

Haploid Selection, Sex Ratio Bias, and Transitions Between Sex-Determination Systems

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Contributions:

Abstract

2 Sex-determination systems are remarkably dynamic; many taxa display
4 shifts in the location of sex-determining loci or the evolution of entirely
6 new sex-determining systems. Predominant theories for why we observe
8 such transitions generally conclude that novel sex-determining systems are
10 favoured by selection if they equalise the sex ratio or increase linkage with
12 a sexually-antagonistic locus. We use population genetic models to extend
14 these theories in two ways: (1) We explicitly consider how selection on very
16 tightly sex-linked loci influences the spread of novel sex-determiners. We
18 find that tightly sex-linked genetic variation can favour the spread of new
20 sex-determination systems in which the heterogametic sex changes (XY to
22 ZW or ZW to XY) and the new sex-determining region is less closely linked
24 (or unlinked) to the sex-linked locus under selection, which is not predicted
26 by previous theory. (2) We also consider selection upon haploid genotypes
28 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 transi-
tions 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 pre-
dicted 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 previously un-
expected genomic locations that experience selection during diploid and/or
haploid phases. These results might be reflected in the lability with which
sex-determination systems evolve.

Introduction

30 Animals and angiosperms exhibit extremely diverse sex-determination systems
31 (reviewed in Bull 1983, Charlesworth and Mank 2010, Beukeboom and Perrin
32 2014, Bachtrog et al. 2014). Among species with genetic sex determination of
33 diploid sexes, some taxa have heterogametic males (XY) and homogametic fe-
34 males (XX), including mammals and most dioecious plants (Ming et al. 2011);
35 whereas other taxa have homogametic males (ZZ) and heterogametic females (ZW),
36 including Lepidoptera and birds. Within several taxa, the chromosome that har-
37 bours the master sex-determining region changes. For example, transitions of the
38 master sex-determining gene between chromosomes or the evolution of new mas-
39 ter sex-determining genes have occurred in Salmonids (Li et al. 2011, Yano et al.
40 2012), Diptera (Vicoso and Bachtrog 2015), and *Oryzias* (Myosho et al. 2012). In
41 addition, many gonochoric clades with genetic sex determination exhibit transi-
42 tions between male (XY) and female (ZW) heterogamety, including snakes (Gam-
43 ble et al. 2017), lizards (Ezaz et al. 2009), eight of 26 teleost fish families (Mank
44 et al. 2006), true fruit flies (Tephritids, Vicoso and Bachtrog 2015), amphibians
45 (Hillis and Green 1990), the angiosperm genus *Silene* (Slancarova et al. 2013),
46 the angiosperm family *Salicaceae* (Pucholt et al. 2015; 2017) and Coleoptera and
47 Hemiptera (Beukeboom and Perrin 2014, plate 2). Indeed, in some cases, both
48 male and female heterogametic sex-determination systems can be found in the
49 same species, as exhibited by some cichlid species (Ser et al. 2010) and *Rana*
50 (*rugosa* (Ogata et al. 2007, Miura 2007)). In addition, multiple transitions have
51 occurred between genetic and environmental sex-determination systems, e.g., in
52 reptiles and fishes (Conover and Heins 1987, Mank et al. 2006, Pokorná and Kra-
53 tochvíl 2009, Ezaz et al. 2009, Pen et al. 2010, Holleley et al. 2015).

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

stronger favourable association to build up between a male-beneficial allele, and
60 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)
62 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-
64 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
66 sex-determination system.

The sex ratio is directly determined by the sex-determination system, and it
68 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 Per-
70 rin 2014, Chapter 7). ‘Fisherian’ sex-ratio selection favours a 1:1 zygotic sex ra-
tio when assuming that males and females are equally costly to produce (Fisher
72 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
74 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
76 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
78 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
80 Y chromosomes are inherited disproportionately often), which causes sex ratios
to become biased (Hamilton 1967). They find that new, unlinked sex-determining
82 loci (masculinizing or feminizing mutations, i.e., neo-Y or neo-W loci) can then
spread, which restore an even sex ratio.

84 Here we use mathematical models to find the conditions under which new
sex-determination systems spread when individuals experience selection at both
86 diploid and haploid stages. Even in animal and plant species that have much
larger and more conspicuous diploid phases than haploid phases, many loci ex-
88 perience 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.

Segregation distortion provides putative evidence of haploid selection and can sometimes be attributed to meiotic drive and/or gametic competition (Lalanne et al. 2004, Fishman and Willis 2005, Leppälä et al. 2008; 2013, Didion et al. 2015; 2016). Where it has been characterized, meiotic drive generally occurs either during the production of male or female gametes only (Úbeda and Haig 2005, Lindholm et al. 2016). Gametic competition is also typically sex specific, occurring primarily among male gametes, because there are typically many more pollen/sperm than required for fertilization. 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, Gossman 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 in animals can alter haploid allele frequencies and increase offspring fitness (Immler et al. 2014, Alavioon et al. 2017).

There are various ways by which genes experiencing 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,
120 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,
122 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
124 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
126 (Lloyd 1974, Conn and Blum 1981, Stehlik and Barrett 2005; 2006, Field et al.
128 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.

130 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
132 by selection on genetically-associated alleles. Consequently, Fisherian sex ratio selection does not dominate and it is possible for selection on linked alleles to
134 drive turnover between sex-determining systems despite causing increases in sex-ratio bias. In addition to considering haploid selection, another novel development
136 in our model is that we consider loci that are in very tight linkage with the ancestral sex-determining region. We show that transitions between male and female
138 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
140 ancestral associations between sex and the alleles favoured in that sex.

Model

142 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
144 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,
146 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**; 148 XX genotypes become females and XY become males (or ZW become females and ZZ become males). To evaluate the evolution of new sex-determination sys- 149 tems, we consider the invasion, fixation, maintenance, and/or loss of novel sex- 150 determining alleles (m) at the **M** locus. We assume that the **M** locus is epistatically 151 dominant over the **X** locus such that zygotes with at least one m allele develop as 152 females with probability k and as males with probability $1 - k$, regardless of the 153 **X** locus genotype. With $k = 0$, the m allele is a masculinizer (i.e., a neo-Y) and 154 with $k = 1$ the m allele is a feminizer (i.e., a neo-W). With intermediate k , we can 155 interpret m as an environmental sex determination (ESD) allele, such that zygotes 156 develop as females in a proportion (k) of the environments they experience.

157 In each generation, we census the genotype frequencies in male and female 158 gametes/gametophytes (hereafter gametes) before gametic competition. A full de- 159 scription of our model, including recursion equations, is given in the Appendix. 160 First, competition occurs among male gametes (sperm/pollen competition) and 161 among female gametes (egg/ovule competition) separately. Selection during ga- 162 metic competition depends on the **A** locus genotype, relative fitnesses are given 163 by w_A^φ and w_a^φ ($\varphi \in \{\text{♀}, \text{♂}\}$; see table 1). We assume that all gametes compete for 164 fertilization during gametic competition, which assumes a polygamous mating sys- 165 tem. Gametic competition in monogamous mating systems is, however, equivalent 166 to meiotic drive in our model (described below), as both only alter the frequency 167 of gametes produced by heterozygotes. After gametic competition, random mating 168 occurs between male and female gametes. The resulting zygotes develop as males 169 or females, depending on their genotypes at the **X** and **M** loci. Diploid males and 170 females then experience selection, with relative fitnesses w_{AA}^φ , w_{Aa}^φ , and w_{aa}^φ . The 171 next generation of gametes is produced by meiosis, during which recombination 172 and sex-specific meiotic drive can occur. Recombination (i.e., an odd number of 173 cross-overs) occurs between loci **X** and **A** with probability r , between loci **A** and 174 **M** with probability R , and between loci **X** and **M** with probability ρ . Any linear 175 order of the loci can be modelled with appropriate choices of r , R , and ρ (see Ta-

ble S.1). Individuals that are heterozygous at the **A** locus may experience meiotic drive; a gamete produced by Aa heterozygotes of sex ♀ bear allele A with probability $\alpha^{\text{♀}}$. 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 $\text{♀} \in \{\text{♀}, \text{♂}\}$

Genotype	Relative fitness during gametic competition
A	$w_A^{\text{♀}} = 1 + t^{\text{♀}}$
a	$w_a^{\text{♀}} = 1$
Genotype	Relative fitness during diploid selection
AA	$w_{AA}^{\text{♀}} = 1 + s^{\text{♀}}$
Aa	$w_{Aa}^{\text{♀}} = 1 + h^{\text{♀}}s^{\text{♀}}$
aa	$w_{aa}^{\text{♀}} = 1$
Genotype	Transmission during meiosis in Aa heterozygotes
A	$\alpha^{\text{♀}} = 1/2 + \alpha_{\Delta}^{\text{♀}}/2$
a	$1 - \alpha^{\text{♀}} = 1/2 - \alpha_{\Delta}^{\text{♀}}/2$

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 homogametic 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 (relabeling the ancestrally-heterogametic sex as female and the ancestrally-homogametic sex as male).

190 **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, $\lambda^2 + b\lambda + c = 0$ (see Appendix for a discussion of other roots - or Sally's proof!). Here, $b = -(\lambda_{mA} + \lambda_{ma}) + (\chi_{mA} + \chi_{ma})$ and $c = (\lambda_{mA} - \chi_{mA})(\lambda_{ma} - \chi_{ma}) - \chi_{mA}\chi_{ma}$, 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 χ_{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 χ_{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^{\varnothing} , and among X-bearing, p_X^{δ} , and among Y-bearing, p_Y^{δ} , 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. We will consider only equilibrium frequencies of alleles, \hat{p}_i^{\varnothing} , and Y-bearing male gametes, \hat{q} , to ensure the eigenvalues of the invasion analysis are valid.

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

neo-Y ($k = 0$)
$\lambda_{mA} = (2\zeta)^{-1} [\hat{p}_X^\varphi w_A^\varphi w_A^\delta w_{AA}^\delta + (1 - \hat{p}_X^\varphi) w_a^\varphi w_A^\delta w_{Aa}^\delta (1 + \alpha_\Delta^\delta)] / (\bar{w}_H^\varphi \bar{w}_H^\delta \bar{w}^\delta)$
$\lambda_{ma} = (2\zeta)^{-1} [(1 - \hat{p}_X^\varphi) w_a^\varphi w_a^\delta w_{aa}^\delta + \hat{p}_X^\varphi w_A^\varphi w_a^\delta w_{Aa}^\delta (1 - \alpha_\Delta^\delta)] / (\bar{w}_H^\varphi \bar{w}_H^\delta \bar{w}^\delta)$
$\chi_{mA} = R(2\zeta)^{-1} [(1 - \hat{p}_X^\varphi) w_a^\varphi w_A^\delta w_{Aa}^\delta (1 + \alpha_\Delta^\delta)] / (\bar{w}_H^\varphi \bar{w}_H^\delta \bar{w}^\delta)$
$\chi_{ma} = R(2\zeta)^{-1} [\hat{p}_X^\varphi w_A^\varphi w_a^\delta w_{Aa}^\delta (1 - \alpha_\Delta^\delta)] / (\bar{w}_H^\varphi \bar{w}_H^\delta \bar{w}^\delta)$
neo-W ($k = 1$)
$\lambda_{mA} = [2(1 - \zeta)]^{-1} [\bar{p}^\delta w_A^\delta w_A^\varphi w_{AA}^\varphi + (1 - \bar{p}^\delta) w_a^\delta w_A^\varphi w_{Aa}^\varphi (1 + \alpha_\Delta^\varphi)] / (\bar{w}_H^\varphi \bar{w}_H^\delta \bar{w}^\varphi)$
$\lambda_{ma} = [2(1 - \zeta)]^{-1} [(1 - \bar{p}^\delta) w_a^\delta w_a^\varphi w_{aa}^\varphi + \bar{p}^\delta w_A^\delta w_a^\varphi w_{Aa}^\varphi (1 - \alpha_\Delta^\varphi)] / (\bar{w}_H^\varphi \bar{w}_H^\delta \bar{w}^\varphi)$
$\chi_{mA} = R[2(1 - \zeta)]^{-1} [(1 - \bar{p}^\delta) w_a^\delta w_A^\varphi w_{Aa}^\varphi (1 + \alpha_\Delta^\varphi)] / (\bar{w}_H^\varphi \bar{w}_H^\delta \bar{w}^\varphi)$
$\chi_{ma} = R[2(1 - \zeta)]^{-1} [\bar{p}^\delta w_A^\delta w_a^\varphi w_{Aa}^\varphi (1 - \alpha_\Delta^\varphi)] / (\bar{w}_H^\varphi \bar{w}_H^\delta \bar{w}^\varphi)$

$\bar{p}^\delta = (1 - \hat{q})\hat{p}_X^\delta + \hat{q}\hat{p}_Y^\delta$ is the average frequency of the A allele among X- and Y-bearing male gametes.

ζ is the zygotic sex ratio (fraction male)

\bar{w}^δ is the mean fitness of diploids of sex δ , see Table S.2

\bar{w}_H^δ is the mean fitness of haploids from sex δ , 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. Given the characteristic polynomial $f(\lambda) = \lambda^2 + b\lambda + c$ and the Perron-Forbenius theorem (guaranteeing that the leading eigenvalue is positive, unique, and real), at least one solution to $f(\lambda) = 0$ is greater than one when the polynomial has a negative slope or negative value at $\lambda = 1$ ($f'(1) = 2 + b < 0$ or $f(1) = 1 + b + c < 0$). Regardless the rate of recombination, at least one of these conditions is true if both haplotypes can spread ($\lambda_{mA}, \lambda_{ma} > 1$) and neither can be true if neither haplotype can spread ($\lambda_{mA}, \lambda_{ma} < 1$). If only one haplotype can spread then the new sex-determining allele increases in frequency on one A

230 background and declines on the other. Invasion then occurs if

$$\chi_{ma}/(\lambda_{ma} - 1) + \chi_{mA}/(\lambda_{mA} - 1) < 1. \quad (1)$$

232 For example, if we assume that only the *mA* haplotype has a positive growth rate
234 ($\lambda_{ma} < 1 < \lambda_{mA}$), the first term on the left-hand side of (1) is negative and invasion
requires that the growth rate of *mA* haplotypes ($\lambda_{ma} - 1$) and the rate at which
236 they are produced by recombination in *ma* haplotypes (χ_{ma}) are sufficiently large
relative to the rate of decline of *ma* haplotypes ($1 - \lambda_{ma}$) and the rate of loss of *mA*
haplotypes due to recombination (χ_{mA}).

238 Table 2 illustrates a number of key points about the invasion of neo-Y and
240 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.,
242 the first factor of the λ_{mi} is greater than one for a neo-Y and less than one for a neo-
W). However, the spread of a neo-Y (neo-W) also depends on the male (female)
244 fitness of associated alleles (terms involving equilibrium allele frequencies, \hat{p} 's).
246 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
248 is because a dominant neo-Y (neo-W) is always found in males (females), and
250 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.
252 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
254 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.

254 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*
256 allele (i.e., \hat{p}_X^q , \hat{p}_X^δ , and \hat{p}_Y^δ) and Y-bearing male gametes (\hat{q}) in the ancestral pop-
ulation. Since only the A locus experiences selection directly, any deterministic

258 evolution requires that there is a polymorphism at the **A** locus. Polymorphisms
259 can be maintained by mutation-selection balance or transiently present during the
260 spread of beneficial alleles. However, polymorphisms maintained by selection can
261 maintain alleles at higher allele frequencies for longer periods. Here, we focus of
262 polymorphisms maintained by selection, where the *A* allele reaches a stable in-
263 termediate equilibrium frequency under the ancestral sex-determination system
264 before the neo-sex-determining allele (*m*) arises. We can analytically calculate the
265 allele frequency of the *A* allele using two alternative simplifying assumptions: (1)
266 the **A** locus is within (or tightly linked to) the non-recombining region around the
267 ancestral SDR ($r \approx 0$) or (2) selection is weak relative to recombination (s^{δ}, t^{δ} ,
268 α_{Δ}^{δ} of order $\epsilon \ll 1$).

Tight linkage with the ancestral sex-determining region

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

277 A neo-Y will never invade an ancestral XY system that already has tight linkage
278 with the locus under selection ($r = 0$, for details see supplementary *Mathematica*
279 file). A neo-Y haplotype with the same allele as the ancestral Y is neutral ($\lambda_{ma} = 1$)
280 and does not change in frequency. The other neo-Y haplotype will not spread
281 ($\lambda_{mA} < 1$) given that the initial equilibrium is stable. Therefore, a neo-Y mutation
282 cannot spread ($\lambda \leq 1$) in an ancestral XY system that is at equilibrium with all se-
283 lected loci within the non-recombining region around the SDR. In essence, through
284 tight linkage with the **A** locus, the ancestral Y becomes strongly specialized on the
285 allele that has the highest fitness across male haploid and diploid phases. Given
286 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.

288 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
 290 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 (Figure 1). In fact, with
 292 tight linkage between the ancestral SDR and the selected locus, haploid selection
 and/or overdominance can favour completely unlinked neo-W alleles ($R = 1/2$),
 294 allowing autosomes to become new sex chromosomes. To develop an intuition for
 how less closely linked neo-W alleles invade, we first focus on cases where there
 296 is no haploid selection and discuss the additional effect of haploid selection in the
 appendix.

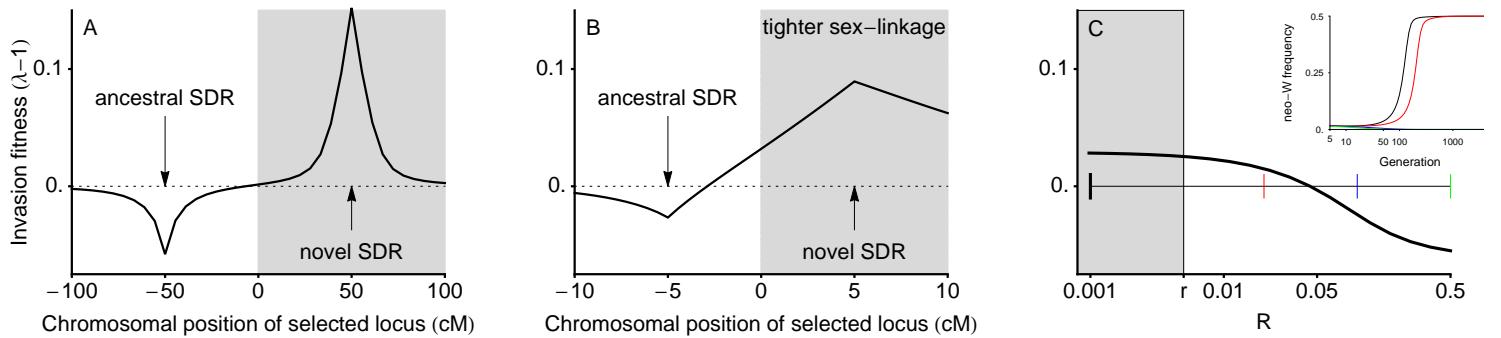


Figure 1: Transitions between XY and ZW systems can occur even when the neo-SDR is less tightly linked to a locus under sexually-antagonistic selection (here, without haploid selection). In panel A, linkage is loose enough relative to selection that the analytical results assuming weak selection hold, 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 analytical results assuming weak selection do not hold, and a neo-W can 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 can show that neo-W invasion fitness is always negative when $R = 1/2$ and there is sex-antagonism but no haploid selection (see supplementary *Mathematica* file). Fitness parameters are shown by an asterisk in Figure 2A: $w_{AA}^g = 1.05$, $w_{aa}^g = 1.2$, $w_{aa}^{\delta} = w_{AA}^{\delta} = 0.85$, $w_{Aa}^{\delta} = 1$, $t^{\delta} = \alpha_{\Delta}^{\delta} = 0$.

298 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

300 with the ancestrally ‘female-beneficial’ allele. Broadly, this is possible because
301 the ancestral X chromosome is sometimes found in males and is therefore unable
302 to perfectly specialise on the ‘female-beneficial’ allele. For example, when the a
303 allele is favoured in males, a polymorphism of A and a alleles can be maintained
304 on the X despite directional selection in favour of the A allele in females ($s^F > 0$,
305 $0 < h^F < 1$). When the a allele is strongly favoured on X chromosomes in males
306 (w_{aa} sufficiently large relative to w_{Aa}), neo-W- A haplotypes can spread ($\lambda_{mA} >$
307 1), see Figure 2A. In this case the a allele is at high frequency among ancestral
308 XX females due to selection upon the X in males. By contrast, W- A haplotypes
309 will only create females with high fitness (AA or Aa genotypes) and can therefore
310 spread.

When only one neo-W haplotype has a positive growth rate (see Figure 2), a
312 neo-W can invade as long as equation (1) is satisfied, which may require that the
313 recombination rate, R , is small enough. Nevertheless, because we assume here that
314 r is small, these results indicate that a more loosely linked sex-determining region
315 ($r < R$) can spread. Therefore, tightly sex-linked loci that experience sexually-
316 antagonistic selection can drive heterogametic transitions in which the neo-SDR
317 is less closely linked to the locus under selection (Figure 1).

Given that the a allele can be considered ancestrally ‘male-beneficial’ because
318 it is fixed on the Y, it is surprising that neo-W- a haplotypes can sometimes be
319 favoured by selection in females ($\lambda_{ma} > 1$). Again, this occurs because ancestral
320 X’s also experience selection in males, in which they will always be paired with a
321 Y- a . Hence, if there is overdominance in males, X- A Y- a males have high fitness
322 and the A allele is favoured by selection on the X in males. Therefore, the X can
323 be polymorphic or even fixed for the A allele despite favouring the a allele during
324 selection in females (e.g., see outlined region in Figure 2B and Lloyd and Webb
325 1977, Otto 2014). In such cases, neo-W- a haplotypes can spread because they
326 create more Aa and aa females when pairing with an X from males and because
327 they bring Y- a haplotypes into females.

In some cases, both W- A and W- a haplotypes can spread, e.g., when AA in-

330 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
332 haplotypes then produce fewer unfit AA females. This is true for the neo-W- A hap-
lotype because it can pair with a Y- a haplotype and still be female. Wherever both
334 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,
336 see Figures S.1 and S.2 for examples).

Assuming that linkage is not tight, van Doorn and Kirkpatrick (2010) showed
338 that invasion by a neo-W occurs under the same conditions as ‘fixation’ (where
fixation indicates that the neo-W reaches its maximum frequency among eggs,
340 which is 1/2). An equivalent analysis is not possible where we assume that linkage
is tight. However, numerical simulations with tight linkage demonstrate that the
342 neo-SDR does not necessarily fix, leading to the stable maintenance of a mixed
sex-determining system, in which X, Y, Z, and W alleles all segregate (e.g., Figure
344 S.9B-D). Within a species, both feminizing and masculinizing alleles have been
reported in houseflies (McDonald et al. 1978), midges (Thompson 1971), frogs
346 (Ogata et al. 2007), cichlid fish (Ser et al. 2010), tilapia (Lee et al. 2004), sea bass
(Vandepitte et al. 2007), and lab-strains of Zebrafish (Liew et al. 2012, Wilson
348 et al. 2014). For example, in the platyfish (*Xiphophorus maculatus*), X, Y, and
W alleles segregate at one locus (or two closely-linked loci) near to potentially
350 sexually-antagonistic genes for pigmentation and sexual maturity (Kallman 1965;
1968, Wolff and Schartl 2001, Schulteis et al. 2006). Our results suggest that several
352 forms of selection on nearby loci (i.e., r and R small) could maintain multiple sex-
determining alleles.

354 **Loose linkage with the ancestral sex-determining region**

Assuming that selection is weak relative to all recombination rates (r , R and ρ),
356 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.
358 To leading order in selection, these are:

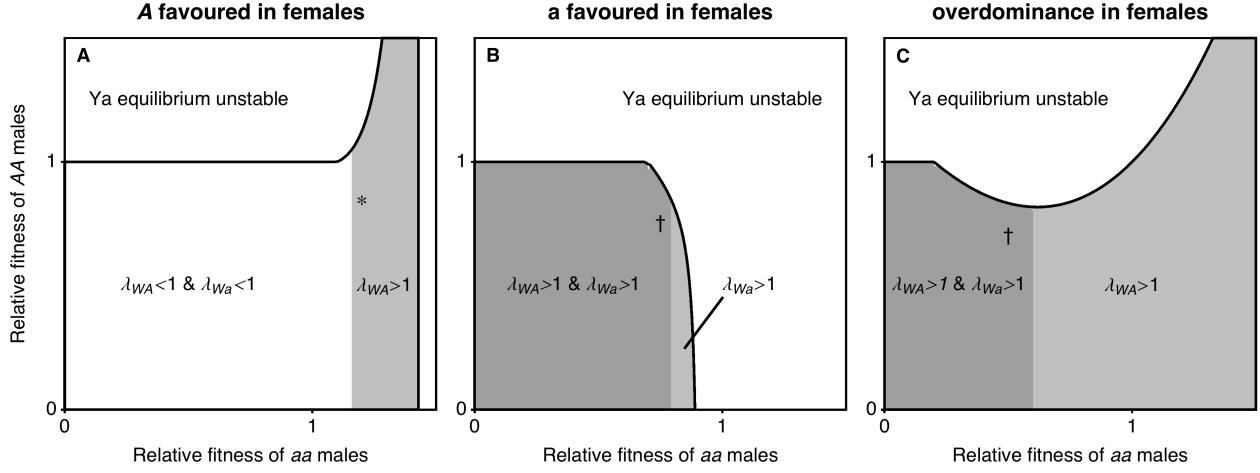


Figure 2: When the ancestral-XY locus is tightly linked to a locus under selection ($r = 0$), one or both neo-W haplotypes can spread. We vary the fitness of male homozygotes relative to heterozygotes ($w_{Aa}^{\varphi} = 1$) and only consider stable equilibria at which both A locus alleles are maintained and the a allele is initially fixed on the Y, region outlined. Here, selection in females can favour the A allele (panel A, $w_{aa}^{\varphi} = 0.85$, $w_{AA}^{\varphi} = 1.05$), favour the a allele (panel B, $w_{aa}^{\varphi} = 1.05$, $w_{AA}^{\varphi} = 0.85$), or be overdominant (panel C, $w_{aa}^{\varphi} = w_{AA}^{\varphi} = 0.6$). 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 $t^{\varphi} = \alpha_{\Delta}^{\varphi} = 0$.

$$\lambda_{Y',XY} = 1 + \frac{1}{4} V_A S_A^2 \frac{(r - R)}{rR} + O(\epsilon^3) \quad (2)$$

and

$$\lambda_{W',XY} = \lambda_{Y',XY} + (2\alpha_{\Delta}^{\delta} - 2\alpha_{\Delta}^{\varphi} + t^{\delta} - t^{\varphi}) (\hat{p}_Y^{\delta} - \hat{p}_X^{\delta}) / 2 + O(\epsilon^3) \quad (3)$$

360 where $V_A = \bar{p}(1 - \bar{p})$ is the variance in the equilibrium frequency of A and $S_A =$
 361 $(D^{\delta} + \alpha_{\Delta}^{\delta} + t^{\delta}) - (D^{\varphi} + \alpha_{\Delta}^{\varphi} + t^{\varphi})$ describes sex differences in selection for the A
 362 versus a across diploid selection, meiosis, and gametic competition. The diploid
 363 selection term, $D^{\varphi} = [\bar{p}s^{\varphi} + (1 - \bar{p})h^{\varphi}s^{\varphi}] - [\bar{p}h^{\varphi}s^{\varphi} + (1 - \bar{p})]$, is the difference
 364 in fitness between A and a alleles in diploids of sex $\varphi \in \{\varphi, \delta\}$, where \bar{p} is the

leading-order probability of mating with an *A*-bearing gamete from the opposite
366 sex (equation S.4). The difference in *A*-allele-frequency among Y-bearing sperm
versus X-bearing sperm is given by $\hat{p}_Y^\delta - \hat{p}_X^\delta = V_A(D^\delta - D^q + \alpha_\Delta^\delta - \alpha_\Delta^q + t^\delta -$
368 $t^q)(1 - 2r)/(2r)$.

The neo-sex-determining allele, *m*, will spread if $\lambda_{m,XY} > 1$. Equation (2)
370 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-
372 determining region (i.e., if $R < r$; note that $V_A S_A^2$ is strictly positive as long as
A is polymorphic). This echoes our tight linkage results above where a neo-Y
374 could never invade if $r \approx 0$. It is also consistent with the results of van Doorn
and Kirkpatrick (2007), who considered diploid selection only and also found that
376 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
378 selection.

With weak selection and no haploid selection ($t^q = \alpha_\Delta^q = 0$), the spread of
380 a neo-W is equivalent to the spread of a neo-Y ($\lambda_{W',XY} = \lambda_{Y',XY}$), such that het-
erogametic transitions (XY to ZW or ZW to XY) can also occur only if the neo-
382 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,
384 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
386 closely linked to the selected locus ($R > r$).

Equation (3) shows that, with weak selection, neo-W alleles can invade an XY
388 system for a large number of selective regimes. To clarify the parameter space un-
der which $\lambda_{W',XY} > 1$, we consider several special cases. Firstly, if the **A** locus is
390 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 no ancestral association be-
392 tween *A* alleles and sex chromosomes in males, $(\hat{p}_Y^\delta - \hat{p}_X^\delta) = 0$, see equation (S.5).
The second term in equation (3) therefore disappears and invasion depends only
394 on the sign of $(r - R)$, as in the case of the neo-Y. Indeed, invasion typically oc-

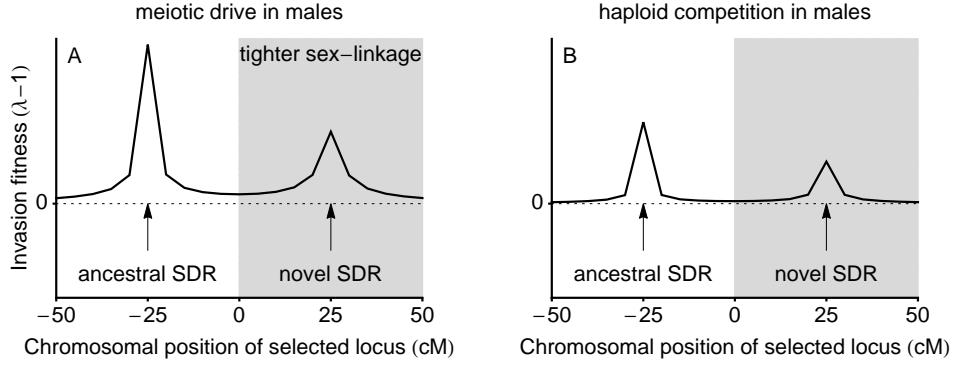


Figure 3: Ploidally-antagonistic selection allows a less tightly linked neo-W to invade. In panel A, male drive ($\alpha_{\Delta}^{\delta} = -1/20$, $t^{\delta} = \alpha_{\Delta}^{\delta} = 0$) opposes selection in diploids (no sex-differences: $s^{\delta} = 1/10$, $h^{\delta} = 7/10$), in which case the neo-sex-determining allele can invade regardless of linkage. In panel B, gametic competition in males ($t^{\delta} = -1/10$, $t^{\varphi} = \alpha_{\Delta}^{\varphi} = 0$) opposes selection in diploids (sex-differences: $s^{\delta} = 3/20$, $s^{\varphi} = 1/20$, $h^{\delta} = 7/10$), 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).

curs when the neo-W is more closely linked to the selected locus than the ancestral
396 sex-determining region (Figure 3).

Secondly, we can simplify the discussion of cases where invasion occurs de-
398 spite looser sex-linkage, $R > r$, by focusing 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
400 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
402 in one sex (e.g., during male meiosis only) and dominance coefficients are equal
in the two sexes, $h^{\varphi} = h^{\delta}$. When there is no gametic competition and meiotic
404 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 ($s^{\varphi}s^{\delta} > 0$, see Figure 3A
406 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
408 in male and female diploid selection and there are sex differences in selection of
one type (e.g., $s^{\varphi}(s^{\delta} - s^{\varphi}) > 0$, see Figure 3B). These special cases indicate that
410 neo-W invasion occurs for a relatively large fraction of the parameter space, even

if the neo-W uncouples the sex-determining locus from a locus under selection.

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	$h^\delta = h^q, t^q = t^\delta = \alpha_\Delta^q = 0$	$s^q s^\delta > 0$
female drive only	$h^\delta = h^q, t^q = t^\delta = \alpha_\Delta^\delta = 0$	$s^q s^\delta > 0$
sperm competition only	$h^\delta = h^q, t^q = \alpha_\Delta^q = \alpha_\Delta^\delta = 0$	$s^q(s^\delta - s^q) > 0$
egg competition only	$h^\delta = h^q, t^\delta = \alpha_\Delta^q = \alpha_\Delta^\delta = 0$	$s^\delta(s^q - s^\delta) > 0$

412 Previous research suggests that when the ancestral sex-determining locus is
413 linked to a locus that experiences haploid selection (e.g., meiotic drive), a new,
414 unlinked sex-determining locus invades in order to restore equal sex ratios (Koziel-
415 ska et al. 2010). Consider, for example, the case where the A locus is linked to the
416 ancestral-SDR ($r < 1/2$) and experiences meiotic drive in males only (e.g., during
417 spermatogenesis but not during oogenesis, $\alpha_\Delta^\delta \neq 0, \alpha_\Delta^q = 0$), without gametic
418 competition ($t^q = t^\delta = 0$). In this case, the zygotic sex ratio can be initially biased
419 only if the ancestral sex-determining system is XY (Figure 4B). We might there-
420 fore expect a difference in the potential for XY to ZW and ZW to XY transitions.
421 However, to leading order with selection weak relative to recombination, we find
422 that sex ratio selection favours the spread of a neo-W (through the first terms in
423 table 2) by an amount that is equal in magnitude to the fitness effects of alleles
424 associated with new sex-determining alleles (second terms in table 2). Thus, inva-
425 sion by a neo-W into an XY system and invasion by a neo-Y into a ZW system
426 occur under the same conditions ($\lambda_{Y',XY} = \lambda_{W',ZW}$ and $\lambda_{Y',ZW} = \lambda_{W',XY}$, at least
427 to order ϵ^2). For example, in Figure 4B neo-W alleles invade an ancestrally-XY
428 system where females are initially rare because the ancestral-Y is associated with
429 a male meiotic drive allele. However, Figure 4A shows that a neo-Y can invade
430 an ancestrally-ZW system under the same conditions. In fact, where $R < 1/2$ the
431 neo-Y becomes associated with the male meiotic drive allele such that the zygotic
432 sex ratio evolves to become biased towards males.

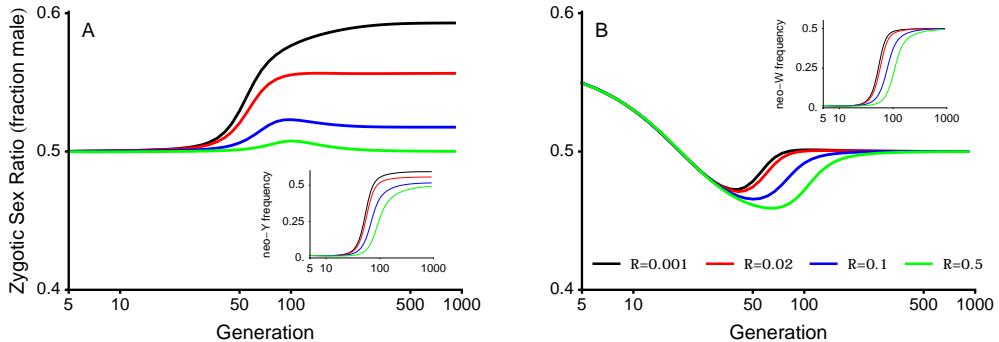


Figure 4: Fisherian sex-ratio selection alone is not a good predictor of turnover between sex-determining systems. In this figure, selection is ploidally antagonistic with haploid selection favouring the a allele during male meiosis. In panel A, male drive in an ancestral ZW system has no effect on the 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: $s^{\varnothing} = s^{\delta} = 0.2$, $h^{\varnothing} = h^{\delta} = 0.7$, $t^{\varnothing} = t^{\delta} = \alpha_{\Delta}^{\varnothing} = 0$, $\alpha_{\Delta}^{\delta} = -0.1$, $r = 0.02$.

The green curves in Figure 4 show transitions between male and female heterogamety even though the new sex-determining region is unlinked to a locus that experiences haploid and diploid selection. We use these green curves 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 sex ratio is ancestrally male biased. In Figure 4A, an unlinked neo-Y spreads despite the fact that the ancestral zygotic sex ratio is even. In this case, 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 ($\hat{p}_W^{\varnothing} - \hat{p}_Z^{\varnothing} > 0$, 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. 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. A freely recombining neo-Y ($R = 1/2$) is equally likely to be segregate with the A or a allele and is therefore unaffected by male meiotic drive. Thus, a key factor in explaining why heterogametic transitions can occur when

$R > r$ is that the neo-SDR determines sex in the diploid phase but recombination
450 occurs before any subsequent haploid selection.

Environmental sex determination

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

462 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
464 on weak selection here. Assuming weak selection, the spread of the new sex-
determining region is given by

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

466 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
468 develop as females and half as males ($k = 1/2$, creating equal sex ratios), the

spread of which is given by

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

470 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
 472 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
 474 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
 476 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
 478 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
 480 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
 482 the same manner as a neo- W .

Significantly, equation (5) is the same whether ESD is invading an ancestrally
 484 XY or ZW system (because $\lambda_{Y',XY} = \lambda_{W',ZW}$ and $\lambda_{W',XY} = \lambda_{Y',ZW}$). Thus, Fisherian sex-ratio selection alone does not explain the invasion of ESD under weak
 486 selection because the sex ratio is only biased by male haploid selection when the
 ancestral sex-determination system is XY. Specifically, with male haploid selec-
 488 tion, 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
 490 ESD may not invade, even if the sex ratio is initially biased (e.g., with drive in
 males only, $r < 1/2$, $h^\varphi = h^\delta$, and $s^\varphi s^\delta < 0$, such that $\lambda_{W',XY} < 1$, see Table 3).

⁴⁹² **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). 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 system. Firstly, we show that selection (including sexually-antagonistic selection) on loci within or near the non-recombinating region of the ancestral sex-determining region can favour heterogametic transitions (XY to ZW or ZW to XY) to new sex-determining systems that are less closely linked to the selected loci (e.g., see Figure 1). Secondly, assuming that selection is weak relative to recombination ('weak selection'), 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-biased zygotic sex-ratio. 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 ga-

metes, 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 alleles that are associated with the neo-sex-determining allele, and these selection pressures are predicted to often be of equal magnitude when selection is weak.

We have shown 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 $|D^\delta - D^0| << |\alpha_\Delta^\delta - \alpha_\Delta^0 + t^\delta - t^0|$ 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

552 could drive transitions between dioecy and hermaphroditism, which are frequent
553 in plants (Käfer et al. 2017, Goldberg et al. 2017).

554 In support of their role in sex chromosome turnover, genes expected to be under
555 sexually-antagonistic selection (e.g., those causing bright male colouration) have
556 been found on recently derived sex chromosomes (Lindholm and Breden 2002,
557 Tripathi et al. 2009, Ser et al. 2010). Our results show that, if loci experiencing
558 overdominance and/or sexually-antagonistic selection can be identified in close
559 linkage with the ancestral sex-determining locus (rather than only the novel sex-
560 determining locus), then they could also be implicated in driving heterogametic
561 transitions between sex-determination systems. In addition, we show haploid se-
562 lection on loci around either the ancestral- or the novel-sex-determining regions
563 could have had a role in driving sex chromosome turnover. A recent transcrip-
564 tome analysis in *Rumex*, suggests a role for gametic competition in the evolution
565 of sex-determination systems, showing that Y-linked genes are have higher expres-
566 sion in haploid pollen than autosomal genes ([check this is accurate](#)). Interestingly,
567 haploid-expression is also more common on the autosome that is orthologous to the
568 sex chromosomes in closely related species suggesting that new sex chromosomes
569 may have been favoured through their association with haploid selected alleles on
570 these chromosomes ([Sandler et al., 2017, Personal Communication](#)).

571 We assume that sex-determining alleles do not experience direct selection ex-
572 cept via their associations with sex and selected alleles. However, in some cases,
573 there may be significant degeneration around the sex-limited allele (Y or W) in the
574 ancestral sex-determining region because recessive deleterious mutations and/or
575 deletions accumulate around the Y or W sex-determining regions (Rice 1996,
576 Charlesworth and Charlesworth 2000, Bachtrog 2006, Marais et al. 2008). During
577 heterogametic transitions (XY to ZW or ZW to XY), but not homogametic transi-
578 tions (XY to XY or ZW to ZW), any recessive deleterious alleles linked to the Y or
579 W are revealed to selection in YY or WW individuals (Bachtrog et al. 2014). This
580 phenomenon was studied by van Doorn and Kirkpatrick (2010), who found that
581 degeneration can prevent fixation of a neo-W or a neo-Y allele, leading to a mixed

582 sex-determination system where the ancestral and new sex-determining loci are
583 both segregating. However, they noted that very rare recombination events around
584 the ancestral sex-determining region can allow these heterogametic transitions to
585 complete. Degeneration around the Y or W could explain why heterogametic transi-
586 tions are not observed to be much more common than homogametic transitions
587 despite the fact that our models demonstrate that they are favoured under a wider
588 range of conditions. For example, Vicoso and Bachtrog (2015) found a dozen
589 sex chromosome configurations among Dipteran species but only one transition
590 between male and female heterogametey.

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

We have shown that tight sex-linkage and haploid selection can drive previ-
608 ously unexpected transitions between sex-determination systems. In particular,
610 both can select for neo-sex-determining loci that are more loosely linked. In ad-
dition, haploid selection alone can cause transitions analogous to those caused by

612 purely sexually-antagonistic selection, eliminating the need for differences in se-
613 lection between male and female diploids. Perhaps counterintuitively, transitions
614 involving haploid selection can be driven by sex-ratio selection or cause sex-ratio
615 biases to evolve. We conclude that haploid selection should be considered as a
616 pivotal factor driving transitions between sex-determination systems. Overall, our
617 results suggest several new scenarios under which new sex-determination systems
618 are favoured, which could help to explain why the evolution of sex-determination
systems is so dynamic.

620 References

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Appendix

876 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^φ and y_i^φ . The superscript $\varphi \in \{\delta, \varphi\}$ specifies the sex of the diploid that the gamete came from. The subscript $i \in \{1, 2, 3, 4\}$ specifies the genotype at the selected locus **A** and at the novel sex-determining locus **M**, where $1 = AM$, $2 = aM$, $3 = Am$, and $4 = am$. The 884 gamete frequencies from each sex sum to one, $\sum_i x_i^\varphi + y_i^\varphi = 1$.

Competition then occurs among gametes of the same sex (e.g., among eggs 886 and among sperm separately) according to the genotype at the **A** locus ($w_1^\varphi = w_3^\varphi = w_A^\varphi$, $w_2^\varphi = w_4^\varphi = w_a^\varphi$, see Table 1). The genotype frequencies after gametic 888 competition are $x_i^{\varphi,s} = w_i x_i^\varphi / \bar{w}_H^\varphi$ and $y_i^{\varphi,s} = w_i y_i^\varphi / \bar{w}_H^\varphi$, where $\bar{w}_H^\varphi = \sum_i w_i x_i^\varphi + w_i y_i^\varphi$ is the mean fitness of male ($\varphi = \delta$) or female ($\varphi = \varphi$) gametes.

890 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 892 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 894 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 896 genotype ji ; for simplicity, we use xx_{ij} and yy_{ij} with $i \neq j$ to denote the average of these frequencies, $xx_{ij} = (x_i^{\varphi,s} x_j^{\delta,s} + x_j^{\varphi,s} x_i^{\delta,s})/2$ and $yy_{ij} = (y_i^{\varphi,s} y_j^{\delta,s} + y_j^{\varphi,s} y_i^{\delta,s})/2$.

898 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 900 k_{bc} . Therefore, the frequencies of XX females are given by $xx_{ij}^\varphi = k_{bc} xx_{ij}$, XY females are given by $xy_{ij}^\varphi = k_{bc} xy_{ij}$, and YY females are given by $yy_{ij}^\varphi = k_{bc} yy_{ij}$. 902 Similarly, XX male frequencies are $xx_{ij}^\delta = (1 - k_{bc}) xx_{ij}$, XY male frequencies are $xy_{ij}^\delta = (1 - k_{bc}) xy_{ij}$, and YY males frequencies are $yy_{ij}^\delta = (1 - k_{bc}) yy_{ij}$. This

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

Selection among diploids then occurs according to the diploid genotype at the
 911 **A** locus, $l \in \{AA, Aa, aa\}$, for an individual of type ij (see Table 1). The diploid
 912 frequencies after selection in sex $\hat{\varphi}$ are given by $xx_{ij}^{\hat{\varphi},s} = w_l^{\hat{\varphi}} xx_{ij}/\bar{w}^{\hat{\varphi}}$, $xy_{ij}^{\hat{\varphi},s} =$
 913 $w_l^{\hat{\varphi}} xy_{ij}/\bar{w}^{\hat{\varphi}}$, and $yy_{ij}^{\hat{\varphi},s} = w_l^{\hat{\varphi}} yy_{ij}/\bar{w}^{\hat{\varphi}}$, where $\bar{w}^{\hat{\varphi}} = \sum_{i=1}^4 \sum_{j=1}^4 w_l^{\hat{\varphi}} xx_{ij} + w_l^{\hat{\varphi}} xy_{ij} +$
 914 $w_l^{\hat{\varphi}} yy_{ij}$ is the mean fitness of individuals of sex $\hat{\varphi}$.

915 Finally, these diploids undergo meiosis to produce the next generation of ga-
 916 metes. Recombination and sex-specific meiotic drive occur during meiosis. Here,
 917 we allow any relative locations for the SDR, **A**, and **M** loci by using three param-
 918 eters to describe the recombination rates between them. R is the recombination
 919 rate between the **A** locus and the **M** locus, ρ is the recombination rate between
 920 the **M** locus and the **X** locus, and r is the recombination rate between the **A** locus
 921 and the **X** locus. Table S.1 shows replacements that can be made for each possi-
 922 ble ordering of the loci assuming that there is no cross-over interference. During
 923 meiosis in sex $\hat{\varphi}$, meiotic drive occurs such that, in Aa heterozygotes, a fraction
 924 $\alpha^{\hat{\varphi}}$ of gametes produced carry the A allele and $(1 - \alpha^{\hat{\varphi}})$ carry the a allele.

Table S.1: Substitutions for different loci orders assuming no interference.

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

925 Among gametes from sex $\hat{\varphi}$, the frequencies of haplotypes (before gametic

competition) in the next generation are given by

$$\begin{aligned}
x_1^{\phi'} = & xx_{11}^{\phi,s} + xx_{13}^{\phi,s}/2 + (xx_{12}^{\phi,s} + xx_{14}^{\phi,s})\alpha^{\phi} \\
& - R(xx_{14}^{\phi,s} - xx_{23}^{\phi,s})\alpha^{\phi} \\
& + (xy_{11}^{\phi,s} + xy_{13}^{\phi,s})/2 + (xy_{12}^{\phi,s} + xy_{14}^{\phi,s})\alpha^{\phi} \\
& - r(xy_{12}^{\phi,s} - xy_{21}^{\phi,s})\alpha^{\phi} - \rho(xy_{13}^{\phi,s} - xy_{31}^{\phi,s})/2 \\
& + [-(R+r+\rho)xy_{14}^{\phi,s} + (R+\rho-r)xy_{41}^{\phi,s} \\
& + (R+r-\rho)xy_{23}^{\phi,s} + (R+\rho-r)xy_{32}^{\phi,s}] \alpha^{\phi}/2
\end{aligned} \tag{S.1a}$$

$$\begin{aligned}
x_2^{\phi'} = & xx_{22}^{\phi,s} + xx_{24}^{\phi,s}/2 + (xx_{12}^{\phi,s} + xx_{23}^{\phi,s})\alpha^{\phi} \\
& - R(xx_{23}^{\phi,s} - xx_{14}^{\phi,s})\alpha^{\phi} \\
& (xy_{22}^{\phi,s} + xy_{24}^{\phi,s})/2 + (xy_{21}^{\phi,s} + xy_{23}^{\phi,s})(1 - \alpha^{\phi}) \\
& - r(xy_{21}^{\phi,s} - xy_{12}^{\phi,s})(1 - \alpha^{\phi}) - \rho(xy_{24}^{\phi,s} - xy_{42}^{\phi,s})/2 \\
& + [-(R+r+\rho)xy_{23}^{\phi,s} + (R+\rho-r)xy_{32}^{\phi,s} \\
& + (R+r-\rho)xy_{14}^{\phi,s} + (R+\rho-r)xy_{41}^{\phi,s}] (1 - \alpha^{\phi})/2
\end{aligned} \tag{S.1b}$$

$$\begin{aligned}
x_3^{\phi'} = & xx_{33}^{\phi,s} + xx_{13}^{\phi,s}/2 + (xx_{23}^{\phi,s} + xx_{34}^{\phi,s})\alpha^{\phi} \\
& - R(xx_{23}^{\phi,s} - xx_{14}^{\phi,s})\alpha^{\phi} \\
& (xy_{33}^{\phi,s} + xy_{31}^{\phi,s})/2 + (xy_{32}^{\phi,s} + xy_{34}^{\phi,s})\alpha^{\phi} \\
& - r(xy_{34}^{\phi,s} - xy_{43}^{\phi,s})\alpha^{\phi} - \rho(xy_{31}^{\phi,s} - xy_{13}^{\phi,s})/2 \\
& + [-(R+r+\rho)xy_{32}^{\phi,s} + (R+\rho-r)xy_{23}^{\phi,s} \\
& + (R+r-\rho)xy_{41}^{\phi,s} + (R+\rho-r)xy_{14}^{\phi,s}] \alpha^{\phi}/2
\end{aligned} \tag{S.1c}$$

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

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

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

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

$$\begin{aligned}
& + [-(R + r + \rho)xy_{23}^{\phi,s} + (R + \rho - r)xy_{32}^{\phi,s}] \\
& + (R + r - \rho)xy_{14}^{\phi,s} + (R + \rho - r)xy_{41}^{\phi,s}] \alpha^\phi / 2
\end{aligned} \tag{S.1g}$$

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

928

The full system is therefore described by 16 recurrence equations (three diallelic
930 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
932 ancestral *XY* sex-determining system, there are *XX* males, *XY* females, or *YY*
females ($x_3^{\delta} = x_4^{\delta} = y_4^{\delta} = y_3^{\delta} = y_i^{\delta} = 0$). In this case, the system only involves six
934 recursion equations, which we assume below to calculate the equilibria.

Resident equilibria and stability

936 In the resident population (allele *M* fixed), we follow the frequency of *A* in X-
bearing female gametes, p_X^{φ} , and X-bearing male gametes, p_X^{δ} , and Y-bearing male
938 gametes, p_Y^{δ} . 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 deter-
940 mine the frequencies of the six resident gamete types: $x_1^{\varphi} = \hat{p}_X^{\varphi}$, $x_2^{\varphi} = 1 - \hat{p}_X^{\varphi}$,
 $x_1^{\delta} = (1 - q)\hat{p}_X^{\delta}$, $x_2^{\delta} = (1 - q)(1 - \hat{p}_X^{\delta})$, $y_1^{\delta} = q\hat{p}_Y^{\delta}$, and $y_2^{\delta} = q(1 - \hat{p}_Y^{\delta})$. Mean
942 fitnesses in the resident population are given in table S.2.

Various forms of selection can maintain a polymorphism at the **A** locus, in-
944 cluding sexually antagonistic selection, overdominance, conflicts between diploid
selection and selection upon haploid genotypes (ploidally antagonistic selection,
946 Immler et al. 2012), or a combination of these selective regimes. [add reference or](#)
[say "see below"](#)

948 In particular special cases, e.g., no sex-differences in selection or meiotic drive

Table S.2: Mean fitnesses and zygotic sex ratio in the resident population (M fixed, XY sex determination).

Sex & Life Cycle Stage	Mean Fitness
female gametes (\bar{w}_H^{\varnothing})	$p_X^{\varnothing} w_A^{\varnothing} + (1 - p_X^{\varnothing}) w_a^{\varnothing}$
male gametes (\bar{w}_H^{δ})	$\bar{p}^{\delta} w_A^{\delta} + (1 - \bar{p}^{\delta}) w_a^{\delta}$
females (\bar{w}_H^{\varnothing})	$(1 - \zeta)^{-1} [p_X^{\varnothing} w_A^{\varnothing} p_X^{\delta} w_A^{\delta} w_{AA}^{\varnothing} + (1 - p_X^{\varnothing}) w_a^{\varnothing} p_X^{\delta} w_A^{\delta} w_{Aa}^{\varnothing} + p_X^{\varnothing} w_A^{\varnothing} (1 - p_X^{\delta}) w_a^{\delta} w_{Aa}^{\varnothing} + (1 - p_X^{\varnothing}) w_a^{\varnothing} (1 - p_X^{\delta}) w_a^{\delta} w_{aa}^{\varnothing}] / (\bar{w}_H^{\varnothing} \bar{w}_H^{\delta})$
males (\bar{w}_H^{δ})	$\zeta^{-1} [p_X^{\varnothing} w_A^{\varnothing} p_Y^{\delta} w_A^{\delta} w_{AA}^{\delta} + (1 - p_X^{\varnothing}) w_a^{\varnothing} p_Y^{\delta} w_A^{\delta} w_{Aa}^{\delta} + p_X^{\varnothing} w_A^{\varnothing} (1 - p_Y^{\delta}) w_a^{\delta} w_{Aa}^{\delta} + (1 - p_X^{\varnothing}) w_a^{\varnothing} (1 - p_Y^{\delta}) w_a^{\delta} w_{aa}^{\delta}] / (\bar{w}_H^{\varnothing} \bar{w}_H^{\delta})$
fraction zygotes male (ζ)	$q [p_Y^{\delta} w_A^{\delta} + (1 - p_Y^{\delta}) w_a^{\delta}] / \bar{w}_H^{\delta}$

($s^{\delta} = s^{\varnothing}$, $h^{\delta} = h^{\varnothing}$, and $\alpha^{\delta} = \alpha^{\varnothing} = 1/2$), the equilibrium allele frequency and stability 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.

954 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:

$$(A) \quad \hat{p}_Y^\delta = 0, \quad \hat{q} = \frac{1}{2} \left(1 - \alpha_\Delta^\delta \frac{w_{Aa}^\delta \phi}{w_{Aa}^\delta \phi + w_{aa}^\delta \psi} \right), \quad (\text{S.2a})$$

$$\hat{p}_X^\delta = \frac{w_a^\delta \phi}{w_a^\delta \phi + w_A^\delta \psi}, \quad \hat{p}_X^\delta = \frac{(1 + \alpha_\Delta^\delta) w_{Aa}^\delta \phi}{(1 + \alpha_\Delta^\delta) w_{Aa}^\delta \phi + w_{aa}^\delta \psi}$$

$$(A') \quad \hat{p}_Y^\delta = 1, \quad \hat{q} = \frac{1}{2} \left(1 + \alpha_\Delta^\delta \frac{w_{Aa}^\delta \phi'}{w_{Aa}^\delta \phi' + w_{AA}^\delta \psi'} \right), \quad (\text{S.2b})$$

$$\hat{p}_X^\delta = 1 - \frac{w_A^\delta \phi'}{w_A^\delta \phi' + w_a^\delta \psi'}, \quad \hat{p}_X^\delta = 1 - \frac{(1 - \alpha_\Delta^\delta) w_{Aa}^\delta \phi'}{(1 - \alpha_\Delta^\delta) w_{Aa}^\delta \phi' + w_{AA}^\delta \psi'}$$

$$(B) \quad \hat{p}_Y^\delta = 0, \quad \hat{p}_X^\delta = 1, \quad \hat{p}_X^\delta = 1, \quad \hat{q} = (1 - \alpha_\Delta^\delta)/2 \quad (\text{S.2c})$$

$$(B') \quad \hat{p}_Y^\delta = 1, \quad \hat{p}_X^\delta = 0, \quad \hat{p}_X^\delta = 0, \quad \hat{q} = (1 + \alpha_\Delta^\delta)/2 \quad (\text{S.2d})$$

$$\begin{aligned} \phi &= (1 + \alpha_\Delta^\delta) w_A^\delta w_{Aa}^\delta [w_a^\delta w_{aa}^\delta + (1 + \alpha_\Delta^\delta) w_a^\delta w_{Aa}^\delta] / 2 - w_a^\delta w_a^\delta w_{aa}^\delta w_{aa}^\delta \\ \psi &= (1 - \alpha_\Delta^\delta) w_a^\delta w_{Aa}^\delta [w_a^\delta w_{aa}^\delta + (1 + \alpha_\Delta^\delta) w_A^\delta w_{Aa}^\delta] / 2 - (1 + \alpha_\Delta^\delta) w_A^\delta w_A^\delta w_{Aa}^\delta w_{AA}^\delta \\ \phi' &= (1 - \alpha_\Delta^\delta) w_a^\delta w_{Aa}^\delta [w_A^\delta w_{AA}^\delta + (1 - \alpha_\Delta^\delta) w_a^\delta w_{Aa}^\delta] / 2 - w_A^\delta w_A^\delta w_{AA}^\delta w_{AA}^\delta \\ \psi' &= (1 + \alpha_\Delta^\delta) w_A^\delta w_{Aa}^\delta [w_A^\delta w_{AA}^\delta + (1 - \alpha_\Delta^\delta) w_a^\delta w_{Aa}^\delta] / 2 - (1 - \alpha_\Delta^\delta) w_a^\delta w_a^\delta w_{Aa}^\delta w_{aa}^\delta \end{aligned}$$

A fifth equilibrium (*C*) also exists where *A* is present at an intermediate frequency
962 on the Y chromosome ($0 < \hat{p}_Y^\delta < 1$). However, equilibrium (*C*) is never locally
stable when $r \approx 0$ and is therefore not considered further. Thus, the Y can either
964 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'*)
966 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
968 interchanged, we discuss only equilibria (*A*) and (*B*), in which the Y is fixed for the
a allele. If there is no haploid selection ($\alpha_\Delta^\delta = 0, w_A^\delta = w_a^\delta = 1$), these equilibria
970 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
972 the ‘small parameter theory’ (Karlin and McGregor 1972*a;b*), these stability prop-

974 erties 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
 974 be stably fixed on the Y we need $\bar{w}_{Y_a}^{\delta} > \bar{w}_{YA}^{\delta}$ where $\bar{w}_{Y_a}^{\delta} = w_a^{\delta}[\hat{p}_X^{\varphi}(1-\alpha_{\Delta}^{\delta})w_A^{\varphi}w_{Aa}^{\delta} +$
 976 $(1 - \hat{p}_X^{\varphi})w_a^{\varphi}w_{aa}^{\delta}]$ and $\bar{w}_{YA}^{\delta} = w_A^{\delta}[\hat{p}_X^{\varphi}w_A^{\varphi}w_{AA}^{\delta} + (1 - \hat{p}_X^{\varphi})(1 + \alpha_{\Delta}^{\delta})w_a^{\varphi}w_{Aa}^{\delta}]$. That is,
 Y- a haplotypes must have higher fitness than Y- A haplotypes. Substituting in \hat{p}_X^{φ}
 978 from equation (S.2), fixation of the a allele on the Y requires that $\gamma_i > 0$ where
 $\gamma_{(A)} = w_a^{\delta}[(1 - \alpha_{\Delta}^{\delta})w_{Aa}^{\delta}\phi + w_{aa}^{\delta}\psi] - w_A^{\delta}[w_{AA}^{\delta}\phi + (1 + \alpha_{\Delta}^{\delta})w_{Aa}^{\delta}\psi]$ for equilibrium
 980 (A) and $\gamma_{(B)} = (1 - \alpha_{\Delta}^{\delta})w_a^{\delta}w_{Aa}^{\delta} - w_A^{\delta}w_{AA}^{\delta}$ for equilibrium (B). Stability of a poly-
 982 morphism 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
 982 equilibrium (A) is not, as it requires $\psi < 0$.

984 Selection weak relative to recombination (weak selection)

986 Here, we assume that selection and meiotic drive are weak relative to recombina-
 tion ($s^{\varphi}, t^{\varphi}, \alpha_{\Delta}^{\varphi}$ of order ϵ). The maintenance of a polymorphism at the A locus
 then requires that

$$0 < -[(1 - h^{\varphi})s^{\varphi} + (1 - h^{\delta})s^{\delta} + t^{\varphi} + t^{\delta} + \alpha_{\Delta}^{\varphi} + \alpha_{\Delta}^{\delta}] \quad (\text{S.3})$$

and $0 < h^{\varphi}s^{\varphi} + h^{\delta}s^{\delta} + t^{\varphi} + t^{\delta} + \alpha_{\Delta}^{\varphi} + \alpha_{\Delta}^{\delta}.$

988 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
 990 frequencies of A in each type of gamete are the same ($\hat{p}_X^{\varphi} = \hat{p}_X^{\delta} = \hat{p}_Y^{\varphi} = \bar{p}$) and
 given, to leading order, by

$$\bar{p} = \frac{h^{\varphi}s^{\varphi} + h^{\delta}s^{\delta} + t^{\varphi} + t^{\delta} + \alpha_{\Delta}^{\varphi} + \alpha_{\Delta}^{\delta}}{(2h^{\varphi} - 1)s^{\varphi} + (2h^{\delta} - 1)s^{\delta}} + O(\epsilon). \quad (\text{S.4})$$

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

$$\begin{aligned}\hat{p}_X^\delta - \hat{p}_X^q &= V_A (D^\delta - D^q + \alpha_\Delta^\delta - \alpha_\Delta^q) + O(\epsilon^2) \\ \hat{p}_Y^\delta - \hat{p}_X^q &= V_A [D^\delta - D^q + \alpha_\Delta^\delta - \alpha_\Delta^q + (1-2r)(t^\delta - t^q)] / 2r + O(\epsilon^2) \quad (\text{S.5}) \\ \hat{p}_Y^\delta - \hat{p}_X^\delta &= V_A (D^\delta - D^q + \alpha_\Delta^\delta - \alpha_\Delta^q + t^\delta - t^q) (1-2r) / 2r + O(\epsilon^2)\end{aligned}$$

where $V_A = \bar{p}(1-\bar{p})$ is the variance in the frequency of A and $D^\delta = [\bar{p}s^\delta + (1-\bar{p})h^\delta s^\delta] - [\bar{p}h^\delta s^\delta + (1-\bar{p})]$ corresponds to the difference in fitness between A and a alleles in diploids of sex $\delta \in \{\text{♀}, \text{♂}\}$ (\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, $q = 1/2 + \alpha_\Delta^\delta (\hat{p}_Y^\delta - \hat{p}_X^\delta)/2 + O(\epsilon^3)$. Without gametic competition or drive ($\alpha_\Delta^\delta = t^\delta = 0$) our results reduce to those of van Doorn and Kirkpatrick (2007).

1002 Invasion conditions

Cover the other parts of the characteristic polynomial here. Waiting for Sally's proof!

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).

The general conditions for the invasion of a neo-sex-determining allele are given in the main text, in terms of the growth rates of the mutant haplotypes in

1016 the absence of recombination (λ_{mi}) and the rate that recombination destroys them
 χ_{mi}). For tight linkage between the ancestral sex-determining locus and the se-
1018 lected locus we can calculate these terms explicitly (see below). For weak selection
we can take a Taylor series of the leading eigenvalue. The leading eigenvalue, λ ,
1020 for any k , is given up to order ϵ^2 by equation (4).

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

1022 Here, we explore the conditions under which a neo-W invades an XY system as-
suming that the A locus is initially in tight linkage with the ancestral sex-determining
1024 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*
1026 notebook for proof).

Starting with the simpler equilibrium (B), the terms of the characteristic poly-
1028 nomial are

$$\lambda_{mA} = [w_A^\delta(1 + \alpha_\Delta^\delta)]^{-1} \frac{w_A^\varphi}{w_A^\varphi} \frac{[w_A^\delta(1 + \alpha_\Delta^\delta)w_{AA}^\varphi + w_a^\delta(1 - \alpha_\Delta^\delta)w_{Aa}^\varphi(1 + \alpha_\Delta^\varphi)]}{2w_{AA}^\varphi} \quad (\text{S.6a})$$

$$\lambda_{ma} = [w_A^\delta(1 + \alpha_\Delta^\delta)]^{-1} \frac{w_a^\varphi}{w_A^\varphi} \frac{[w_A^\delta(1 + \alpha_\Delta^\delta)w_{Aa}^\varphi(1 - \alpha_\Delta^\varphi) + w_a^\delta(1 - \alpha_\Delta^\delta)w_{aa}^\varphi]}{2w_{AA}^\varphi} \quad (\text{S.6b})$$

$$\chi_{mA} = \frac{1}{2} [w_A^\delta(1 + \alpha_\Delta^\delta)]^{-1} \frac{w_A^\varphi}{w_A^\varphi} \frac{[w_a^\delta(1 - \alpha_\Delta^\delta)w_{Aa}^\varphi(1 + \alpha_\Delta^\varphi)]}{w_{AA}^\varphi} R \quad (\text{S.6c})$$

$$\chi_{ma} = \frac{1}{2} [w_A^\delta(1 + \alpha_\Delta^\delta)]^{-1} \frac{w_a^\varphi}{w_A^\varphi} \frac{[w_A^\delta(1 + \alpha_\Delta^\delta)w_{Aa}^\varphi(1 - \alpha_\Delta^\varphi)]}{w_{AA}^\varphi} R \quad (\text{S.6d})$$

Haploid selection impacts the spread of neo-W haplotypes in three ways. Firstly,
1030 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
1032 drive in males. Specifically, at equilibrium (B), the fraction female is $1 - \zeta =$
 $w_A^\delta(1 + \alpha_\Delta^\delta)/(2\bar{w}_H^\delta)$ where $2\bar{w}_H^\delta = [w_a^\delta(1 - \alpha_\Delta^\delta) + w_A^\delta(1 + \alpha_\Delta^\delta)]$ has been canceled

1034 out in equations (S.6) to leave the term $[w_A^\delta(1 + \alpha_\Delta^\delta)]^{-1}$. Male biased sex ratios
 1035 facilitate the spread of a neo-W because neo-W alleles cause the zygotes that carry
 1036 them to develop as the rarer, female, sex.

1037 Secondly, haploid selection in females selects on neo-W haplotypes directly. At
 1038 equilibrium (B), the fitness of female gametes under the ancestral sex-determining
 1039 system is $w_A^?$ such that the relative fitnesses of neo-W- A and neo-W- a haplotypes
 1040 during female gametic competition are $w_A^?/w_A^?$ and $w_a^?/w_A^?$ (see terms in equation
 1041 S.6). Meiotic drive in females will also change the proportion of gametes that carry
 1042 the A versus a alleles, which will be produced by heterozygous females in propor-
 1043 tions $(1 + \alpha_\Delta^?)$ /2 and $(1 - \alpha_\Delta^?)$ /2, respectively. These terms are only associated with
 1044 heterozygous females, i.e., they are found alongside $w_{Aa}^?$.

1045 Thirdly, haploid selection in males affects the diploid genotypes of females
 1046 by altering the allele frequencies in the male gametes that female gametes pair
 1047 with. At equilibrium (B), neo-W female gametes will mate with X- A male ga-
 1048 metes with probability $w_A^\delta(1 + \alpha_\Delta^\delta)/(2\bar{w}_H^\delta)$ and Y- a male gametes with probability
 1049 $w_a^\delta(1 - \alpha_\Delta^\delta)/(2\bar{w}_H^\delta)$, where the $2\bar{w}_H^\delta$ terms have been canceled in equation (S.6)
 1050 (as mentioned above). Thus, for example, neo-W- A haplotypes are found in AA
 1051 female diploids with probability $w_A^\delta(1 + \alpha_\Delta^\delta)/(2\bar{w}_H^\delta)$ (first term in square brack-
 1052 ets in the numerator of equation S.6a) and in Aa female diploids with probability
 1053 $w_a^\delta(1 - \alpha_\Delta^\delta)/(2\bar{w}_H^\delta)$ (see equation S.6c and the second term in square brackets in
 1054 the numerator of equation S.6a).

1055 The other terms in equations (S.6) are more easily interpreted if we assume that
 1056 there is no haploid selection in either sex, in which case $\lambda_{mA} > 1$ when $w_{Aa}^? > w_{AA}^?$
 1057 and $\lambda_{ma} > 1$ when $(w_{Aa}^? + w_{aa}^?)/2 > w_{AA}^?$. These conditions cannot be met under
 1058 purely sexually-antagonistic selection, where A is directionally favoured in females
 1059 ($w_{AA}^? > w_{Aa}^? > w_{aa}^?$) and a is directionally favoured in males ($w_{AA}^\delta > w_{Aa}^\delta > w_{aa}^\delta$).
 1060 Essentially, the X is then already as specialized as possible for the female beneficial
 1061 allele (A is fixed on the X), and the neo-W often makes daughters with the Y- a
 1062 haplotype, increasing the flow of a alleles into females, which reduces the fitness
 1063 of those females.

1064 If selection doesn't uniformly favour A in females, however, neo-W- A haplo-
 types and/or neo-W- a haplotypes can spread ($\lambda_{mA} > 1$ and/or $\lambda_{ma} > 1$) at this
 1066 equilibrium. A neo-W can spread alongside the A allele ($\lambda_{mA} > 1$), despite the
 fact that a neo-W brings Y- a haplotypes into females, when $w_{Aa}^{\varphi} > w_{AA}^{\varphi}$, as stated
 1068 above. 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 (i.e., to keep A fixed on the X),
 1070 $X-a$ cannot be overly favoured in females and $X-A$ must be sufficiently favoured
 in males (for example, by overdominance in males, remembering that a is fixed
 1072 on the Y). Specifically, from the stability conditions for equilibrium (B), we must
 have $w_{Aa}^{\varphi} < 2w_{AA}^{\varphi}$ and $w_{Aa}^{\delta}/[(w_{aa}^{\delta} + w_{Aa}^{\delta})/2] > w_{Aa}^{\varphi}/w_{AA}^{\varphi}$.

1074 Still considering $w_{Aa}^{\varphi} > w_{AA}^{\varphi}$, the neo-W can also spread alongside the a allele
 ($\lambda_{ma} > 1$) if w_{aa}^{φ} is large enough such that $(w_{Aa}^{\varphi} + w_{aa}^{\varphi})/2 > w_{AA}^{\varphi}$. This can occur
 1076 with overdominance or directional selection for a in females (Figure 2B,C). In this
 case, a is favoured in females (comparing Aa to AA genotypes in females) but A
 1078 is fixed on the X due to selection in males. The neo-W- a haplotype can spread
 because it produces females with higher fitness Aa and aa genotypes.

1080 Similar equations can be derived for equilibrium (A) by substituting the equi-
 librium allele frequencies into Table 2

$$\lambda_{mA} = \frac{a}{b} [w_{AA}^{\varphi} w_{Aa}^{\delta} w_A^{\delta} (1 + \alpha_{\Delta}^{\delta}) \phi + w_{Aa}^{\varphi} (1 + \alpha_{\Delta}^{\varphi}) w_a^{\delta} c] / (2w_a^{\varphi}) \quad (\text{S.7a})$$

$$\lambda_{ma} = \frac{a}{b} [w_{Aa}^{\varphi} (1 - \alpha_{\Delta}^{\varphi}) w_{Aa}^{\delta} w_A^{\delta} (1 + \alpha_{\Delta}^{\delta}) \phi + w_{aa}^{\varphi} w_a^{\delta} c] / (2w_A^{\varphi}) \quad (\text{S.7b})$$

$$\chi_{mA} = \frac{aR}{b2} [w_{Aa}^{\varphi} (1 + \alpha_{\Delta}^{\varphi}) w_a^{\delta} c] / w_a^{\varphi} \quad (\text{S.7c})$$

$$\chi_{ma} = \frac{aR}{b2} [w_{Aa}^{\varphi} (1 - \alpha_{\Delta}^{\varphi}) w_{Aa}^{\delta} w_A^{\delta} (1 + \alpha_{\Delta}^{\delta}) \phi] / w_A^{\varphi} \quad (\text{S.7d})$$

1082 where

$$a = w_a^\varphi \phi + w_A^\varphi \psi \quad (\text{S.8a})$$

$$b = w_{AA}^\varphi [w_{Aa}^\delta w_A^\delta (1 + \alpha_\Delta^\delta)] \phi^2 + w_{Aa}^\varphi [w_{Aa}^\delta w_A^\delta (1 + \alpha_\Delta^\delta) + w_{aa}^\delta w_a^\delta] \psi \phi + w_{aa}^\varphi (w_{aa}^\delta w_a^\delta) \psi^2 \quad (\text{S.8b})$$

$$c = w_{Aa}^\delta (1 - \alpha_\Delta^\delta) \phi + 2w_{aa}^\delta \psi \quad (\text{S.8c})$$

As with equilibrium (B), haploid selection again modifies invasion fitnesses
 1084 by altering the sex-ratio and the diploid genotypes of females and directly selecting
 upon female gametes. The only difference is that resident XX females are no
 1086 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 fit-
 1088 ness between neo-W haplotypes and resident X haplotypes, as both can be on any
 diploid or haploid background.

1090 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
 1092 and only if

$$2(w_{Aa}^\varphi - w_{aa}^\varphi)w_{aa}^\delta \psi^2 > (w_{AA}^\varphi - w_{Aa}^\varphi)w_{Aa}^\delta \phi(\phi - \psi) \quad (\text{S.9})$$

where $\phi - \psi = w_{AA}^\varphi w_{Aa}^\delta - w_{aa}^\varphi w_{aa}^\delta$ and both ϕ and ψ are positive when equilibrium
 1094 (A) is stable. In contrast to equilibrium (B), a neo-W haplotype can spread under
 purely sexually-antagonistic selection ($w_{aa}^\varphi < w_{Aa}^\varphi < w_{AA}^\varphi$ and $w_{AA}^\delta < w_{Aa}^\delta < w_{aa}^\delta$).
 1096 The neo-W-*A* can spread as long as it becomes associated with females that bear
 more *A* alleles than observed at equilibrium (A).

1098 Without haploid selection, the neo-W-*a* haplotype spreads ($\lambda_{ma} > 1$) if and
 only if

$$(w_{aa}^\varphi + w_{Aa}^\varphi - 2w_{AA}^\varphi)w_{Aa}^\delta \phi^2 + (w_{aa}^\varphi - w_{Aa}^\varphi)(w_{Aa}^\delta + 2w_{aa}^\delta) \phi \psi > 0 \quad (\text{S.10})$$

1100 This condition cannot be met with purely sexually antagonistic selection (as both
1101 terms on the left-hand side would then be negative), but it can be met under other
1102 circumstances. For example, with overdominance in males there is selection for
1103 increased A frequencies on X chromosomes in males, which are always paired
1104 with Y- a haplotypes. Directional selection for a in females can then maintain a
1105 polymorphism at the A locus on the X. This scenario selects for a modifier that
1106 increases recombination between the sex chromosomes (e.g., blue region of Figure
1107 2d in Otto 2014) and facilitates the spread of neo-W- a haplotypes, which create
1108 more females bearing more a alleles than the ancestral X chromosome does.

Tight Linkage and Haploid Selection

1110 is this specific in any way to tight linkage, $r \approx 0$?

Generally, haploid selection expands the scenarios under which neo-W alleles can spread. For example, when selection is sexually-antagonistic in diploids ($s^{\delta} s^{\delta} < 0$ and $0 < h^{\delta} < 1$) an unlinked neo-W ($R = 1/2$) cannot invade unless there is also haploid selection (Figures 1 and S.3). Secondly, with haploid selection, overdominance ($w_{aa}^{\delta} < w_{Aa}^{\delta}$ & $w_{AA}^{\delta} < w_{Aa}^{\delta}$) is not required for neo-W- a haplotypes to spread ($\lambda_{ma} > 1$) (Figures S.4-S.7). Finally, haploid selection can maintain a polymorphism in the face of directional selection in male and female diploids (ploidally-antagonistic selection). When selection is ploidally-antagonistic, neo-W alleles often spread, for at least some values of R (Figure S.8).

As discussed above, male haploid selection alters the sex ratio and the alleles carried by male gametes that female gametes pair with. Male haploid selection in favour of the a allele ($\alpha_{\Delta}^{\delta} < 0$, $w_A^{\delta} < w_a^{\delta}$) generates male-biased sex ratios at equilibria (A) and (B), where Y- a is fixed ($\hat{p}_Y^{\delta} = 0$). Male-biased sex-ratios facilitate the spread of neo-W- A and neo-W- a haplotypes (increasing λ_{WA} and λ_{Wa}). Panels A-C in Figures S.4 and S.5 show that neo-W haplotypes tend to spread for a wider range of parameters when sex ratios are male biased, compared to Figure 2 without haploid selection. By contrast, male haploid selection in favour of the A allele generates female-biased sex ratios and reduces λ_{WA} and λ_{Wa} , as

demonstrated by panels D-F in Figures S.4 and S.5.

1130 Female haploid selection generates direct selection on the neo-W-*A* and neo-W-*a* haplotypes as they spread in females. Thus, female haploid selection in favour
1132 of the *a* allele tends to increase λ_{W_a} and decrease λ_{W_A} , as shown by panels A-C in
1134 Figures S.6 and S.7. Conversely, female haploid selection in favour of the *A* allele
increases λ_{W_A} and decreases λ_{W_a} , see panels D-F in Figures S.6 and S.7.

Supplementary Figures

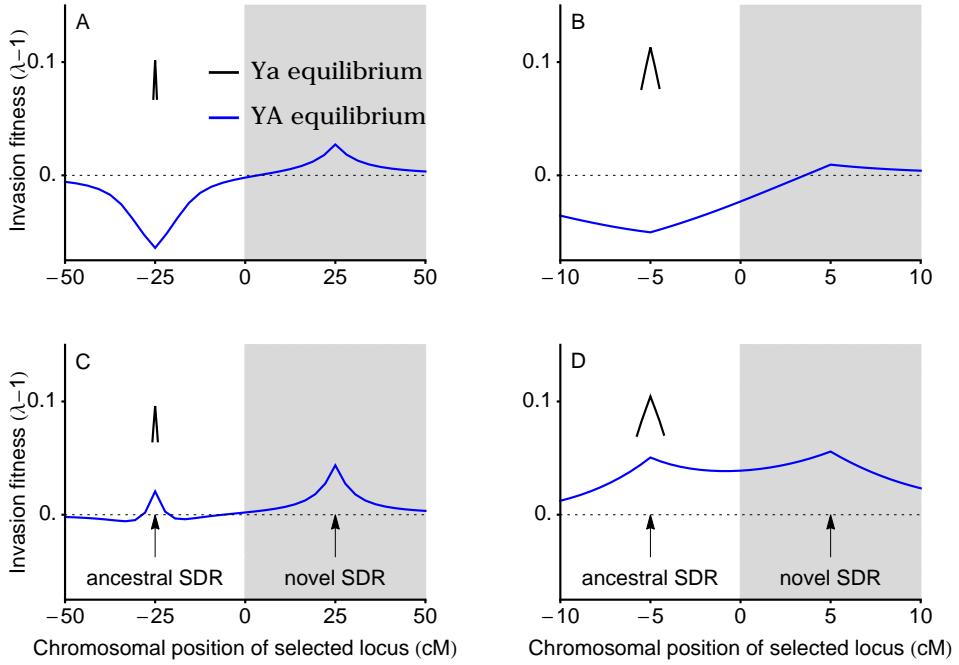


Figure S.1: Neo-W alleles can spread when loci under diploid selection are tightly linked to the ancestral sex determining locus ($r \approx 0$). In panels A and B, the a allele is favoured in females ($w_{aa}^{\varnothing} = 1.05$, $w_{Aa}^{\delta} = 1$, $w_{AA}^{\varnothing} = 0.85$) and selection in males is overdominant ($w_{aa}^{\delta} = w_{AA}^{\delta} = 0.75$). In panels C and D, selection in males and females is overdominant ($w_{aa}^{\varnothing} = w_{AA}^{\varnothing} = 0.6$, $w_{aa}^{\delta} = 0.5$, $w_{AA}^{\delta} = 0.7$, $w_{Aa}^{\delta} = 1$). There is no haploid selection $t^{\delta} = \alpha_{\Delta}^{\delta} = 0$. These parameters are marked by daggers in Figure 2B and C, which show that neo-W invasion is expected for any \bar{R} ($\lambda_{WA}, \lambda_{Wa} > 1$) when the a allele is nearly fixed on the Y (black lines in this figure; not stable for $r \gg 0$). Equilibria where the A allele is more common among Y-bearing male gametes can also be stable and allow neo-W invasion 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, in the absence of haploid selection, neo-W alleles should spread if and only if they are more tightly linked to the selected locus (positive invasion fitness if and only if the selected locus is in the grey region). However, when linkage is tight (panels B and D and when the selected locus is near the SDRs in all panels), this weak selection prediction can break down.

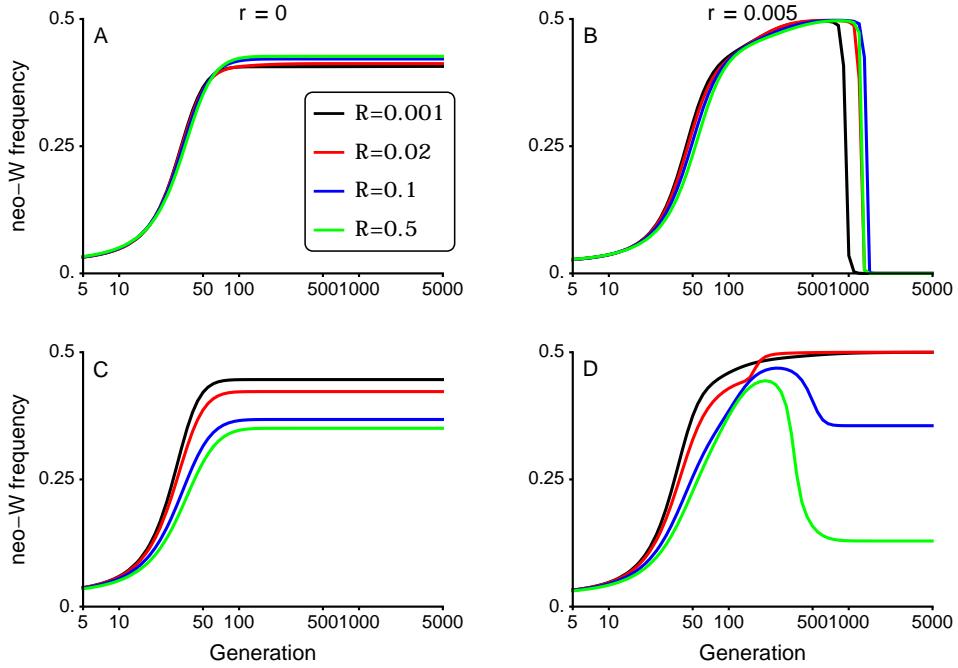


Figure S.2: Following invasion by a neo-W allele, there can be a complete transition to a new sex-determination system, maintenance of polymorphism at both ancestral-XY and neo-ZW sex determining regions, or loss of the new sex-determining allele. Here we plot the frequency of the neo-W allele among 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 by 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 than the A allele on the Y ($Y-a$ is fixed when $r = 0$). When $r > 0$ (panels B and D), Y- A haplotypes created by recombination can become more common than Y- a haplotypes as the neo-W spreads. In B, this leads to loss of the neo-W and the system goes to an equilibrium with X- a and Y- A haplotypes fixed (equilibrium A'), such that all females have the high fitness genotype aa and all males are Aa . For the parameters in B, neo-W alleles have negative invasion fitness when the Y- A haplotype is ancestrally more common than Y- a (see blue lines in Figure S.1A and S.1B near the ancestral SDR). In contrast, the neo-W is not lost in panel D as it is favoured near $r \approx 0$ (see blue lines in Figure S.1C and S.1D near the ancestral SDR). Fitness parameters are the same as in Figure S.1; in panels A and B the a allele is favoured in females ($w_{aa}^{\varphi} = 1.05$, $w_{Aa}^{\varphi} = 1$, $w_{AA}^{\varphi} = 0.85$) while there is overdominance in males ($w_{aa}^{\delta} = w_{AA}^{\delta} = 0.75$) and in panels C and D, there is overdominance in both sexes ($w_{aa}^{\varphi} = w_{AA}^{\varphi} = 0.6$, $w_{aa}^{\delta} = 0.5$, $w_{AA}^{\delta} = 0.7$, $w_{Aa}^{\delta} = 1$). These parameters are marked by a dagger in Figure 2. Here, there is no haploid selection $\iota^{\varphi} = \alpha_{\Delta}^{\varphi} = 0$.

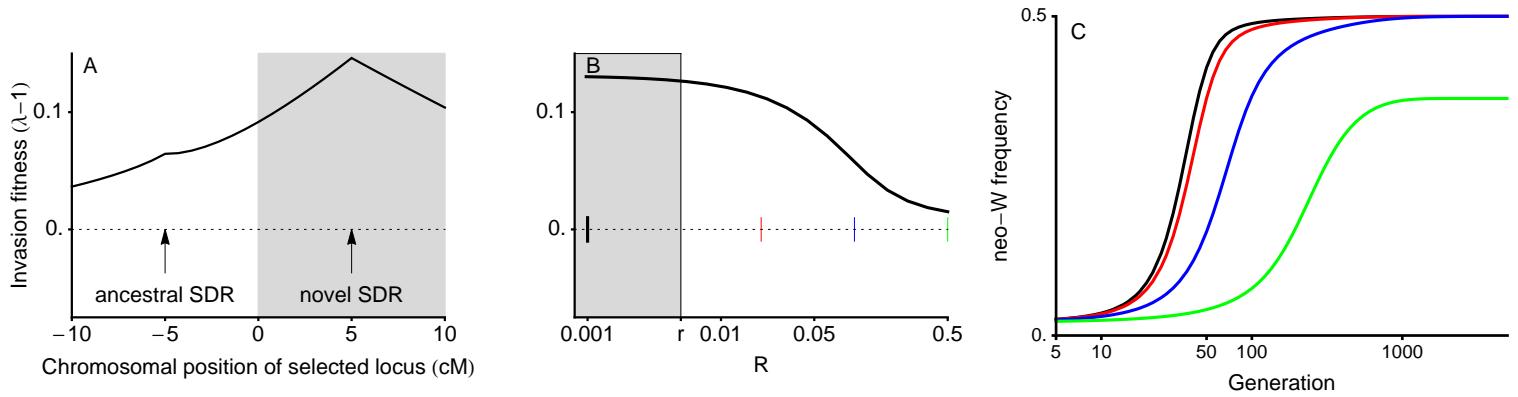


Figure S.3: When there is sexually-antagonistic selection and haploid selection, a neo-W may invade for any R . Panel A shows that the invasion fitness of a neo-W is positive where linkage is tight, even when $r < R$ (unshaded region). (remove A?) In panel B, we vary the recombination rate between the 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 neo-W invasion are plotted in panel C (black $R = 0.001$, red $R = 0.02$, blue $R = 0.1$, green $R = 0.5$). The diploid selection parameters used in this plot are the same as in Figure 1, marked by an asterisk in Figure S.4A: $w_{AA}^{\delta} = 1.05$, $w_{Aa}^{\delta} = 1$, $w_{aa}^{\delta} = 0.85$, $w_{AA}^{\vartheta} = 0.85$, $w_{Aa}^{\vartheta} = 1.05$, $w_{aa}^{\vartheta} = -0.08$, except that there is also male meiotic drive in favour of the a allele, $\alpha_{\Delta}^{\delta} = -0.08$. When $R = 0.5$ (green curve), the neo-W does not reach fixation and X,Y,Z, and W alleles are all maintained in the population, see Figure S.9C.

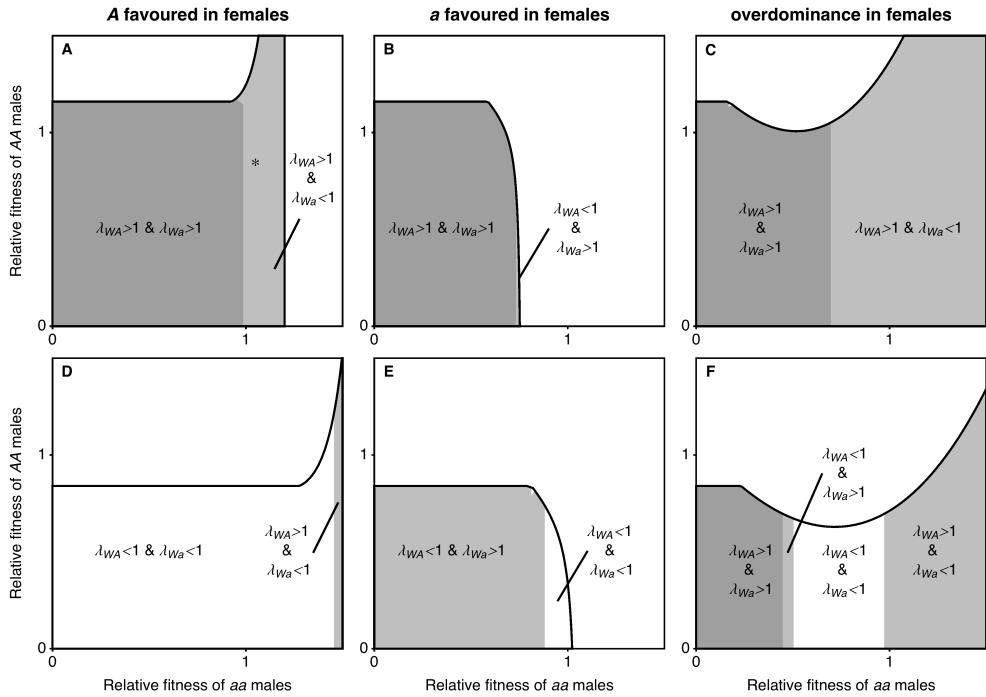


Figure S.4: Meiotic drive in males affects whether neo-W-*A* and neo-W-*a* haplotypes spread when the ancestral-XY locus is tightly linked to a locus under selection ($r = 0$). We vary the fitness of male homozygotes relative to heterozygotes ($w_{Aa}^{\varnothing} = 1$) and only consider stable equilibria at which both *A* locus allele are maintained and the *a* allele is initially fixed on the Y, region outlined. In panels A-C, meiotic drive in males favours the *a* allele ($\alpha_{\Delta}^{\delta} = -0.16$), creating male-biased sex ratios and generally increasing λ_{WA} and λ_{Wa} . By contrast, λ_{WA} and λ_{Wa} tend to be reduced when meiotic drive in males favours the *A* allele ($\alpha_{\Delta}^{\delta} = 0.16$), panels D-F. We consider three forms of selection in females: directional selection in favour of the *A* allele (panels A and D, $w_{aa}^{\varnothing} = 0.85$, $w_{AA}^{\varnothing} = 1.05$), direction selection in favour of the *a* allele (panels B and E, $w_{aa}^{\varnothing} = 1.05$, $w_{AA}^{\varnothing} = 0.85$), and overdominance (panels C and F, $w_{aa}^{\varnothing} = w_{AA}^{\varnothing} = 0.6$).

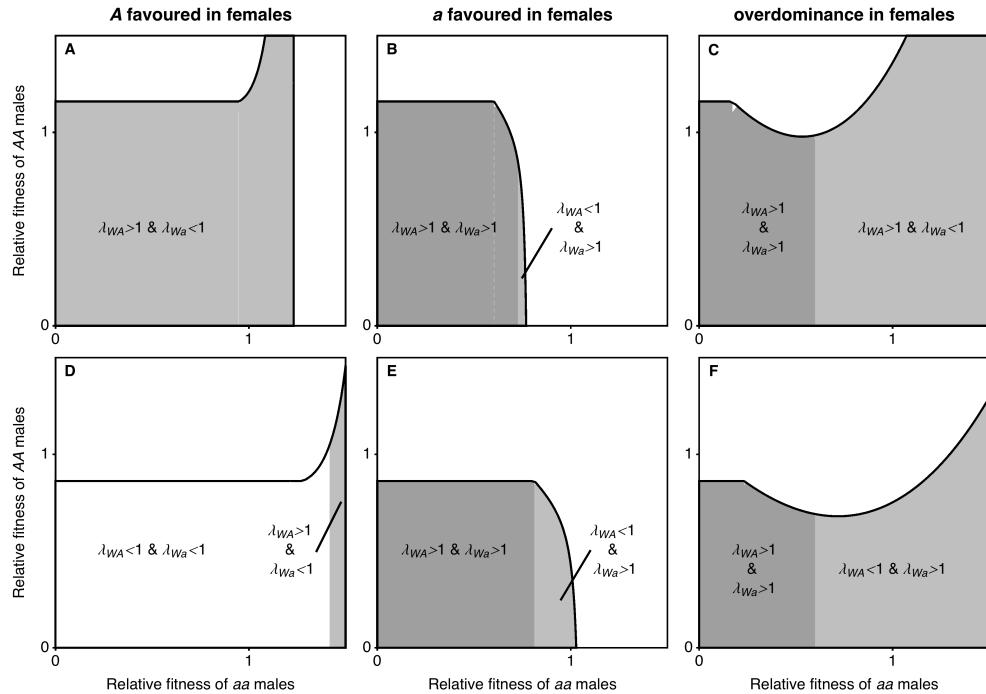


Figure S.5: Parameters for which neo-W-*A* and neo-W-*a* haplotypes spread when there is male gametic competition at a locus that is tightly linked to the ancestral-XY locus. Diploid selection parameters (w_{ij}^δ) are the same as those in Figure S.4. The *a* allele is favoured during male gametic competition in Panels A-C ($w_a^\delta = 1.16$, $w_A^\delta = 1$), which creates male biased sex-ratios and increases λ_{WA} and λ_{Wa} . On the other hand, the *A* allele is favoured during male gametic competition in Panels D-F ($w_a^\delta = 1$, $w_A^\delta = 1.16$) and λ_{WA} and λ_{Wa} tend to be reduced. Compared to the meiotic drive parameters in Figure S.4, the effect of these male gametic competition parameters on the sex ratio is smaller. For example, in Figure S.4A-C, the ancestral sex ratio is $\alpha^\delta = 0.58$ at equilibrium (B) and in panels A-C of this plot, the ancestral sex ratio is $w_a^\delta/(w_A^\delta + w_a^\delta) = 0.537$ at equilibrium (B).

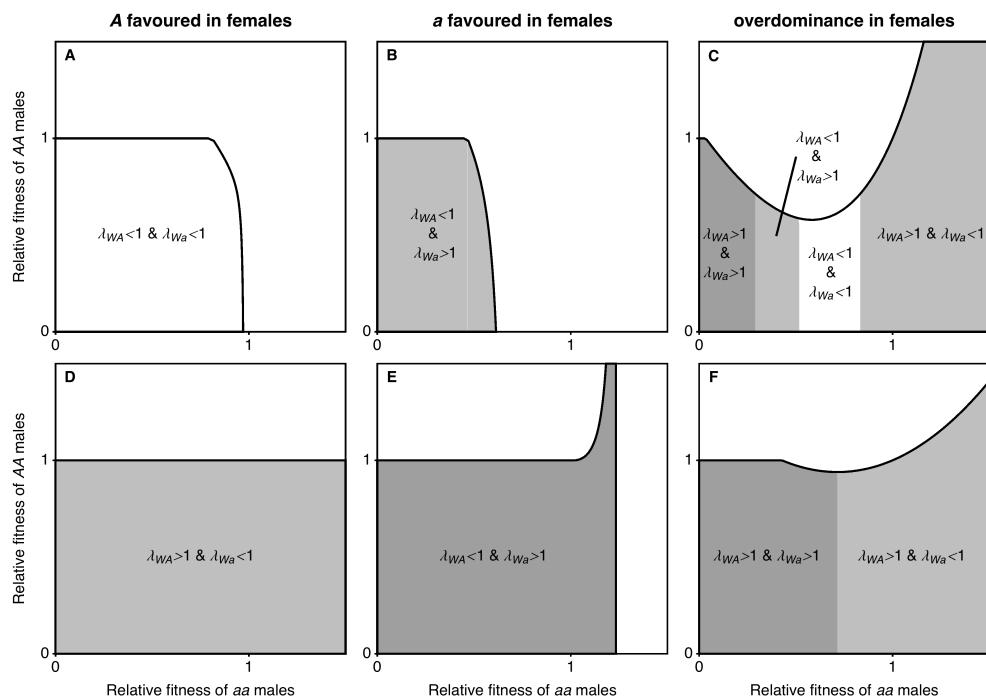


Figure S.6: Parameters for which neo-W-*A* and neo-W-*a* haplotypes spread when there is female meiotic drive at a locus that is tightly linked to the ancestral-XY locus. Diploid selection parameters (w_{ij}^ϕ) are the same as those in Figure S.4 and S.5. The *a* allele is favoured by meiotic drive in females in Panels A-C ($\alpha_\Delta^\phi = -0.16$), which increases λ_{Wa} and decreases λ_{WA} . Female meiotic drive in favour of the *A* allele (panels D-F, $\alpha_\Delta^\phi = -0.16$) has the opposite effect.

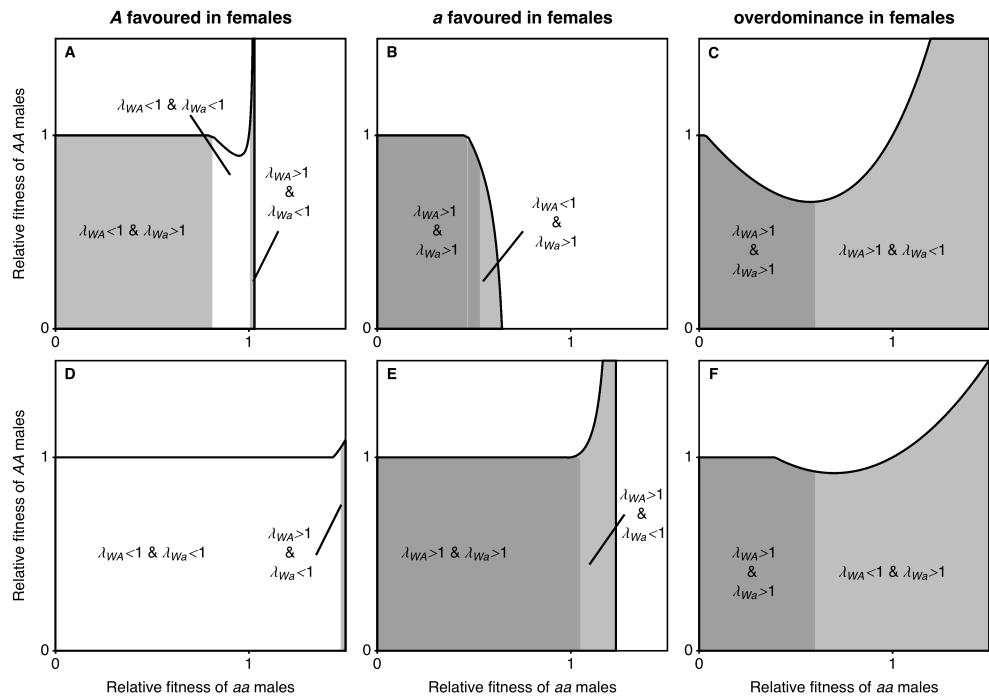


Figure S.7: Parameters for which neo-W-*A* and neo-W-*a* haplotypes spread when there is female gametic competition at a locus that is tightly linked to the ancestral-XY locus. Diploid selection parameters (w_{ij}^ϕ) are the same as those in Figure S.4, S.5, and S.6. The *a* allele is favoured during female gametic competition in females in Panels A-C ($w_a^\phi = 1.16$, $w_A^\phi = 1$), which increases λ_{Wa} and decreases λ_{WA} . The *A* allele is favoured during gametic competition in panels D-F ($w_a^\phi = 1$, $w_A^\phi = 1.16$), giving the opposite effect on λ_{Wa} and λ_{WA} .

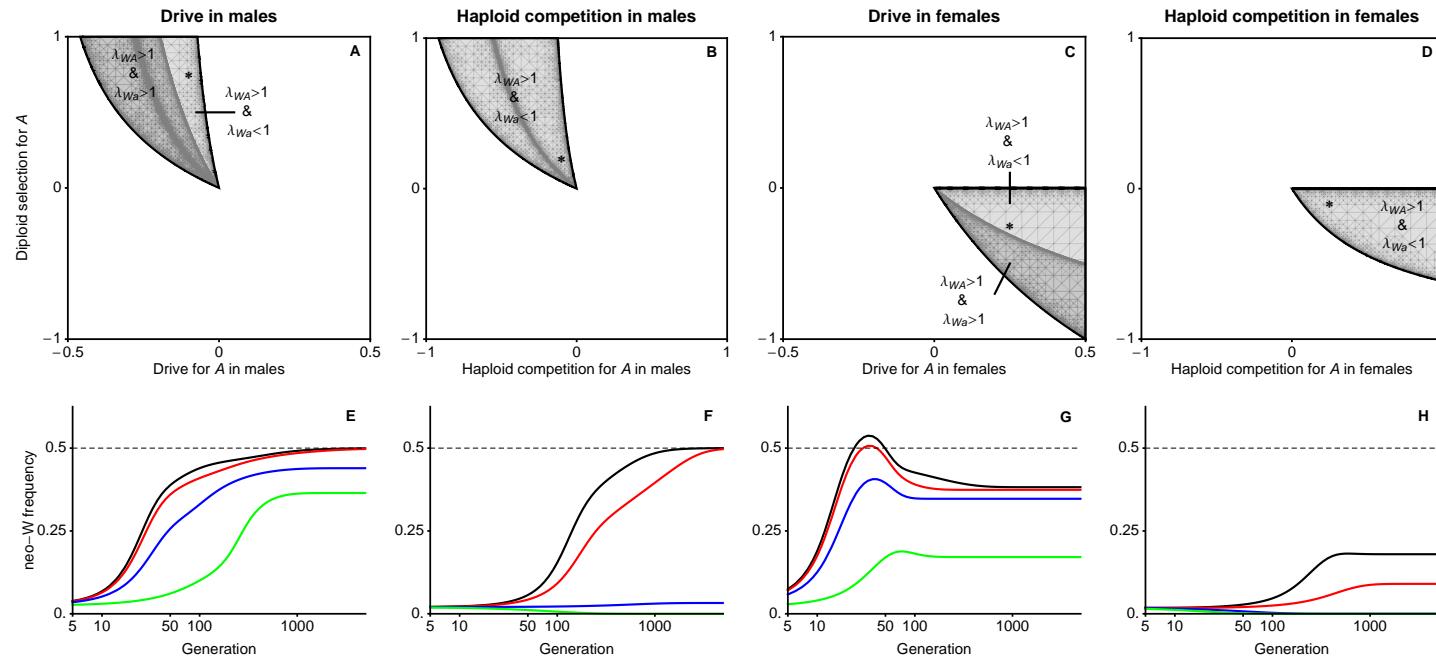


Figure S.8: A-D show when each of the neo-W haplotypes invade an internally stable equilibrium with a fixed on the Y (found by setting $r = 0$). The y-axis shows directional selection in diploids of both sexes, $s^{\varphi} = s^{\delta}$, and the x-axes show sex-specific drive, $\alpha_{\Delta}^{\varphi}$, or haploid competition, t^{φ} . The top left and bottom right quadrants therefore imply ploidally-antagonistic selection (and these are the only places where neo-W haplotypes can invade). Dominance is equal in both sexes, $h^{\varphi} = h^{\delta} = 3/4$. E-F show the temporal dynamics of neo-W frequency in females with parameters given by the asterisks in the corresponding A-D plot, with $r = 1/200$, for four different R . Black $R = 1/1000$, Red $R = 2/100$, Blue $R = 1/10$, Green $R = 1/2$. Dashed line in E-H gives “fixation” of neo-W (all females heterozygous ZW).

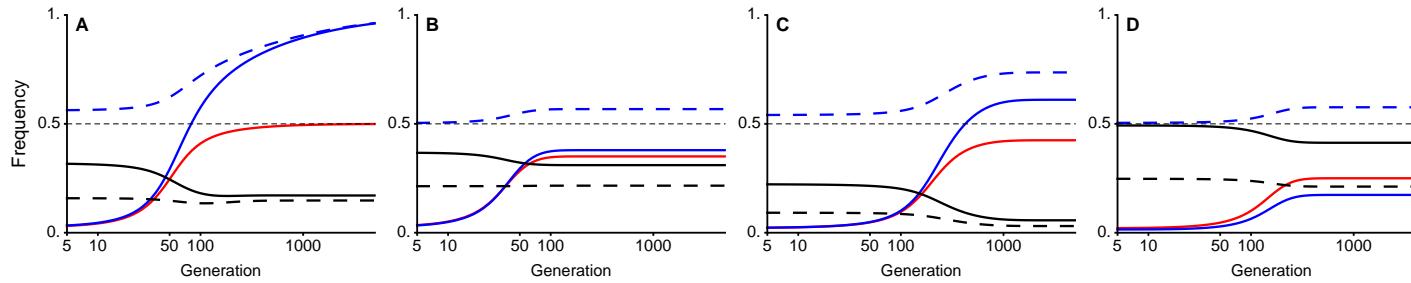


Figure S.9: Dynamics of sex-determining alleles during invasion by a neo-W allele. The curves show the frequencies of the neo-W (red), ancestral-Y (Blue), and A allele among female gametes (solid curves) and among male gametes (dashed curves). In panel A, there is a complete transition from XY sex determination (XX-ZZ females and XY-ZZ males) to ZW sex determination (YY-ZW females and YY-ZZ males). In panels B-D polymorphism is maintained at both the ancestral XY locus and the neo-ZW locus, such that there are males with genotypes XY-ZZ or YY-ZZ and females with genotypes XX-ZZ, XX-ZW, XY-ZW, or YY-ZW. In panel A, selection is ploidally antagonistic with drive in males (parameters as in the green curve in Figure 4B). In panel B, there is overdominance in both sexes (parameters as the green curve in Figure S.2C). In panel C, there is male meiotic drive and sexually-antagonistic selection in diploids (parameters as the green curve in Figure S.4C). (remove D?) Panel D has the same parameters as the red curve in Figure S.8F, except $r = 0$ (ploidy-antagonism with pollen competition). In all cases, the initial equilibrium frequency has a near fixed on the Y.