

Gametic Selection, Meiotic Drive, Sex Ratio Bias, and Transitions Between Sex Determination Systems

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Contributions:

Abstract

2 Sex determination systems are remarkably dynamic; many studied taxa
display transitions of sex-determining genes between chromosomes or the
4 evolution of entirely new sex-determining systems. Predominant theories in
which new sex-determining systems are favoured by selection generally con-
6 clude that that novel sex determination systems are favoured if they equalise
the sex ratio or increase linkage between the sex-determining region and a
8 sexually-antagonistic locus. We use population genetic models to extend
these theories in two ways: (1) We explicitly consider how selection on very
10 tightly sex-linked loci influences the spread of novel sex-determiners. We
find that tightly sex-linked genetic variation can favour the spread of new
12 sex-determination systems in which the heterogametic sex changes (XY to
ZW or ZW to XY) and the new sex-determining region is less closely linked
14 (or unlinked) to the sex linked locus under selection; a result that is not found
with loose sex-linkage. (2) We also consider selection upon haploid geno-
16 types either during gametic competition (e.g., pollen/sperm competition) or
meiosis (i.e., non-Mendelian segregation); selective processes that typically
18 occur in one sex or the other. As well as having sex-specific fitness conse-
quences, haploid selection can cause the zygotic sex ratio to become biased
20 because sex ratios are determined by the production and fertilization success
of X- versus Y-bearing pollen/sperm (or Z- versus W-bearing ovules/eggs).
22 Consequently, selection for XY to ZW transitions and ZW to XY transitions
can be assymetrical when linkage between the ancestral sex-determining lo-
24 cus and a locus under haploid selection is tight, in which case ancestral sex
ratio biases can be strong. With looser linkage and haploid selection, we
26 again find that transitions between male and female heterogamety (XY to
ZW or ZW to XY) can occur even if the new sex-determining region is less
28 closely linked to the locus under selection. That is, favourable associations
that develop between the ancestral sex-determining locus and selected loci
30 can be broken during the spread of a new sex-determining region. Overall,
our models provide new predictions for the types of selection and the ge-
32 nomic location of loci that can drive transitions between sex-determination

systems.

34 abstract word count: ≈ 350

Introduction

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

Predominant theories in accounting for the spread of new sex determination
60 systems by selection involve fitness differences between sexes (e.g., sexually antag-
onistic selection) or sex ratio selection. van Doorn and Kirkpatrick (2007; 2010)
62 show that new sex-determining loci can be favoured if they arise in closer link-
age with a locus that experiences sexual antagonism. For example, linkage allows
64 favourable associations to build up between a male-beneficial allele and a neo-Y

chromosome. Such associations can favour a new master sex-determining gene on
66 a new chromosome (van Doorn and Kirkpatrick 2007) and can also favour a transition between male and female heterogamety (e.g., a ZW to XY transition, van
68 Doorn and Kirkpatrick 2010). However, any sexually-antagonistic loci that are more closely linked to the ancestral sex-determination locus will develop similar,
70 favourable associations and select against the spread of a new sex-determination system. Here we extend these studies by explicitly calculating the the equilibrium
72 allele frequencies of loci that are very tightly linked to the ancestral sex-determining region.

74 The sex ratio is directly affected by the sex determination system, it has therefore been suggested that sex ratio selection is a dominant force in the evolution of
76 sex determination (e.g., Bull 1983, p66-67; Beukeboom and Perrin 2014, Chapter 7). ‘Fisherian’ sex ratio selection favours a 1:1 zygotic sex ratio when assuming
78 that males and females are equally costly to produce (Fisher 1930, Charnov 1982). This follows from the fact that, for an autosomal locus, half of the genetic material
80 is inherited from a male, and half from a female (West 2009). Thus, if the population sex ratio is biased towards females, the average per-individual contribution of
82 genetic material to the next generation from males is greater than the contribution from females (and vice versa for male-biased sex ratios). Therefore, a mutant that
84 increases investment in males (e.g., increases the proportion of males produced) will spread via the higher per-individual contributions made by males. In the case
86 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
88 Y chromosomes are inherited disproportionately often), which causes sex ratios to become biased (Hamilton 1967). They find that new, unlinked sex-determining
90 loci (masculinizing or feminizing mutations, i.e., neo-Y or neo-W loci) can then spread, which restore an even sex ratio.

92 Here, we use mathematical models to find the conditions under which new sex determination systems are favoured when loci experience haploid selection.
94 Haploid genotypes at many loci experience selection during gamete competition

and/or meiotic drive (Mulcahy et al. 1996, Joseph and Kirkpatrick 2004). We
96 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 com-
98 petition’ to refer to selection upon haploid genotypes within a gamete/gametophyte
pool (potentially from by multiple parents); the term ‘haploid selection’ encom-
100 passes both processes. Meiotic drive generally occurs either during the production
of male or female gametes only (Úbeda and Haig 2005, Lindholm et al. 2016). Be-
102 cause there are typically many more pollen/sperm than required for fertilization,
gametic competition is also typically sex specific, occurring primarily among male
104 gametes. Gametic competition may be particularly common in plants, in which 60-
70% of all genes are expressed in the male gametophyte and these genes exhibit
106 stronger signatures of selection than random genes (Borg et al. 2009, Arunkumar
et al. 2013, Gossmann et al. 2014). In addition, artificial selection pressures ap-
108 plied to male gametophytes are known to cause a response to selection (e.g., Hor-
maza and Herrero 1996, Ravikumar et al. 2003, Hedhly et al. 2004, Clarke et al.
110 2004) and gametic selection appears to occur during the creation of F2 crosses
(Kumar, 2007). A much smaller proportion of genes are thought to be expressed
112 and selected during competition in animal sperm, although precise estimates are
uncertain (Zheng et al. 2001, Joseph and Kirkpatrick 2004, Vibranovski et al. 2010,
114 Immler et al. 2014).

There are various ways in which a period of haploid selection could influence
116 transitions between sex determination systems. If we assume that haploid selec-
tion at any particular locus predominantly occurs in one sex (e.g., meiotic drive
118 during spermatogenesis), then such loci experience a form of sex-specific selec-
tion. In this respect, we might expect that haploid selection would affect transitions
120 between sex determination systems in a similar manner to sex-specific diploid se-
lection (as explored by van Doorn and Kirkpatrick 2007; 2010). That is, new
122 masculinizing mutations (neo-Y chromosomes) could be favoured via associations
with alleles that are beneficial in the male haploid stage. However, sex ratios can
124 also become biased by linkage between the sex-determining region and a locus that

harbours genetic variation in haploid fitness. For example, there are several known
126 cases of sex ratio bias caused by sex-linked meiotic drive alleles (Burt and Trivers
2006, Chapter 3) or selection among X- and Y-bearing pollen (Lloyd 1974, Conn
128 and Blum 1981, Stehlik and Barrett 2005; 2006, Field et al. 2012; 2013). It is not
immediately clear how the spread of new sex determination systems would be in-
130 fluenced by the combination of sex ratio biases and associations between haploid
selected loci and sex-determining regions.

132 Our models tracking the spread of new sex determination systems therefore
have two important new features. Firstly, we consider loci that are under selec-
134 tion and also in very tight linkage with the ancestral sex-determining region. Sec-
ondly, we allow sex-specific haploid selection to occur on a locus in tight or loose
136 linkage with the ancestral sex-determining region. We find that sex ratio biases
caused by haploid selection can exert Fisherian sex ratio selection upon novel sex-
138 determiners but that their spread is also determined by the fitness of the alleles that
are associated with them. Indeed, it is only when haploid selected loci are tightly
140 linked to the ancestral sex-determining region (and so sex ratio biases are initially
large) that we see an asymmetry between selection for XY to ZW transitions and
142 ZW to XY transitions, e.g., because haploid selection in males only causes bi-
ased zygotic sex ratios in an ancestrally XY system. In addition, we show that
144 transitions between male and female heterogamety can evolve even when the neo-
sex-determining locus is less closely linked to a locus under selection and therefore
146 disrupts favourable ancestral associations between sex and the alleles selected in
that sex. Such transitions are not favoured in models lacking tight linkage and/or
148 haploid selection.

Model

150 We consider the transition between ancestral and novel sex determination systems
using a three locus model. Locus **X** is the ancestral sex-determining region, with
152 alleles *X* and *Y* (or *Z* and *W*). Locus **A** is a locus under selection, with alleles

A and a . Locus \mathbf{M} is a novel sex-determining region, at which the null allele (M)
 154 is initially fixed in the population such that sex of zygotes is determined by the
 genotype at the ancestral sex-determining region, \mathbf{X} ; XX genotypes become fe-
 156 males and XY become males (or ZW become females and ZZ become males).
 To evaluate the evolution of new sex-determination systems, we consider the inva-
 158 sion, fixation, maintenance, and/or loss of novel sex-determining alleles (m) at the
 \mathbf{M} locus. We assume that the \mathbf{M} locus is epistatically dominant over the \mathbf{X} locus
 160 such that zygotes with at least one m allele develop as females with probability
 k and as males with probability $1 - k$, regardless of the \mathbf{X} locus genotype. With
 162 $k = 0$, the m allele is a masculinizer (i.e., a neo-Y) and with $k = 1$ the m allele is a
 feminizer (i.e., a neo-W). With intermediate k , the m allele confers environmental
 164 sex determination (ESD) such that zygotes develop as females in a proportion (k)
 of the environments they (randomly) experience. Finally, we also analyze a model
 166 of maternally-controlled environmental sex-determination, where mothers with at
 least one m allele produce daughters with probability k .

168 In each generation, we census the genotype frequencies in male and female
 gametes/gametophytes (hereafter gametes) before gametic competition. A full de-
 170 scription of our model, including recursion equations, is given in the Appendix.
 First, competition occurs among male gametes (sperm/pollen competition) and
 172 among female gametes (egg/ovule competition) separately. Selection during ga-
 metic competition depends on the \mathbf{A} locus genotype, relative fitnesses are given
 174 by w_A^{\varnothing} and w_a^{\varnothing} ($\varnothing \in \{\varnothing, \delta\}$; see table 1). We assume that all gametes compete for
 fertilization during gametic competition, which is not the case for monogamous
 176 mating systems where gametes from only one mating partner are present. Gametic
 competition in monogamous mating systems is equivalent to meiotic drive in our
 178 model, which only alters the frequency of gametes produced by heterozygotes. Af-
 ter gametic competition, random mating occurs between male and female gametes.
 180 The resulting zygotes develop as males or females, depending on their genotypes
 at the \mathbf{X} and \mathbf{M} loci (and the \mathbf{M} genotype of their mother in the case of maternal
 182 control) as described above. Diploid males and females then experience selection,

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

Table 1: Relative fitness of different genotypes in sex $\mathfrak{f} \in \{\mathfrak{f}, \mathfrak{m}\}$

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

Results

194 The only asymmetry between males and females in our model is that, under the
ancestral sex determination system, males develop with genotype XY (or ZZ)
196 and females with genotype XX (or ZW). Therefore, the model outlined above
describes both ancestrally- XY and ancestrally- ZW sex determination systems if

198 we relabel the two sexes as being ancestrally ‘heterogametic’ or ancestrally ‘ho-
 200 mogametic’. Without loss of generality, we primarily refer to the ancestrally het-
 202 erogametic sex as male and the ancestrally homogametic sex as female. That is,
 we describe an ancestral XY sex determination system but our model can easily
 be applied to an ancestral ZW sex determination system.

Generic invasion by a neo-Y or neo-W

204 The evolution of a new sex determination system requires that a rare mutant al-
 lele, m , at the novel sex-determining locus increases in frequency when rare. The
 206 spread of a rare mutant m at the \mathbf{M} locus is determined by the leading eigenvalue, λ ,
 of the system of eight equations describing the next generation frequency of eggs
 208 and sperm carrying the mutation, (S.1c, S.1d, S.1g, S.1h). This system simpli-
 fies substantially in a number of cases of interest. Dominant neo-Y (when $k = 0$)
 210 or neo-W alleles (when $k = 1$) are only found in male diploids (neo-Y) or fe-
 male diploids (neo-W) such that their growth rate ultimately depends only on the
 212 change in frequency of m -bearing gametes produced by males (for a neo-Y) or
 by females (for a neo-W). Furthermore, if the m allele is fully epistatically dom-
 214 inant over the ancestral sex-determining system, phenotypes are not affected by
 the genotype at the ancestral sex-determining region (\mathbf{X} locus). Thus, the inva-
 216 sion of rare dominant neo-Y or neo-W alleles is determined by the largest eigen-
 value that solves the quadratic characteristic polynomial $\lambda^2 + b\lambda + c = 0$. Here,
 218 $b = -(\lambda_{mA} + \lambda_{ma}) + (\rho_{mA} + \rho_{ma})$ and $c = (\lambda_{mA} - \rho_{mA})(\lambda_{ma} - \rho_{ma}) - \rho_{mA}\rho_{ma}$,
 where λ_{mi} is the (multiplicative) growth rate of mutant haplotypes on background
 220 $i \in \{A, a\}$, without accounting for loss due to recombination, and ρ_{mi} is the rate at
 which mutant haplotypes on background $i \in \{A, a\}$ recombine onto the other \mathbf{A}
 222 locus background in heterozygotes (see table 2). The spread of the mutant m allele
 depends on the frequency of alleles at the other two loci in the ancestral popula-
 224 tion. In the ancestral population, it is convenient to follow the frequency of the A
 allele in female gametes (eggs) from an XX female, p_X^ϕ , and in X-bearing, p_X^δ , and
 226 Y-bearing, p_Y^δ , male gametes (sperm). We also track the fraction of male gametes

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

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

$\bar{p}^\delta = p_Y^\delta q + p_X^\delta (1 - q)$ is the average frequency of the *A* allele among X- and Y-bearing male gametes.
 R is the probability of recombination between loci **A** and **M**.
 ζ is the zygotic sex ratio (fraction female)
 \bar{w}^\varnothing is the mean fitness of diploids of sex ♂, see Table S.2
 \bar{w}_H^\varnothing is the mean fitness of haploids from sex ♂, see Table S.2

230 We are particularly concerned with the conditions under which a rare neo-sex-
determining allele increases in frequency, which occurs when the largest eigen-
232 value, λ , is greater than one. If the average change in frequency of the two haplo-
types that carry the *m* allele (*Am* and *am*) is positive, invasion will always occur
234 (i.e., if $\{(\lambda_{mA} - 1) + (\lambda_{ma} - 1)\} / 2 > 0$ then $\lambda > 1$. If neither haplotype increases
in frequency ($\lambda_{mA}, \lambda_{ma} < 1$), the *m* allele will not invade. Otherwise, the new sex-
236 determining allele increases in frequency on one **A** background and declines on

the other, and invasion requires

$$\frac{\rho_{mA}}{\lambda_{mA} - 1} + \frac{\rho_{ma}}{\lambda_{ma} - 1} > 0. \quad (1)$$

For example, if we assume that only the mA haplotype has a positive growth rate ($\lambda_{mA} > 1$ and $\lambda_{ma} < 1$), the second term in (1) is negative and invasion requires that number of recombinants from the fitter mA haplotypes is larger than that of the less fit ma haplotypes, relative to their growth rates.

Table 2 illustrates a number of key points about the invasion of neo-Y and neo-W mutations. Firstly, Fisherian sex ratio selection will favour the spread of a neo-Y if the ancestral zygotic sex ratio is biased towards females, $\zeta > 1/2$, and vice versa for a neo-W (terms in square brackets increase λ_{mi}). However, the spread of a neo-Y (neo-W) also depends on the male (female) fitness of alleles that they are associated with, see terms in curly brackets. Secondly, since a dominant neo-Y is always found in males, the allele frequencies at the neo-Y (**M**) locus only change in males. Therefore, invasion by a neo-Y allele does not involve any female diploid selection terms (w_g°). Similarly, invasion by a neo-W is driven by the fitness of female gametes and diploids and does not involve any direct selection in male diploids.

Finally, the diploid fitness terms in Table 2 are weighted by the probability of producing those genotypes through matings with gametes of the opposite sex. For example, matings between a neo-Y-bearing male gamete and an A -bearing female gamete occur with probability $p_X^\circ w_A^\circ / \bar{w}_H^\circ$. The probability that a neo-W bearing female gamete mates with an A -bearing male gamete is $\bar{p}^\delta w_A^\delta / \bar{w}_H^\delta$, where $\bar{p}^\delta = p_Y^\delta q + p_X^\delta (1 - q)$ is the frequency of the A allele among both X- and Y-bearing male gametes. That is, in the case of a neo-W, female diploids can result from matings with either an X-bearing or a Y-bearing sperm, resulting in zygotes that will develop as females. However, females that do not carry the neo-W only result from matings with X-bearing sperm. Therefore, eggs with and without a neo-W can differ in the frequency of A alleles they obtain from matings with male gametes. Invasions by a neo-Y and a neo-W differ in this respect because sperm

with or without a neo-Y allele both mate with X-bearing female gametes only.

266 In order to explicitly determine the conditions under which a rare neo-sex-determining allele spreads, we must calculate the frequency of the A allele in the
 268 ancestral population (i.e., p_X^q , p_X^δ , and p_Y^δ). We assume that the A allele reaches a stable equilibrium frequency under the ancestral sex-determination system before
 270 the neo-sex-determining allele (m) arises. We can analytically calculate the allele frequency of the A allele using two alternative simplifying assumptions: (1) as-
 272 suming that the A locus is within the non-recombining region around the ancestral SDR (or within tight linkage, $r \approx 0$) or (2) assuming that selection is weak relative
 274 to recombination (s^δ , t^δ , α_Δ^δ of order ϵ).

Tight linkage with the ancestral sex-determining region

276 When there is tight linkage between the ancestral sex-determining region and the A locus ($r = 0$), either the A allele or the a allele must be fixed on the Y. Because
 278 the labelling of alleles is arbitrary, we will assume that the a locus is fixed on the Y without loss of generality ($p_Y^\delta = 0$). If there are two alleles maintained at the
 280 A locus, the X can either be fixed for the A allele ($p_X^q = p_X^\delta = 1$) or polymorphic ($0 < p_X^q, p_X^\delta < 1$). These equilibrium allele frequencies and their stability conditions
 282 are given in the appendix.

A neo-Y will never invade an ancestral XY system that already has tight linkage
 284 with the locus under selection ($r = 0$). A neo-Y haplotype with the same allele as the ancestral Y is neutral and does not change in frequency ($\lambda_{ma} = 1$). The
 286 other neo-Y haplotype will not spread given that the initial equilibrium is stable ($\lambda_{mA} < 1$). Therefore, a neo-Y mutation cannot spread ($\lambda \leq 1$).

288 Neo-W alleles, on the other hand, can invade an ancestral XY system under some conditions (given in detail in the appendix). Given the ancestral allele fre-
 290 quencies in the population, neo-W- A and/or neo-W- a haplotypes can increase in frequency ($\lambda_{ma} > 1$ and/or $\lambda_{mA} > 1$). Firstly, haploid selection causes the zygotic
 292 sex ratio to be male biased ($\zeta < 1/2$) when the a allele (which is fixed on the Y) is favoured during haploid competition or by meiotic drive. This facilitates the

294 spread of a neo-W because neo-W alleles cause zygotes to develop as the rarer fe-
 male sex. However, neo-W alleles can also be favoured via their associations with
 296 A locus alleles that confer a fitness advantage in females. We will first explore
 these situations by assuming that there is no haploid selection, which means that
 298 there are no zygotic sex ratio biases.

... this holds for moderate amounts of recombination between the neo-W and
 300 the selected locus, $0 < R \ll 1$, indicating that, contrary to the conclusions of
 van Doorn and Kirkpatrick (2010), neo sex chromosomes that reduce linkage with
 302 selected loci can invade.

Loose linkage with the ancestral sex-determining region

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

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

308 and

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

where $V_A = \bar{p}(1 - \bar{p})$ is the variance in the frequency of A and $S_A = (D^\delta + \alpha_\Delta^\delta + t^\delta) -$
 310 $(D^\varphi + \alpha_\Delta^\varphi + t^\varphi)$ is the difference in fitness in males versus females for the A allele
 against the a allele across diploid selection, gametic competition, and meiosis.
 312 $D^\varphi = (\bar{p}s^\varphi + (1 - \bar{p})h^\varphi s^\varphi) - (\bar{p}h^\varphi s^\varphi + (1 - \bar{p}))$ is the difference in fitness between
 A and a alleles in diploids of sex $\varphi \in \{\varphi, \delta\}$; \bar{p} is the leading-order probability of
 314 mating with an A -bearing gamete from the opposite sex (see Appendix).

The neo-sex-determining allele m will spread if $\lambda_{m,XY} > 1$. Equation (2)
 316 demonstrates that a neo-Y will invade if and only if it is more closely linked to

the selected locus than the ancestral sex-determining region (i.e., if $R < r$, note
 318 that V_A and S_A^2 are strictly positive as long as \mathbf{A} is polymorphic). This result echoes
 that of van Doorn and Kirkpatrick (2007), who considered diploid selection only
 320 and also found that homogametic transitions (XY to XY or ZW to ZW) can oc-
 cur when the neo-sex-determining locus is more closely linked to a locus under
 322 sexually-antagonistic selection.

Equation (3) shows that if there is no haploid selection ($t^\phi = \alpha_\Delta^\phi = 0$), as con-
 324 sidered by van Doorn and Kirkpatrick (2010), the spread of a neo-W is equivalent
 to the spread of a neo-Y ($\lambda_{W',XY} = \lambda_{Y',XY}$) such that heterogametic transitions (XY
 326 to ZW or ZW to XY) can also occur only if the neo-sex-determining region is more
 closely linked to a locus under selection ($R < r$). However, if there is any hap-
 328 loid selection, 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
 330 region is less closely linked to the selected locus ($R > r$). These transitions are
 unusual because, when $R > r$, associations that have built up between alleles more
 332 favourable in one sex and that sex will be weakened. Therefore, mean fitness can
 decrease (Figure 2B,D).

We find that neo-W alleles can invade an XY system for a large number of
 334 selective regimes. To clarify the parameter space under which $\lambda_{W',XY} > 1$, we
 consider several special cases. Firstly, if the \mathbf{A} locus is unlinked to the ancestral
 336 sex-determining region ($r = 1/2$), a more closely linked neo-W ($R < 1/2$) can
 always invade because $(\hat{p}_Y^\phi - \hat{p}_X^\phi) = 0$ such that the second term in equation (3)
 338 disappears and invasion depends only on the sign of $(r - R)$. Indeed, invasion
 typically occurs when the neo-W is more closely linked to the selected locus than
 340 the ancestral sex-determining region (Figure 3). Secondly, we can simplify cases
 where invasion occurs despite $R > r$ using the special case where $R = 1/2$ and $r <$
 342 $1/2$ (e.g., in the ancestor the selected locus is on an autosome and the novel sex-
 determining allele arises on it). In table 3 we give the conditions where invasion
 344 occurs when we further assume that haploid selection only occurs in one sex (e.g.,
 during male meiosis only) and dominance coefficients are equal in the two sexes,
 346

$h^{\varnothing} = h^{\delta}$. Where there is no gametic competition and meiotic drive in one sex
 348 only, an unlinked neo-W can invade as long as the same allele is favoured during
 diploid selection in males and females ($s^{\varnothing}s^{\delta} > 0$, see Figure 3B). When there
 350 is no meiotic drive and gametic competition occurs in one sex only, an unlinked
 neo-W can invade as long as the same allele is favoured in male and female diploid
 352 selection and there are sex differences in selection of one type (e.g., $s^{\varnothing}(s^{\delta} - s^{\varnothing}) > 0$,
 see Figure 3C,D). These special cases indicate that neo-W invasion can occur for
 354 a relatively large fraction of 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	$h^{\delta} = h^{\varnothing}, t^{\varnothing} = t^{\delta} = \alpha_{\Delta}^{\varnothing} = 0$	$s^{\varnothing}s^{\delta} > 0$
female drive only	$h^{\delta} = h^{\varnothing}, t^{\varnothing} = t^{\delta} = \alpha_{\Delta}^{\delta} = 0$	$s^{\varnothing}s^{\delta} > 0$
sperm competition only	$h^{\delta} = h^{\varnothing}, t^{\varnothing} = \alpha_{\Delta}^{\varnothing} = \alpha_{\Delta}^{\delta} = 0$	$s^{\varnothing}(s^{\delta} - s^{\varnothing}) > 0$
egg competition only	$h^{\delta} = h^{\varnothing}, t^{\delta} = \alpha_{\Delta}^{\varnothing} = \alpha_{\Delta}^{\delta} = 0$	$s^{\delta}(s^{\varnothing} - s^{\delta}) > 0$

356 Previous research suggests that when the ancestral sex-determining locus is
 linked to a locus that experiences haploid selection (e.g., meiotic drive), a new, un-
 358 linked sex-determining locus invades in order to restore equal sex ratios (Kozielska
 et al. 2010). Our model provides a good opportunity to determine whether Fish-
 360 erian sex ratio selection provides a useful explanation for the evolution of new
 sex-determining loci in other contexts. Consider, for example, the case where the
 362 **A** locus is linked to the ancestral-SDR ($r < 1/2$) and experiences meiotic drive
 in males only (e.g., during spermatogenesis but not during oogenesis, $\alpha^{\delta} \neq 1/2$,
 364 $\alpha^{\varnothing} = 1/2$). We will also disregard gametic competition ($t^{\varnothing} = t^{\delta} = 0$) such that
 zygotic sex ratios are only biased by meiotic drive in males. In this case, the zy-
 366 gotic sex ratio can be initially biased only if the ancestral sex-determining system
 is XY (Figure 1B). If the ancestral sex-determining system is ZW, the zygotic sex
 368 ratio will be 1:1 because diploid sex is determined by the proportion of Z-bearing
 versus W-bearing eggs (and meiosis in females is fair, Figure 1D). Thus, if the

zygotic sex ratio is crucial to the evolution of new genetic sex-determining systems, invasion into ZW and XY systems will be distinct. However, we find that invasion by a homogametic neo-sex-determining allele (XY to XY, or ZW to ZW) or by a heterogametic neo-sex-determining allele (XY to ZW or ZW to XY) occur under the same conditions. That is, we can show that $\lambda_{Y',XY} = \lambda_{W',ZW}$ and $\lambda_{Y',ZW} = \lambda_{W',XY}$ (at least up to order ϵ^3 ; for a numerical example, compare Figure 1A,B to Figure 1C,D).

Environmental sex determination

We next consider the case where the new sex-determining mutation, m , causes sex to be determined stochastically or by environmental conditions (environmental sex determiner, ESD). We assume that individuals carrying the m allele develop as females in a fraction, k , of the environments they (randomly) experience. Assuming weak selection, the spread of these mutations is given by

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

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

Under Fisherian sex ratio selection, autosomal modifiers favour equal investment in male and female offspring, i.e., a 1:1 sex ratio (Fisher 1930, Charnov 1982, West 2009). A novel environmental sex-determiner that causes half of its carriers to become female and half to become male ($k = 1/2$) will be in males half of the time and in females half of the time (like an autosome). In addition, these novel sex-determination alleles equalize the sex ratio and so one might expect them to be favoured by Fisherian sex ratio selection when the resident sex ratio is biased. However, assuming weak selection, we find that the growth rate of a rare, dominant offspring-controlled neo-ESD allele that produces males or

females with equal probability ($k = 1/2$) is

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

394 where we have indicated that $\lambda_{Y',XY}$ and $\lambda_{W',XY}$ are evaluated at $R = 1/2$. Re-
combination between the selected locus and the novel sex-determining locus, R ,
396 doesn't enter into the $k = 1/2$ results because sex is essentially randomized each
generation, preventing associations from building up between allele A and sex.

398 Equation (5) shows that invasion by a novel 'perfect' ESD (equal sex ratio,
 $k = 1/2$) mutation is the same for an ancestrally XY or ZW system (since $\lambda_{Y',XY} =$
400 $\lambda_{W',ZW}$, $\lambda_{W',XY} = \lambda_{Y',ZW}$). Thus, by the same argument as above (if drive occurs
in males only then the sex ratio is only biased when the ancestral sex-determination
402 system is XY), Fisherian sex ratio selection does not explain invasion by an offspring-
controlled neo-ESD locus. Rather, the neo-ESD gets half of the fitness of a femi-
404 nizing mutation (neo- W) and half of the fitness of a masculinizing mutation (neo- Y),
but only has an effect one half of the time (the other half of the time it produces
406 the same sex as the ancestral system would have, to leading order). The net result
can be that perfect ESD will not invade, even if current sex ratios are biased. For
408 example, if there is haploid selection in males (either drive or pollen/sperm com-
petition) but the conditions in table 3 are not met, perfect ESD will not invade,
410 even though it would equalize the zygotic sex ratio from an initially biased case
(assuming $r < 1/2$).

412 Fisherian sex ratio selection is sometimes considered in terms of balancing
parental investment in male versus female offspring (Charnov 1982). In addition,
414 under environmental sex-determination, the proportion of males/females is some-
times controlled by the mother, e.g., the proportion of eggs laid in warm versus
416 cold environments could determine the sex ratio of offspring. We therefore also
considered the invasion of a neo-sex-determining allele (m) in a model in which
418 mothers that have at least one m allele produce daughters with probability k . As
with offspring-controlled ESD, for all $k \in \{0, 1/2, 1\}$, we find that invasion into

420 an ancestrally XY system is the same as invasion into an ancestrally ZW system
(at least up to order ϵ^3 , assuming weak selection), implying transitions between
422 genetic sex determination and maternally controlled environmental sex determi-
nation are not driven by Fisherian sex ratio selection on biased zygotic sex ratios.
424 (maternal analysis still lacks meiotic drive)

Discussion

426 Because linkage between haploid selected loci and sex-determining regions causes
biased zygotic sex ratios (Hamilton 1967, Burt and Trivers 2006, Field et al. 2012;
428 2013), one might expect Fisherian sex ratio selection to drive the spread of new
sex-determining systems that bring the sex ratio closer to 50:50. Fisherian sex
430 ratio selection follows from the fact that, for an autosomal locus, half of the ge-
netic material is inherited from a male, and half from a female (Fisher 1930, West
432 2009). Thus, if the population sex ratio is biased towards females, the average
per-individual contribution of genetic material to the next generation from males
434 is greater than the contribution from females (and vice versa for male-biased sex
ratios). Therefore, a mutant that increases investment in males will spread via
436 the higher per-individual contributions made by males. An implicit assumption
of Fisherian sex ratio selection is that the mutant allele is autosomal and has the
438 same inheritance pattern as the non-mutant allele. The mutations we consider
here, neo-sex-determining alleles, break this assumption. For example, the suc-
440 cess of neo-Y/neo-W mutations depends only on the number of alleles contributed
by males/females (Table 2). In this respect, a neo-W is similar to a cytoplasmic el-
442 ement, which also does not experience selection to balance sex ratios (Frank 1989,
Werren and Beukeboom 1998, Chase 2007). Even mutants that are equally likely
444 to be found in males or females, such as an environmental sex determination mu-
tation (equation 5), are not strictly autosomal if they determine sex. Thus, despite
446 the fact that sex ratio biases caused by gametic competition or meiotic drive have
been shown to exert Fisherian sex ratio selection on various autosomal modifiers

448 (Stalker 1961, Smith 1975, Frank 1989, Hough et al. 2013, Úbeda et al. 2015, Otto
et al. 2015), we do not find evidence of Fisherian sex ratio selection acting dur-
450 ing invasion by neo-sex-determination systems (e.g., see Figure 1 and Úbeda et al.
2015, in which a neo-Y invades despite biasing sex ratios).

452 We note two other ways in which sex determination has been shown to relate
to zygotic sex ratios. Firstly, female-biased sex ratios can be favoured when there
454 is local mate competition, where all matings are between siblings and assuming
one male can inseminate many females (Hamilton 1967). Therefore, with local
456 mate competition, feminizing mutations can spread because they bias the sex ratio
towards females (Wilson and Colwell 1981, Vuilleumier et al. 2007). Secondly,
458 environmental conditions (e.g., maternal condition, mate quality, age, or host size)
can differentially affect the fitness of males versus females such that the optimal al-
460 location to males/females depends on the environment (Trivers and Willard 1973,
Charnov and Bull 1977, Charnov 1982). In such cases, flexible sex determination
462 systems may evolve in order to allow the zygotic sex ratio to be determined in a
way that depends on the environment (Charnov and Bull 1977, Werren and Taylor
464 1984, Pen et al. 2010). In this study, we do not consider environmental condi-
tion dependence or local mate competition (reviewed in Charnov 1982, Bull 1983,
466 West 2009).

It has previously been demonstrated that new sex-determining systems can
468 evolve if there is genetic variation maintained by sexually-antagonistic selection
(van Doorn and Kirkpatrick 2007; 2010). In particular, transitions to new sex-
470 determining systems can occur when new sex-determining regions are more closely
linked to a sexually-antagonistic locus. Our results show that genetic variation at
472 loci that experience haploid selection can also generate selection in favour of new
sex-determining systems. New sex-determining alleles are again favoured if they
474 are linked with a locus under haploid selection and the ancestral sex-determination
locus is not. However, with haploid selection, heterogametic transitions (XY to
476 ZW or ZW to XY) can also occur when the new sex-determining region is less
closely linked to the locus under selection.

478 Neo-W (neo-Y) alleles invade when their fitness in females (males) is greater
than the mean fitness of females (males) under the ancestral sex determination
480 system. With sexually antagonistic selection (between diploid sexes) only, linkage
between a selected locus and the sex-determining region strengthens associations
482 between male beneficial alleles and the male-determining allele (Y or Z) and be-
tween female beneficial alleles and the female-determining allele (X or W). Thus,
484 the mean fitness of both males and females increases with closer linkage to the sex-
determining region. Therefore, new sex-determining alleles only invade if they are
486 more closely linked than the ancestral sex-determining region. However, if there
is haploid selection on loci linked to an XY (ZW) sex-determining region, selec-
488 tion can maintain polymorphisms at which the mean fitness of females (males)
or males is lower than it would be without sex-linkage. In these cases, unlinked
490 neo-W (neo-Y) alleles can invade, see figure 2.

We assume that sex-determining alleles do not experience direct selection ex-
492 cept via their associations with sex and alleles at a selected locus. However, in
some cases, there may be significant degeneration around the sex-limited allele (Y
494 or W) in the ancestral sex determining region because recessive deleterious muta-
tions and/or deletions may fix around the Y or W allele (Rice 1996, Charlesworth
496 and Charlesworth 2000, Bachtrog 2006, Marais et al. 2008). During heterogametic
transitions (XY to ZW or ZW to XY), the formally sex-limited allele fixes such
498 that all individuals have YY or WW genotypes (Figure 1). Any recessive deleter-
ious alleles linked to the Y or W will therefore be revealed to selection during a
500 heterogametic transition. This phenomenon was studied by van Doorn and Kirk-
patrick (2010), who found that degeneration can prevent fixation of a neo-W or
502 a neo-Y allele, leading to a mixed sex determination system where the ancestral-
and neo- sex-determining loci are both polymorphic. However, they noted that
504 very rare recombination events around the ancestral sex-determining region can
allow these heterogametic transitions to complete. While not explicitly studied,
506 we also predict that Y or W degeneration would prevent fixation of the new sex-
determiners considered here.

508 In addition, our model of meiotic drive is simple, involving a single locus with
two alleles. However, many meiotic drive systems involve an interaction with an-
510 other locus at which alleles may ‘suppress’ the action of meiotic drive (Burt and
Trivers 2006, Lindholm et al. 2016). Thus, the dynamics of meiotic drive alleles
512 can be heavily dependent on the interaction between two loci and the recombina-
tion rate between them, which in turn can be affected by sex-linkage if there is re-
514 duced recombination between sex chromosomes (Hurst and Pomiankowski 1991).
Furthermore, in some cases, a driving allele may act by killing any gametes that
516 carry a ‘target’ allele at another locus, in which case there is a two-locus drive sys-
tem and the total number of gametes produced can be reduced by meiotic drive.
518 Where gamete number is reduced by meiotic drive, the number of mates com-
peting for fertilization (mating system) can affect the equilibrium frequency of a
520 meiotic drive allele (Holman et al. 2015). In polygamous mating systems, the in-
tensity of pollen/sperm competition can depend on the density of males available to
522 donate pollen/sperm, which can itself depend on the sex ratio (Taylor and Jaenike
2002). Since the sex ratio is partly determined by the sex determination system, the
524 evolution of new sex determination system could be influenced by these dynam-
ics. How the evolution of new sex-determining mechanisms could be influenced
526 by two-locus meiotic drive and/or by ecological feedbacks under different mating
systems remains to be studied.

528 The hypotheses presented here can be empirically investigated in a similar
manner to the idea that transitions between sex-determining systems are favoured
530 by linkage to sexually antagonistic variation. In the case of sexually antagonis-
tic variation, one supporting observation is that genes that appear to experience
532 sexually-antagonistic selection have been found on recently derived sex chromo-
somes (Lindholm and Breden 2002, Tripathi et al. 2009, Ser et al. 2010). However,
534 it is possible that sexually antagonistic variation accumulated after sex chromo-
some transitions because linkage with the sex-determining regions allows sexu-
536 ally antagonistic selection to maintain polymorphisms under a larger parameter
space (Rice 1987, Jordan and Charlesworth 2011). We note that linkage with sex

538 chromosomes is not, a priori, more permissive to the maintenance of ploidy an-
tagonistic variation (Immler et al. 2012). However, as with sexually-antagonistic
540 variation, a comparison between closely related clades could indicate whether
a polymorphism pre-dates a transition in sex-determination or arose afterwards.
542 Secondly, we have shown that new sex-determination systems can be favoured if
either the ancestral sex-determining region or the new sex-determining region are
544 linked to loci under haploid selection. Therefore, the presence of haploid selected
loci around ancestral- or new- sex-determining regions could support their role in
546 sex chromosome turnover.

Taken at face value, our results indicate that transitions in heterogamety (XY
548 to ZW or vice versa) are more likely to be favoured by selection if there is selection
upon both haploid and diploid genotypes rather than diploid selection alone. This
550 prediction could be examined using a suitable proxy for haploid selection, for ex-
ample, Lenormand and Dutheil (2005) use the outcrossing rate in plants as a proxy
552 for the strength of pollen competition. In animals, one might expect gametic com-
petition to be stronger in species where sperm is required to live for a long time
554 after spermatogenesis because transcripts shared during spermatogenesis may be-
come depleted, revealing the haploid phenotype of the sperm (Immler et al. 2014).
556 Given the caveats mentioned above about the form of meiotic drive modelled, we
would also expect that heterogametic transitions in sex determination would be
558 more common in clades where there is meiotic drive.

We have shown that haploid selection can drive transitions between sex de-
560 termination systems, such that haploid selection should be incorporated into the
factors that influence the evolution of sex determination. However, the particular
562 way in which transitions are affected by haploid selection is not intuitively obvious.
Firstly, sex-specific haploid selection affects turnovers between sex determination
564 systems in a manner that is qualitatively different from diploid sex-specific selec-
tion. In particular, closer linkage between a sex-determining locus and a selected
566 locus is not always favoured during heterogametic transitions when there is hap-
loid selection. Secondly, even though haploid selection is a source of zygotic sex

ratio biases, Fisherian sex ratio selection does not have good explanatory power in our models in determining whether various sex-determination systems evolve; this result is surprising given that sex ratios are ultimately determined via the sex-determination system.

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Figures

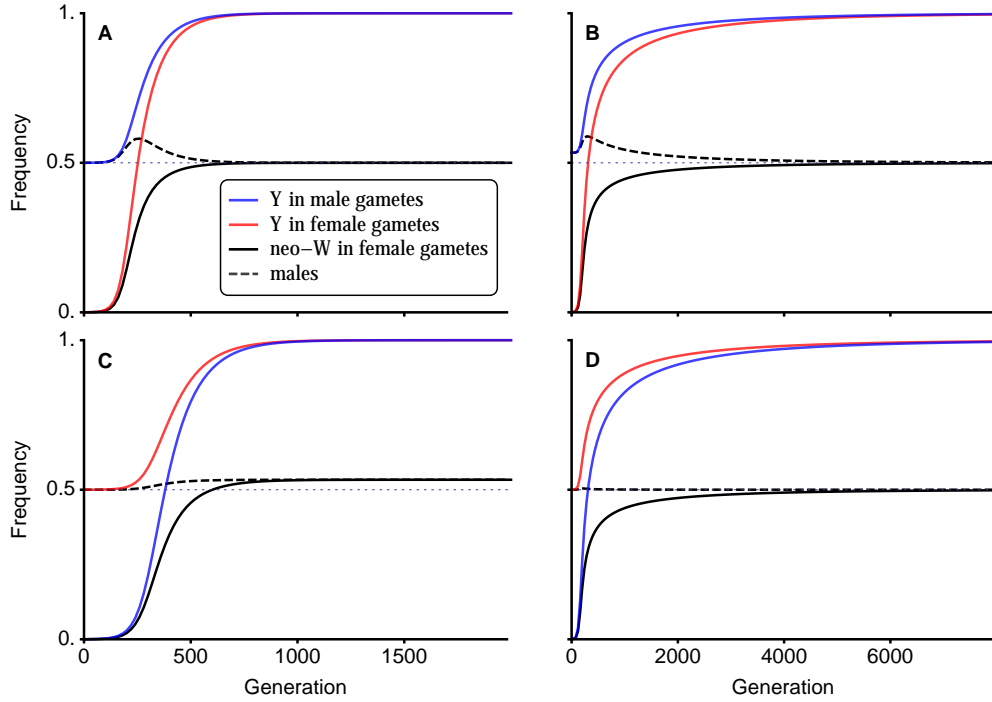


Figure 1: Heterogametic transitions from XY to ZW sex determination (neo-W frequency shown by black lines, panels A and B) or from ZW to XY (neo-Y frequency shown by black lines, panels C and D) occur similarly regardless of sex ratio biases present before (B versus D) or after (C versus A, dashed lines show male frequency). During invasion by a neo-ZW sex determination system (A and B), the ancestral Y fixes in both males and females (blue and red lines). Similarly, the ancestral W allele fixes in males and females (blue and red lines) during a ZW to XY transition. In this plot, there is no gametic competition ($t^{\varnothing} = t^{\sigma} = 0$) and meiotic drive occurs during male meiosis only ($\alpha_{\Delta}^{\varnothing} = 0$, $\alpha_{\Delta}^{\sigma} = -1/5$). Therefore, sex ratio biases can only arise when the A locus is linked to an XY sex-determining locus. In panels A and C, the neo-sex-determining locus is more closely linked to the A locus than the ancestral sex-determining region ($r = 1/2$, $R = 1/20$) such that a neo-Y can cause biased sex ratios (panel C). In panels B and D, the ancestral sex-determining locus is more closely linked to the A locus than the neo-sex-determining locus ($r = 1/20$, $R = 1/2$). Therefore, an ancestral XY sex determination can have a biased zygotic sex ratio that becomes unbiased after an unlinked neo-W invades (B). However, in panel D, a unlinked neo-Y invades an ancestral ZW sex determination system in a similar manner but no biases to the zygotic sex ratio occur. With diploid selection alone, neo-sex-determining loci do not spread if they are less closely linked to the A locus than the ancestral sex-determining locus (see equation (3) and Figure 3A). In this plot there are no sex differences in selection and an equilibrium is maintained because selection in diploids opposes meiotic drive, $s^{\varnothing} = s^{\sigma} = 1/5$, $h^{\varnothing} = h^{\sigma} = 7/10$. Aesthetic adjustments: Could add titles to the columns/rows: neo-W for row 1, neo-Y for row 3, $r = 0.5$, $R = 0.05$ for column 1 and $r = 0.05$, $R = 0.5$ for column 2. Could adjust padding (too much whitespace where there is no axis label). It also seems could increase ratio of font size relative to plot size to make figure more compact. Matt - could you uncomment the line legends in the Mathematica file (function not included in my Mathematica version).

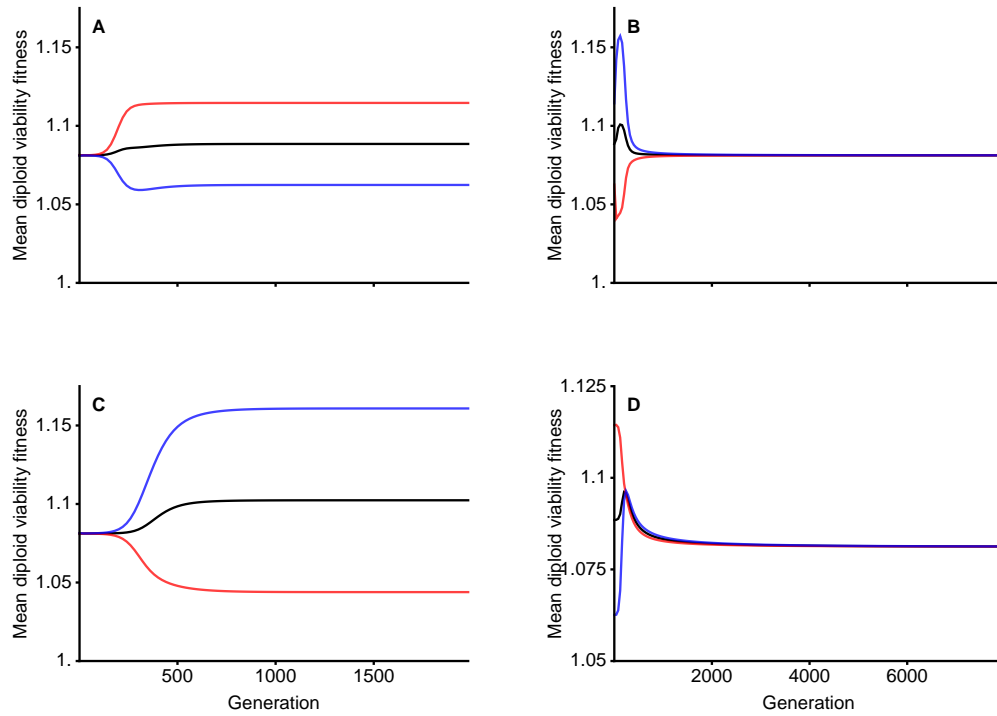


Figure 2: Here, we plot how male mean fitness (blue lines), female mean fitness (red lines), and population mean fitness (male mean fitness plus female mean fitness, black lines) changes during the transitions between sex-determination systems shown in Figure 1. Here we multiply male mean fitness and female mean fitness by two so that we can show it on the same scale as population mean fitness. The mean fitness of females increases during the spread of neo-W alleles (A and B) and the mean fitness of males increases during the spread of neo-Y alleles (C and D). However, when a neo-sex determining system evolves that is less closely linked to a locus under selection (B and D), population mean fitness decreases. **Could add titles to the columns/rows: neo-W for row 1, neo-Y for row 3, $r = 0.5$, $R = 0.05$ for column 1 and $r = 0.05$, $R = 0.5$ for column 2. & possibly adjust padding (too much whitespace?). Matt - could you uncomment the line legends in the Mathematica file (function not included in my Mathematica version).**

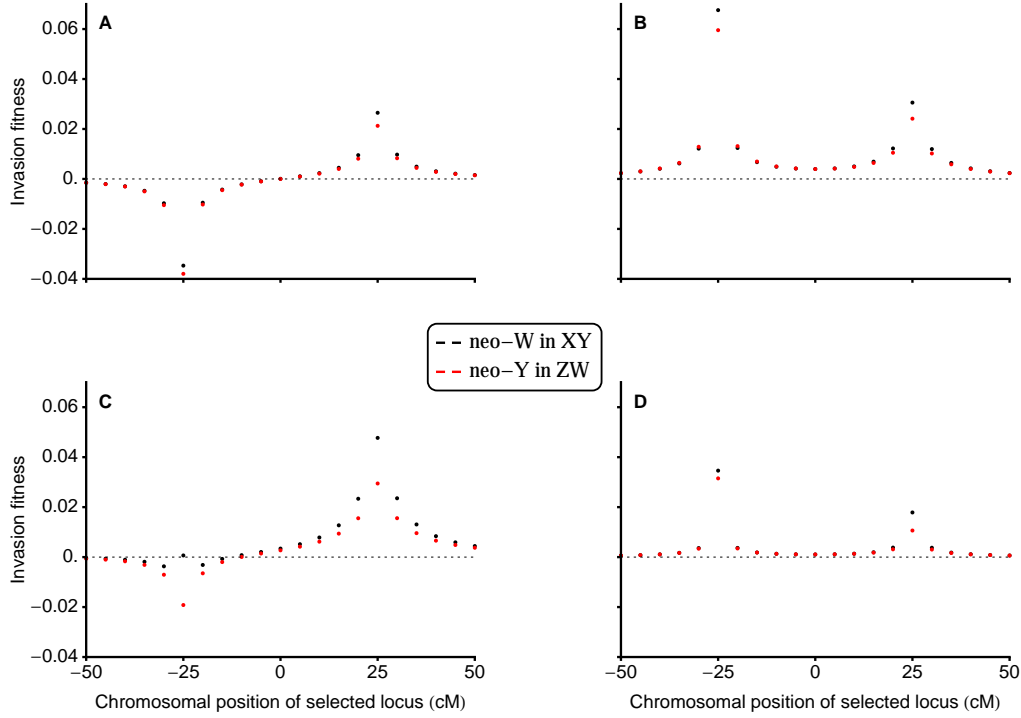


Figure 3: The invasion fitness of a neo-W allele plotted against the relative location of a locus under direct selection, **A**, for various selective regimes. We assume that the ancestral sex-determining locus is located at -0.25, the novel sex-determining locus is located at 0.25 and that there is a polymorphism at the **A** locus maintained by selection. We used Haldane's map function (Equation 3 in Haldane 1919) to convert from map distance (centiMorgans) to the probability of a cross-over event. In **A**, there is no haploid selection ($r^\delta = \alpha_\Delta^\delta = 0$) and selection in diploids is sexually antagonistic (following van Doorn and Kirkpatrick 2010), in which case a neo-W can only invade if it is more closely linked to the selected locus ($s^\varnothing = 1/10$, $h^\varnothing = 7/10$, $s^\delta = -1/10$, $h^\delta = 3/10$). In **B-D** we include haploid selection and assume that selection in diploids is not sexually-antagonistic ($s^\varnothing s^\delta > 0$). A polymorphism can then be maintained by opposing selection between the haploid and diploid phases. In **B**, there is drive in favour of the *a* allele in males ($\alpha_\Delta^\delta = -1/10$), no female meiotic drive or gametic competition, $r^\delta = \alpha_\Delta^\delta = 0$, and equal selection in diploid sexes ($s^\varnothing = s^\delta = 1/10$, $h^\varnothing = h^\delta = 7/10$). In this case, a neo-W can invade even when the selected locus is more closely linked to the ancestral sex determining locus (see Table 3 and Figure 1). In **C** and **D**, there is gametic competition among male gametes only (favouring *a*, $r^\delta = -1/10$) and no meiotic drive or gametic competition in females ($r^\varnothing = \alpha_\Delta^\delta = 0$). In this case, the neo-W does not invade if $s^\varnothing > s^\delta$ (panel **C**: $s^\varnothing = 3/20$, $s^\delta = 1/20$) but does if $s^\varnothing < s^\delta$ (panel **D**: $s^\varnothing = 1/20$, $s^\delta = 3/20$), see Table 3. **I suspect that panel C has a region where no equilibrium is maintained (CHECK! Maybe include different parameters here or remove the part when no equilibrium).** Currently use different parameters for **B** than using in figure 1 (selection/drive twice as strong in turnover figure). This plot would also benefit from titles giving, e.g., “sexually-antagonistic selection, $s^\varnothing s^\delta < 0$ ” for **A**, “male meiotic drive, $s^\varnothing s^\delta > 0$ ” for **B**

772 Appendix

Recursion Equations

774 In each generation we census the genotype frequencies in male and female gametes/gametophytes (hereafter, gametes) between meiosis (and any meiotic drive)
 776 and gametic competition. At this stage we denote the frequencies of X- and Y-bearing gametes from males and females X_{ij}^{ϕ} and Y_{ij}^{ϕ} , where $\phi \in \{\delta, \varphi\}$ specifies the sex of the diploid that the gamete came from, $i \in \{A, a\}$ specifies the allele at the selected locus **A**, and $j \in \{M, m\}$ specifies the allele at the novel sex-determining locus **M**. The gamete frequencies from each sex sum to one,
 780 $\sum_{i,j} x_{ij}^{\phi} + y_{ij}^{\phi} = 1$.

782 Competition then occurs among gametes of the same sex (e.g., among eggs and among sperm separately) according to the **A** locus allele, i (see Table 1). The
 784 genotype frequencies after gametic competition are $x_{ij}^{\phi,s} = w_i x_{ij}^{\phi} / \bar{w}_H^{\phi}$ and $y_{ij}^{\phi,s} = w_i y_{ij}^{\phi} / \bar{w}_H^{\phi}$, where $\bar{w}_H^{\phi} = \sum_{i,j} w_i x_{ij}^{\phi} + w_i y_{ij}^{\phi}$ is the mean fitness of male ($\phi = \delta$) or
 786 female ($\phi = \varphi$) gametes.

Random mating then occurs between gametes to produce diploid zygotes. To
 788 shorten notation we now use index i (and j) to denote the alleles at both the **A** and **M** loci and label $MA = 1$, $Ma = 2$, $mA = 3$, and $ma = 4$, such that
 790 $i, j \in \{1, 2, 3, 4\}$. The frequencies of XX zygotes are then denoted as xx_{ij} , XY zygotes as xy_{ij} , and YY zygotes as yy_{ij} . In XX and YY zygotes, individuals with
 792 diploid genotype ij are equivalent to those with diploid genotype ji ; for simplicity, we use xx_{ij} and yy_{ij} to denote the average of these frequencies, $xx_{ij} = (X_i^{\varphi,s} X_j^{\delta,s} +$
 794 $X_j^{\varphi,s} X_i^{\delta,s})/2$ and $yy_{ij} = (Y_i^{\varphi,s} Y_j^{\delta,s} + Y_j^{\varphi,s} Y_i^{\delta,s})/2$.

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

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

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

Finally, these diploids undergo meiosis to produce the next generation of gametes. Recombination and sex-specific meiotic drive occur during meiosis. Here, we allow the relative locations of the SDR, \mathbf{A} , and \mathbf{M} loci to be generic by using three parameters to describe the recombination rates between them. R is the recombination rate between the \mathbf{A} locus and the \mathbf{M} locus, χ is the recombination rate between the \mathbf{M} locus and the \mathbf{X} locus, and r is the recombination rate between the \mathbf{A} locus and the \mathbf{X} locus. Table S.1 shows how χ can be substituted to give any linear order of loci. During meiosis in sex ϕ , meiotic drive occurs such that, in Aa heterozygotes, a fraction α^{ϕ} of gametes produced carry the A allele and $(1 - \alpha^{\phi})$ carry the a allele.

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

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

Among gametes from sex ϕ (sperm/pollen when $\phi = \sigma$, eggs/ovules when

824 $\phi = \varphi$), the frequencies of haplotypes (before gametic competition) in the next generation are given by

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

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

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

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

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

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

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

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

826

The full system is therefore described by 16 recurrence equations (three diallelic
828 loci in two sexes, $2^3 \times 2 = 16$). However, some diploid types are not produced
under a given sex determination system. For example, with the M allele fixed and
830 ancestral XY sex determination, there are no m alleles, XX males, XY females,
or YY females ($xx_{11}^{\delta} = xx_{12}^{\delta} = xx_{22}^{\delta} = xy_{11}^{\delta} = xy_{12}^{\delta} = xy_{21}^{\delta} = xy_{22}^{\delta} = yy_{11}^{\delta} =$
832 $yy_{12}^{\delta} = yy_{22}^{\delta} = 0$). In this case, the system only involves six recursion equations,
which yields equilibrium (S.3).

834 Resident equilibrium and stability

In the resident population (allele M fixed), we choose to follow the frequency
836 of A in female gametes (eggs) from an XX female, p_X^{δ} , and in X -bearing, p_X^{δ} ,
and Y -bearing, p_Y^{δ} , male gametes (sperm). We also track the total frequency of
838 Y among male gametes, q , which may deviate from $1/2$ due to meiotic drive in
males. These four variables determine the frequencies of the six resident gamete
840 types: $X_{MA}^{\delta} = p_X^{\delta}$, $X_{Ma}^{\delta} = 1 - p_X^{\delta}$, $X_{MA}^{\delta} = (1 - q)p_X^{\delta}$, $X_{Ma}^{\delta} = (1 - q)(1 - p_X^{\delta})$,
 $Y_{MA}^{\delta} = qp_Y^{\delta}$, and $Y_{Ma}^{\delta} = q(1 - p_Y^{\delta})$. Mean fitnesses in the resident population are
842 given in table S.2.

Various forms of selection can maintain a polymorphism at the A locus, in-
844 cluding sexually antagonistic selection, overdominance, conflicts between diploid
selection and selection upon haploid genotypes (ploidy antagonistic selection,
846 Immler et al. 2012), and a combination of these selective regimes.

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

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

In particular special cases, e.g., no sex-differences in selection or meiotic drive
 848 ($s^\delta = s^\varphi$, $h^\delta = h^\varphi$, and $\alpha^\delta = \alpha^\varphi = 1/2$), the equilibrium allele frequency and sta-
 bility can be calculated analytically without assuming anything about the relative
 850 strengths of selection and recombination. However, here, we focus on two regimes
 (tight linkage and weak selection) in order to make fewer assumptions about fit-
 852 nesses.

Recombination weak relative to selection (tight linkage)

854 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
 856 order ϵ). The **A** locus will not affect evolution at the novel sex-determining locus,
M, if one **A** allele is fixed on all backgrounds. We therefore focus on the five
 858 equilibria that maintain both *A* and *a* alleles, of which four are given to leading
 order by:

$$\begin{aligned}
(A) \quad \hat{p}_Y^\delta &= 0, \quad \hat{q} = \frac{1}{2} - \frac{(\alpha^\delta - 1/2)w_{Aa}^\delta \phi}{w_{Aa}^\delta \phi + w_{aa}^\delta \psi}, \\
\hat{p}_X^\varnothing &= \frac{w_a^\varnothing \phi}{w_a^\varnothing \phi + w_A^\varnothing \psi}, \quad \hat{p}_X^\delta = \frac{2\alpha^\delta w_{Aa}^\delta \phi}{2\alpha^\delta w_{Aa}^\delta \phi + w_{AA}^\delta \psi} \\
(A') \quad \hat{p}_Y^\delta &= 1, \quad \hat{q} = \frac{1}{2} + \frac{(\alpha^\delta - 1/2)w_{Aa}^\delta \phi'}{w_{Aa}^\delta \phi' + w_{AA}^\delta \psi'}, \\
\hat{p}_X^\varnothing &= 1 - \frac{w_A^\varnothing \phi'}{w_A^\varnothing \phi' + w_a^\varnothing \psi'}, \quad \hat{p}_X^\delta = 1 - \frac{2(1 - \alpha^\delta)w_{Aa}^\delta \phi'}{2(1 - \alpha^\delta)w_{Aa}^\delta \phi' + w_{aa}^\delta \psi'} \\
(B) \quad \hat{p}_Y^\delta &= 0, \quad \hat{p}_X^\varnothing = 1, \quad \hat{p}_X^\delta = 1, \quad \hat{q} = 1 - \alpha^\delta \\
(B') \quad \hat{p}_Y^\delta &= 1, \quad \hat{p}_X^\varnothing = 0, \quad \hat{p}_X^\delta = 0, \quad \hat{q} = \alpha^\delta
\end{aligned}$$

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

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

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

872 properties are unaffected by small amounts of recombination between the SDR and
 A locus, although equilibrium frequencies may be slightly altered. For the a allele
 874 to be stably fixed on the Y requires that $\bar{w}_{Ya}^\delta > \bar{w}_{YA}^\delta$ where $\bar{w}_{Ya}^\delta = w_a^\delta(2p_X^\varphi(1 - \alpha^\delta)w_A^\varphi w_{Aa}^\delta + (1 - p_X^\varphi)w_a^\varphi w_{aa}^\delta)$ and $\bar{w}_{YA}^\delta = w_A^\delta(p_X^\varphi w_A^\varphi w_{AA}^\delta + 2(1 - p_X^\varphi)\alpha^\delta w_a^\varphi w_{aa}^\delta)$.
 876 That is, Ya haplotypes must have higher fitness than YA haplotypes. Substituting
 in $p_X^\varphi = \hat{p}_X^\varphi$ from above, fixation of the A allele on the Y requires that $\gamma_i > 0$
 878 where $\gamma_{(A)} = w_a^\delta(2(1 - \alpha^\delta)w_{Aa}^\delta\phi + w_{aa}^\delta\psi) - w_A^\delta(2\alpha^\delta w_{Aa}^\delta\phi + w_{aa}^\delta\psi)$ for equilibrium
 (A) and $\gamma_{(B)} = 2(1 - \alpha^\delta)w_a^\delta w_{Aa}^\delta - w_A^\delta w_{AA}^\delta$ for equilibrium (B). Stability of a
 880 polymorphism on the X chromosome (equilibrium A) further requires that $\phi > 0$
 and $\psi > 0$. Fixation of the a allele on the X (equilibrium (B)) is mutually exclusive
 882 with equilibrium (A) and requires $\psi < 0$ and $w_A^\varphi w_{AA}^\varphi > (1 - \alpha^\varphi)w_a^\varphi w_{Aa}^\varphi$.

Selection weak relative to recombination (weak selection)

884 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
 886 then requires that

$$0 < -((1 - h^\varphi)s^\varphi + (1 - h^\delta)s^\delta + t^\varphi + t^\delta + \alpha_\Delta^\varphi + \alpha_\Delta^\delta) \quad (\text{S.2})$$

and $0 < (h^\varphi s^\varphi + h^\delta s^\delta + t^\varphi + t^\delta + \alpha_\Delta^\varphi + \alpha_\Delta^\delta).$

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

888 Given that a polymorphism is maintained at the A locus by selection, with
 weak selection and drive the frequencies of A in each type of gamete are the same
 890 ($\hat{p}_X^\varphi = \hat{p}_X^\delta = \hat{p}_Y^\delta = \bar{p}$) and given, to leading order, by

$$\bar{p} = \frac{h^\varphi s^\varphi + h^\delta s^\delta + t^\varphi + t^\delta + \alpha_\Delta^\varphi + \alpha_\Delta^\delta}{(2h^\varphi - 1)s^\varphi + (2h^\delta - 1)s^\delta} + O(\epsilon). \quad (\text{S.3})$$

Differences in frequency between gamete types are of order ϵ and given, to leading
 892 order, by

$$\begin{aligned}
\hat{p}_X^\delta - \hat{p}_X^\varphi &= V_A(D^\delta - D^\varphi + \alpha_\Delta^\delta - \alpha_\Delta^\varphi) + O(\epsilon^2) \\
\hat{p}_Y^\delta - \hat{p}_X^\varphi &= V_A(D^\delta - D^\varphi + \alpha_\Delta^\delta - \alpha_\Delta^\varphi + (1 - 2r)(t^\delta - t^\varphi))/2r + O(\epsilon^2) \quad (\text{S.4}) \\
\hat{p}_Y^\delta - \hat{p}_X^\delta &= V_A(D^\delta - D^\varphi + \alpha_\Delta^\delta - \alpha_\Delta^\varphi + t^\delta - t^\varphi)(1 - 2r)/2r + O(\epsilon^2)
\end{aligned}$$

where $V_A = \bar{p}(1 - \bar{p})$ is the variance in the frequency of A and $D^\varphi = (\bar{p}s^\varphi + (1 - \bar{p})h^\varphi s^\varphi) - (\bar{p}h^\varphi s^\varphi + (1 - \bar{p}))$ corresponds to the difference in fitness between A and a alleles in diploids of sex $\varphi \in \{\varphi, \delta\}$ (\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 ($\alpha_\Delta^\varphi = t^\varphi = 0$) our results reduce to those of van Doorn and Kirkpatrick (2007).

902 **Invasion conditions**

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

904 Here, we explore the conditions under which a neo- W invades an XY system assuming that the A locus is initially in close linkage with the ancestral sex-determining region ($r \approx 0$). We disregard neo- Y mutations, which never spread given that the ancestral population is at a stable equilibrium. At equilibrium (B) we have

$$\lambda_{mA} = \frac{w_A^\delta w_{AA}^\varphi \alpha^\delta + 2w_a^\delta w_{Aa}^\varphi \alpha^\varphi (1 - \alpha^\delta)}{2w_A^\delta w_{AA}^\varphi \alpha^\delta} \quad (\text{S.5a})$$

$$\lambda_{ma} = \frac{w_a^\varphi (w_a^\delta w_{aa}^\varphi (1 - \alpha^\delta) + 2w_A^\delta w_{Aa}^\varphi (1 - \alpha^\varphi) \alpha^\delta)}{2w_A^\delta w_A^\varphi w_{AA}^\varphi \alpha^\delta} \quad (\text{S.5b})$$

$$\rho_{mA} = \frac{Rw_a^\delta w_{Aa}^\varphi \alpha^\varphi (1 - \alpha^\delta)}{w_A^\delta w_{AA}^\varphi \alpha^\delta} \quad (\text{S.5c})$$

$$\rho_{ma} = \frac{Rw_a^\varphi w_{Aa}^\varphi (1 - \alpha^\varphi)}{w_A^\varphi w_{AA}^\varphi} \quad (\text{S.5d})$$

908 In this case, the zygotic sex ratio (ζ) is given by the difference in haploid selection
in males on a (fixed on the Y) and A (fixed on the X) alleles, i.e., there are more
910 males than females ($\zeta < 1/2$) if $\alpha^\delta < 1/2$ and/or $w_a^\delta > w_A^\delta$. Populations with
a male biased zygotic sex ratio are more permissive to invasion by a neo-W (λ_{mA}
912 and λ_{ma} larger). In addition, the spread rate of neo-W haplotypes is determined
by their fitness in females. Zygotes carrying dominant neo-W alleles will develop
914 as females regardless of their genotype at the XY locus. Therefore, females result
from matings with either X- A or Y- a male gametes. The relative proportion of
916 these male gametes is also determined by haploid selection in males; mating with
a Y- a male gamete is more likely if the a allele is favoured during male gamete
918 production or competition ($\alpha^\delta < 1/2$ and/or $w_a^\delta > w_A^\delta$).

Furthermore, haploid selection in females can directly select upon neo-W- A
920 or neo-W- a haplotypes. An A -bearing female gamete has the same fitness during
haploid competition as the resident A -bearing female gametes. On the other hand,
922 a -bearing female gametes can be favoured or disfavoured during female haploid
competition (favoured if $w_a^\varphi > w_A^\varphi$). Meiotic drive in females (α^φ) similarly affects
924 the fitness of these haplotypes, except that meiotic drive only occurs in heterozy-
gotes.

926 The other terms in equations (S.5) are more easily interpreted if we assume
that there is no haploid selection in either sex, in which case $\lambda_{mA} > 1$ when $w_{Aa}^\varphi >$

928 w_{AA}^{φ} and $\lambda_{ma} > 1$ when $(w_{Aa}^{\varphi} + w_{aa}^{\varphi})/2 > w_{AA}^{\varphi}$. These conditions cannot be met
under purely sexually antagonistic selection, where a is directionally favoured in
930 males ($w_{AA}^{\delta} > w_{Aa}^{\delta} > w_{aa}^{\delta}$) and A is directionally favoured in females ($w_{AA}^{\varphi} >$
 $w_{Aa}^{\varphi} > w_{aa}^{\varphi}$). Essentially, the X is already as specialized as possible for the female
932 beneficial allele (X-A is fixed), and the neo-W often makes daughters with the Y-a
haplotype, increasing the flow of a alleles into females, which reduces the fitness
934 of those females.

If selection doesn't uniformly favour A in females, however, neo-W-A haplo-
936 types and/or neo-W- a haplotypes can spread at this equilibrium. If $\lambda_{mA} > 1$ (re-
quiring $w_{Aa}^{\varphi} > w_{AA}^{\varphi}$), the implication is that a is favoured by selection in females
938 despite A being fixed on the X, which must require that X-A is sufficiently favoured
in males to drive the frequency of X-A to one (specifically, from the stability con-
940 ditions, we must have $w_{Aa}^{\delta}/((w_{Aa}^{\delta} + w_{AA}^{\delta})/2) > w_{Aa}^{\varphi}/w_{AA}^{\varphi}$).

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

946 Similar equations can be derived for equilibrium (A) by subbing the equilib-
rium allele frequencies into Table 2. This gives

$$\lambda_{mA} = \frac{a}{b} \left[w_{AA}^{\varphi} w_{Aa}^{\delta} w_A^{\delta} \alpha^{\delta} \phi + 2w_{Aa}^{\varphi} \alpha^{\varphi} w_a^{\delta} \frac{c}{d} \right] / w_a^{\varphi} \quad (\text{S.6a})$$

$$\lambda_{ma} = \frac{a}{b} \left[2w_{Aa}^{\varphi} (1 - \alpha^{\varphi}) w_{Aa}^{\delta} w_A^{\delta} \alpha^{\delta} \phi + w_{aa}^{\varphi} w_a^{\delta} \frac{c}{d} \right] / w_A^{\varphi} \quad (\text{S.6b})$$

$$\rho_{mA} = \frac{a}{b} R \left[2w_{Aa}^{\varphi} \alpha^{\varphi} w_a^{\delta} \frac{c}{d} \right] / w_a^{\varphi} \quad (\text{S.6c})$$

$$\rho_{ma} = \frac{a}{b} R \left[2w_{Aa}^{\varphi} (1 - \alpha^{\varphi}) w_{Aa}^{\delta} w_A^{\delta} \alpha^{\delta} \phi \right] / w_A^{\varphi} \quad (\text{S.6d})$$

948 where

$$a = w_a^\varnothing \phi + w_A^\varnothing \psi \quad (\text{S.7a})$$

$$b = w_{AA}^\varnothing \phi (2w_{Aa}^\delta w_A^\delta \alpha_\delta \phi) + w_{Aa}^\varnothing \psi (2w_{Aa}^\delta w_A^\delta \alpha_\delta \phi + w_{AA}^\delta w_a^\delta \psi) + w_{aa}^\varnothing \psi (w_{AA}^\delta w_a^\delta \psi) \quad (\text{S.7b})$$

$$c = 2(w_{Aa}^\delta \phi)^2 (1 - \alpha^\delta) \alpha_\delta + w_{Aa}^\delta \phi (w_{AA}^\delta \psi + w_{aa}^\delta \psi \alpha^\delta) + w_{aa}^\delta \psi w_{AA}^\delta \psi \quad (\text{S.7c})$$

$$d = 2w_{Aa}^\delta \alpha^\delta \phi + w_{aa}^\delta \psi \quad (\text{S.7d})$$

Without haploid selection $\lambda_{mA} > 1$ if and only if

$$2(w_{Aa}^\varnothing - w_{aa}^\varnothing)w_{AA}^\delta \psi^2 > (w_{AA}^\varnothing - w_{Aa}^\varnothing)w_{Aa}^\delta \phi(\phi - \psi) \quad (\text{S.8})$$

950 NOTES: $\phi - \psi = w_{AA}^\varnothing w_{Aa}^\delta - w_{aa}^\varnothing w_{aa}^\delta$ and both ϕ and ψ are positive by the equilibrium conditions. Most important advance on the descriptions given for the (B)
 952 equilibrium is that this can be met with ‘purely’ sexually antagonistic selection (directional but opposite in both sexes). Basically, because W-A haplotypes never
 954 produce *aa* females, that can be an advantage, even though they also produce a lot of *Aa* females through obtaining the *a* from Y-gametes. Can be seen from the fact
 956 that the condition will be more easily met if there is a large benefit from never producing *aa* females (LHS larger, although note that w_{Aa}^\varnothing and w_{aa}^\varnothing enter into ϕ and ψ
 958 terms too). Even if $R \neq 0$, there can be invasion with purely sexually antagonistic selection.

960 Without haploid selection $\lambda_{ma} > 1$ if and only if

$$w_{Aa}^\delta \phi^2 (w_{aa}^\varnothing + w_{Aa}^\varnothing - 2w_{AA}^\varnothing) + (w_{aa}^\varnothing - w_{Aa}^\varnothing) (w_{Aa}^\delta + 2w_{AA}^\delta) \phi \psi > 0 \quad (\text{S.9})$$

NOTES: Not met with purely sexually antagonistic selection but met in some other
 962 circumstances.

With $R = 0$ the two eigenvalues are λ_{mA} and λ_{ma} . The neo-W can then invade
 964 on the *A* background when $\lambda_{mA} > 1$ and the neo-W can invade on the *a* background

when $\lambda_{ma} > 1$. Even in this case it is difficult to see from equation S.6 when the
966 neo-W will invade. Below we discuss why λ_{mA} and λ_{ma} might be larger than one
and confirm the logic numerically.

968 For simplicity, consider the case of no haploid selection. A polymorphism
at the **A** locus then requires sexually-antagonistic selection (van Doorn and Kirk-
970 patrick 2007). Given that *a* is fixed on the Y, one can consider the *a* allele ‘male
beneficial’ and the *A* allele to be ‘female beneficial’. Because X chromosomes
972 spend some time in males the frequency of *A* on the X can reach an intermediate
equilibrium (equilibrium *A*).

974 We can therefore reason that when a neo-W invades equilibrium (*A*), it is likely
to spread on the *A* background as W chromosomes are always in females. The
976 neo-W can outcompete the ancestral, ‘compromising’ X because it can specialize
on females by fixing the ‘female beneficial’ allele. We call this the ‘sex-specialist
978 hypothesis’. This hypothesis should only work when the benefit of specializing
outweighs the cost of bringing Y chromosomes into females (the neo-W is epistat-
980 ically dominant over the X/Y locus).

One could also reason that, when the neo-W spreads, it does so precisely be-
982 cause it brings Y chromosomes, and their associated alleles, into females, some-
thing the X cannot do. However, this requires a somewhat particular (perhaps
984 ‘perverse’) equilibrium, where XX females do worse than XY females despite as-
sociations on the X and Y being built up by selection. One example of such a per-
986 verse equilibrium is produced by overdominance in both sexes. Overdominance in
females selects for an allele frequency of 0.5 on the X (*A* and *a* equally frequent,
988 maximizing the number of heterozygotes). However, given that *a* is fixed on the
Y, overdominance in males selects for the X to become more associated with the
990 *A*. Thus, a compromising equilibrium is reached on the X chromosome and fe-
males fitness suffers due to the overproduction of *AA* homozygotes. This sets up
992 a scenario in which a neo-W can invade on the *a* background, despite the fact that
a is fixed on the Y and in that sense ‘male beneficial’. We call this the ‘perverse
994 hypothesis’.

Figure S.1 shows where the sex-specialist (red) and perverse (blue) hypotheses are valid. The left panel demonstrates that both hypotheses can be simultaneously valid with overdominance in both sexes and sex differences in selection, which overlaps the parameter region where there is selection for increased recombination between the sex chromosomes (compare with figure 2a in Otto 2014). The right panel shows that the perverse hypothesis is no longer valid when selection is exactly the same in both sexes, despite the fact that there is selection for increased recombination between the sex chromosomes with sufficiently strong overdominance (compare with figure 3 in Otto 2014).

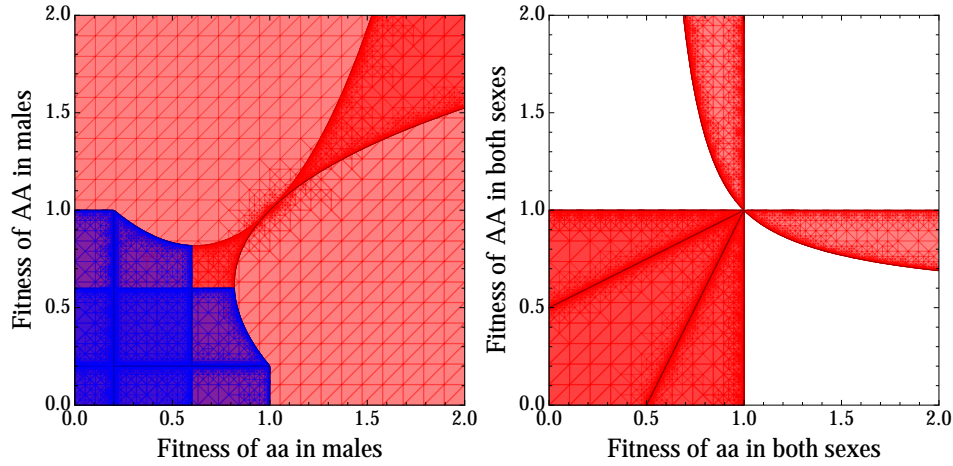


Figure S.1: Numerical exploration of where sex-specialist (red) and perverse (blue) hypotheses are valid, i.e., where an internally stable resident equilibrium can be invaded by a neo-W that is perfectly linked with the allele not fixed on the Y (red) or the allele that is fixed on the Y (blue). **(Left)** The perverse equilibrium is only valid with overdominance while the sex-specialist hypothesis is valid over the entire range shown. Both hypotheses are simultaneously valid over much of the parameter space where increased recombination between the sex chromosomes is selected (Otto 2014, figure 2a). **(Right)** Only the sex-specialist hypothesis is valid with no sex-differences in selection, despite selection for increased recombination between the sex-chromosomes with strong overdominance (Otto 2014, figure 3). Parameters: $w_{Aa}^{\phi} = 1$, $w_a^{\phi} = w_A^{\phi} = 1$, $\alpha^{\phi} = 1/2$, $r = R = 0$, and in left panel $w_{aa}^{\phi} = w_{AA}^{\phi} = 0.6$.

1004 Selection weak relative to recombination (weak selection)

With weak selection the leading eigenvalue for any k is given, up to order ϵ^2 , by
 1006 equation 4.