loss of the neo-W and the system goes to an equilibrium with Xa and YA haplotypes fixed (A'), such that all females have the high fitness genotype aa and all males Aa. For the parameters in B, neo-W alleles have negative invasion fitness when the YA haplotype is ancestrally more common than Ya (see blue line in Figure S.2A and S.2B). In contrast, the neo-W is not lost in panel D (see blue line in Figure S.2C and S.2D). Fitness parameters are the same as in Figure S.2, the a allele is favoured in females ($w^{\female}_{aa} = 1.05$, $w^{\female}_{Aa} = 1$, $w^{\female}_{AA} = 0.85$) and there is overdominant selection in males ($w^{\male}_{aa} = w^{\male}_{AA} = 0.75$) in panels A and B. In panels C and D, selection in males and females is overdominant ($w^{\female}_{aa} = w^{\female}_{AA} = 0.6$, $w^{\male}_{aa} = 0.5$, $w^{\male}_{AA} = 0.7$, $w^{\male}_{Aa} = 1$). These parameters are marked by a dagger in Figure 2. Here, there is no haploid selection $t^{\male} = \alpha^{\male}_{\Delta} = 0$.

Add Sally's figure showing lambda for small r near equil A versus near equil B. Add references to this figure to appendix where we discuss whether lambdas can be greater than 1 with sexually antagonistic selection.

Check that we mention Sally's result that invasion cannot occur with sexually-antagonistic selection and $R = 1/2$

We could also give versions of Figure 2 where there is also haploid selection of various types. I suggest using $\alpha_{\Delta}^{\male\female} = 1/20$ and $t^{\male\female} = 1/10$. Haploid selection can favour A or a, so this would involve 4x 6-panel figures. Started looking at this in RegionPlots.nb but haven't added gametic competition or labels for λs. Try to integrate into the discussion of haploid selection?

Perhaps it would also be useful to add an 8 panel figure that features ploidally antagonistic selection. For each type of haploid selection (gametic competition/ meiotic drive in males/females), give a regionplot where $h^{\male} = h^{\female}$, e.g., $h^{\male} = h^{\female} = 0.75$ (or perhaps the value of h we use in the regionplots we have, in which $w_{aa} = 0.85$, $w_{Aa} = 1$, $w_{AA} = 1.05$). Matt made a figure like this before but both Ya and YA equilibria were plotted and there was no outline showing where the Ya equilibrium is stable (as in Figure 2). In Matts plot the axes were $s^{\male\female}$ and $\alpha_{\Delta}^{\male\female}$. Add an asterisk to each region plot and show invasion in another panel, using those parameters and various R (e.g., in the stye of S.2). In an email, Sally has an example of ploidally-antagonistic selection where the neo-W fixes and $R = 1/2$. This would cover that case and more.

Perhaps, for one set of parameters, we should plot the dynamics of all the different alleles. E.g., we could use the same parameters used in 4. The main purpose would be to show what happens to the ancestral SDR during turnover. We could also show an example where XY and ZW sex determining systems are both polymorphic and stable.