

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 involve sex ra-
6 tio selection or sex-specific selection (e.g., sexually antagonistic selection).
These studies generally conclude that novel sex determination systems are
8 favoured if they equalise the sex ratio or increase linkage between the sex-
determining region and a sexually-antagonistic locus. We use population
10 genetic models to extend these theories in two ways: (1) We explicitly con-
sider how selection on very tightly sex-linked loci influences the spread of
12 novel sex-determiners. We find that tightly sex-linked genetic variation can
favour the spread of new sex-determination systems in which the heteroga-
14 metric sex changes (XY to ZW or ZW to XY) and the new sex-determining
region is less closely linked (or unlinked) to the sex linked locus under selec-
16 tion; a result that is not found with loose sex-linkage. (2) We also consider
selection upon haploid genotypes either during gametic competition (e.g.,
18 pollen/sperm competition) or meiosis (i.e., non-Mendelian segregation); se-
lective processes that typically occur in one sex or the other. As well as
20 having sex-specific fitness consequences, haploid selection can cause the zy-
gotic sex ratio to become biased because sex ratios are determined by the
22 production and fertilization success of X- versus Y-bearing pollen/sperm (or
Z- versus W-bearing ovules/eggs). With relatively weak linkage, we find that
24 transitions between male and female heterogamety (XY to ZW or ZW to XY)
can again occur despite breaking up favourable associations that build up be-
26 tween the ancestral sex-determining locus and selected loci, which does not
occur with diploid selection alone. In addition, when linkage between the
28 ancestral sex-determining locus and a locus under haploid selection is tight,
sex ratio biases can be strong such that there is an asymmetry between in-
30 vasion of ancestrally XY and ancestrally ZW systems because, e.g., haploid
selection in males only causes biased zygotic sex ratios in an ancestrally XY
32 system. Overall, our models add to the view that sex-determination is dy-

34 namic by indicating that various selective benefits of novel sex-determining
systems may have been underestimated, especially when the heterogametic
sex changes, and offer several new insights to be explored as information
36 about sex determination in non-model taxa accumulates.

Introduction

38 Animals and angiosperms exhibit extremely diverse sex determination systems (re-
viewed in Bull 1983, Charlesworth and Mank 2010, Beukeboom and Perrin 2014,
40 Bachtrog et al. 2014). Among species with genetic sex determination of diploid
sexes, some taxa have heterogametic males (XY) and homogametic females (XX),
42 including mammals and most dioecious plants (Ming et al. 2011); whereas other
taxa have homogametic males (ZZ) and heterogametic females (ZW), including
44 Lepidoptera and birds. Within several taxa, the chromosome that harbours the
master sex-determining region changes. For example, transitions of the master
46 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),
48 Diptera (Vicoso and Bachtrog 2015), and *Oryzias* (Myosho et al. 2012). In ad-
dition, many gonochoric clades with genetic sex determination exhibit transitions
50 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-
52 tids, Vicoso and Bachtrog 2015), amphibians (Hillis and Green 1990), the an-
giosperm genus *Silene* (Slancarova et al. 2013), and Coleoptera and Hemiptera
54 (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,
56 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
58 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
60 et al. 2010, Holleley et al. 2015).

Predominant theories in accounting for the spread of new sex determination
62 systems by selection involve fitness differences between sexes (e.g., sexually antag-
onistic selection) or sex ratio selection. van Doorn and Kirkpatrick (2007; 2010)
64 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
66 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
68 a new chromosome (van Doorn and Kirkpatrick 2007) and can also favour a tran-
sition between male and female heterogamety (e.g., a ZW to XY transition, van
70 Doorn and Kirkpatrick 2010). However, any sexually-antagonistic loci that are
more closely linked to the ancestral sex-determination locus will develop similar,
72 favourable associations and select against the spread of a new sex-determination
system. Here we extend these studies by explicitly calculating the the equilib-
74 rium allele frequencies of loci that are very tightly linked to the ancestral sex-
determining region.

76 It has been suggested that sex ratio selection is a dominant force in the evolu-
tion of sex determination (e.g., Bull 1983, p66-67; Beukeboom and Perrin 2014,
78 Chapter 7). The default mode of sex ratio selection is ‘Fisherian’ sex ratio se-
lection, which favours equal investment in male and female offspring (i.e., a 1:1
80 zygotic sex ratio when assuming that males and females are equally costly to pro-
duce, Fisher 1930, Charnov 1982). Given that the sex determination system can
82 directly affect the sex ratio, we might expect Fisherian sex ratio selection to influ-
ence the spread of new sex determination systems. For example, Kozielska et al.
84 (2010) consider systems in which the ancestral sex chromosomes experience mei-
otic drive (e.g., where driving X or Y chromosomes are inherited disproportion-
86 ately often), which causes sex ratios to become biased (Hamilton 1967). They find
that new, unlinked sex-determining loci (masculinizing or feminizing mutations,
88 i.e., neo-Y or neo-W loci) can then spread, which restore an even sex ratio.

Here, we use mathematical models to find the conditions under which new
90 sex determination systems are favoured when loci experience haploid selection.
Haploid genotypes at many loci experience selection during gamete competition
92 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
94 genotypes during gamete production (from one parent) and the term ‘gametic com-
petition’ to refer to selection upon haploid genotypes within a gamete/gametophyte
96 pool (potentially from by multiple parents); the term ‘haploid selection’ encom-

passes both processes. Meiotic drive generally occurs either during the production
98 of male or female gametes only (Úbeda and Haig 2005, Lindholm et al. 2016). Be-
cause there are typically many more pollen/sperm than required for fertilization,
100 gametic competition is also typically sex specific, occurring primarily among male
gametes. Gametic competition may be particularly common in plants, in which 60-
102 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
104 et al. 2013, Gossmann et al. 2014). In addition, artificial selection pressures ap-
plied to male gametophytes are known to cause a response to selection (e.g., Hor-
106 maza and Herrero 1996, Ravikumar et al. 2003, Hedhly et al. 2004, Clarke et al.
2004) and gametic selection appears to occur during the creation of F2 crosses
108 (Kumar, 2007). A much smaller proportion of genes are thought to be expressed
and selected during competition in animal sperm, although precise estimates are
110 uncertain (Zheng et al. 2001, Joseph and Kirkpatrick 2004, Vibranovski et al. 2010,
Immler et al. 2014).

112 There are various ways in which a period of haploid selection could influence
transitions between sex determination systems. If we assume that haploid selec-
114 tion at any particular locus predominantly occurs in one sex (e.g., meiotic drive
during spermatogenesis), then such loci experience a form of sex-specific selec-
116 tion. In this respect, we might expect that haploid selection would affect transitions
between sex determination systems in a similar manner to sex-specific diploid se-
118 lection (as explored by van Doorn and Kirkpatrick 2007; 2010). That is, new
masculinizing mutations (neo-Y chromosomes) could be favoured via associations
120 with alleles that are beneficial in the male haploid stage. However, sex ratios can
also become biased by linkage between the sex-determining region and a locus that
122 harbours genetic variation in haploid fitness. For example, there are several known
cases of sex ratio bias caused by sex-linked meiotic drive alleles (Burt and Trivers
124 2006, Chapter 3) or selection among X- and Y-bearing pollen (Lloyd 1974, Conn
and Blum 1981, Stehlik and Barrett 2005; 2006, Field et al. 2012; 2013). It is not
126 immediately clear how the spread of new sex determination systems would be in-

fluenced by the combination of sex ratio biases and associations between haploid
128 selected loci and sex-determining regions.

Surprisingly, our models show that haploid selection influences the evolution
130 of new sex determination systems in a way that is distinct from both diploid sex-
specific selection and Fisherian sex ratio selection. We find that the spread of
132 new sex determination systems are independent of there being a zygotic sex ratio
bias caused by associations between sex-determining regions and haploid selected
134 loci. In addition, we find that associations that build up between an ancestral sex-
determining locus and a haploid-selected locus can favour sex chromosome tran-
136 sitions between male and female heterogamety (e.g., a neo-W allele arising at a
previously autosomal locus spreads in an ancestrally XY system), despite the fact
138 that these ancestral associations were built up by selection. Such transitions are
not favoured in models lacking haploid selection.

140 **Model**

We consider the transition between ancestral and novel sex determination systems
142 using a three locus model. Locus **X** is the ancestral sex-determining region, with
alleles X and Y (or Z and W). Locus **A** is a locus under selection, with alleles
144 A and a . Locus **M** is a novel sex-determining region, at which the null allele (M)
is initially fixed in the population such that sex of zygotes is determined by the
146 genotype at the ancestral sex-determining region, **X**; XX genotypes become fe-
males and XY become males (or ZW become females and ZZ become males).
148 To evaluate the evolution of new sex-determination systems, we consider the inva-
sion, fixation, maintenance, and/or loss of novel sex-determining alleles (m) at the
150 **M** locus. We assume that the **M** locus is epistatically dominant over the **X** locus
such that zygotes with at least one m allele develop as females with probability
152 k and as males with probability $1 - k$, regardless of the **X** locus genotype. With
 $k = 0$, the m allele is a masculinizer (i.e., a neo-Y) and with $k = 1$ the m allele is a
154 feminizer (i.e., a neo-W). With intermediate k , the m allele confers environmental

sex determination (ESD) such that zygotes develop as females in a proportion (k)
 156 of the environments they (randomly) experience. Finally, we also analyze a model
 of maternally-controlled environmental sex-determination, where mothers with at
 158 least one m allele produce daughters with probability k .

In each generation, we census the genotype frequencies in male and female
 160 gametes/gametophytes (hereafter gametes) before gametic competition. A full de-
 scription of our model, including recursion equations, is given in the Appendix.
 162 First, competition occurs among male gametes (sperm/pollen competition) and
 among female gametes (egg/ovule competition) separately. Selection during ga-
 164 metic competition depends on the **A** locus genotype, relative fitnesses are given
 by w_A^{ϕ} and w_a^{ϕ} ($\phi \in \{\varphi, \sigma\}$; see table 1). We assume that all gametes compete for
 166 fertilization during gametic competition, which is not the case for monogamous
 mating systems where gametes from only one mating partner are present. Ga-
 168 metic competition in monogamous mating systems is equivalent to meiotic drive
 in our model, which only alters the frequency of gametes produced by heterozy-
 170 gotes. After gametic competition, random mating occurs between male and female
 gametes. The resulting zygotes develop as males or females, depending on their
 172 genotypes at the **X** and **M** loci (and the **M** genotype of their mother in the case of
 maternal control) as described above. Diploid males and females then experience
 174 selection, relative fitnesses are given by w_g^{ϕ} , where g is the diploid genotype at the
A locus ($g \in \{AA, Aa, aa\}$). The next generation of gametes is then produced
 176 by meiosis, during which recombination and sex-specific meiotic drive can occur.
 Recombination (i.e., an odd number of cross-overs) occurs between loci **X** and **A**
 178 with probability r , between loci **A** and **M** with probability R , and between loci **X**
 and **M** with probability χ . Any linear order of the loci can be modelled with ap-
 180 propriate choices of r , R , and χ (see Table S.1). Individuals that are heterozygous
 at the **A** locus may experience meiotic drive; Aa heterozygotes of sex ϕ produce
 182 gametes bearing allele A with probability α^{ϕ} . Thus, the **A** locus can experience
 sex-specific gametic competition, diploid selection, and/or meiotic drive.

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

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

184 Results

The only asymmetry between males and females in our model is that, under the
 186 ancestral sex determination system, males develop with genotype XY (or ZZ) and
 females with genotype XX (or ZW). Therefore, without loss of generality, we
 188 primarily present results for an ancestral XY sex determination system. Ancestral
 ZW sex determination can be considered by changing the notation such that X
 190 becomes Z , Y becomes W , and the labelling of male and female selection terms
 are reversed.

192 Turnover between sex-determination systems

The evolution of a new sex determination system requires that a rare mutant al-
 194 lele, m , at the novel sex-determining locus increases in frequency when rare. The
 spread of a rare mutant m at the \mathbf{M} locus is determined by the leading eigenvalue, λ ,
 196 of the system of eight equations describing the next generation frequency of eggs
 and sperm carrying the mutation, (S.1c, S.1d, S.1g, S.1h). This system simpli-
 198 fies 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
 200 diploids (neo-W) such that their growth rate ultimately depends only on the change
 in frequency of m -bearing gametes produced by males (for a neo-Y) or by females
 202 (for a neo-W). Furthermore, if the m allele is fully epistatically dominant over the
 ancestral sex-determining system, phenotypes are not affected by the genotype at
 204 the ancestral sex-determining region (\mathbf{X} locus). Thus, the invasion of rare domi-
 nant neo-Y or neo-W alleles is determined by the largest eigenvalue that solves the
 206 quadratic characteristic polynomial $\lambda^2 + b\lambda + c = 0$. In this case $b = -(\lambda_{mA} + \lambda_{ma})$
 and $c = \lambda_{mA}\lambda_{ma} - \rho_{mA}\rho_{ma}$, where λ_{mi} is the (multiplicative) growth rate of mutant
 208 haplotypes on background $i \in \{A, a\}$, accounting for loss due to recombination,
 and ρ_{mi} is the rate of addition of mutant haplotypes onto background $i \in \{A, a\}$
 210 due to recombination (see table 2). The spread of the mutant m allele depends
 on the frequency of alleles at the other two loci in the ancestral population. In
 212 the ancestral population, it is convenient to follow the frequency of the A allele
 in female gametes (eggs) from an XX female, p_X° , and in X-bearing, p_X^δ , and Y-
 214 bearing, p_Y^δ , male gametes (sperm). We also track the fraction of male gametes
 that are Y-bearing, q , which may deviate from $1/2$ due to meiotic drive in males.

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

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

$\bar{p}^\delta = p_Y^\delta q + p_X^\delta (1 - q)$ 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**.

See Table S.2 for expressions of mean haploid, \bar{w}_H^\varnothing , and diploid, \bar{w}^δ , fitnesses.

Table 2 illustrates a number of key points about the invasion of neo-Y and neo-W mutations. For a neo-Y, invasion is driven by the fitness of male gametes and diploids, where the latter is weighted by the chance that diploid arises, which depends on the frequency of A in eggs. For example, matings with A -bearing female gametes occur with probability $p_X^\varnothing w_A^\varnothing / \bar{w}_H^\varnothing$. Since a 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^\varnothing). 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. However, in the case of a neo-W, female diploids can result from matings with either an X-bearing or a Y-bearing sperm. In either case, the zygote will develop as a female due to the presence of a neo-W. For example, neo-W females will inherit an A allele from

230 a male gamete with probability $\bar{p}^\delta w_A^\delta / \bar{w}_H^\delta$, 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. By con-
 232 trast, females that do not carry the neo-W only result from matings with X-bearing
 sperm. They will therefore inherit an A from a male gamete with probability
 234 $(1 - q) \bar{p}_X^\delta w_A^\delta / \bar{w}_H^\delta$. If the A locus is initially linked to the ancestral sex-determining
 locus, \mathbf{X} , the frequency of the A allele among X- and Y-bearing sperm can differ
 236 (equation S.4). Thus, eggs with and without a neo-W differ in the frequency of A
 alleles they obtain from mating with male gametes.

238 We are particularly concerned with whether or not a rare neo-sex-determining
 allele increases in frequency, which occurs when the largest eigenvalue, λ , is greater
 240 than one. In the Appendix, we derive these conditions without assuming that se-
 lection is weak relative to recombination. Here, we explicitly determine the con-
 242 ditions under which invasion occurs by assuming that the A allele reaches an equi-
 librium frequency under the ancestral sex-determination system before the neo-
 244 sex-determination system (m) arises. The equilibrium frequency of A on different
 ancestral backgrounds (\hat{p}_Y^δ , \hat{p}_X^δ , and \hat{p}_Δ^δ) is given by equations (S.3) and (S.4) where
 246 we assume selection and meiotic drive are weak relative to recombination (s^δ , t^δ ,
 α_Δ^δ of order ϵ ; table 1). Under weak selection, we denote the leading eigenvalues
 248 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, which are given by

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

250 and

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

where $V_A = \bar{p}(1 - \bar{p})$ is the variance in the frequency of A and $S_A = (D^\delta + \alpha_\Delta^\delta + t^\delta) -$
 252 $(D^\varphi + \alpha_\Delta^\varphi + t^\varphi)$ is the difference in fitness in males versus females for the A allele
 against the a allele across diploid selection, gametic competition, and meiosis.

254 $D^{\phi} = (\bar{p}s^{\phi} + (1 - \bar{p})h^{\phi}s^{\phi}) - (\bar{p}h^{\phi}s^{\phi} + (1 - \bar{p}))$ is the difference in fitness between
 256 A and a alleles in diploids of sex $\phi \in \{\varphi, \sigma\}$; \bar{p} is the leading-order probability of
 mating with an A -bearing gamete from the opposite sex (see Appendix).

The neo-sex-determining allele m will spread if $\lambda_{m,XY} > 1$. Equation (1)
 258 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
 260 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
 262 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
 264 sexually-antagonistic selection.

Equation (2) shows that if there is no haploid selection ($t^{\phi} = \alpha_{\Delta}^{\phi} = 0$), as con-
 266 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
 268 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-
 270 loid selection, the additional term in equation (2) can be positive, which can allow,
 for example, neo-W invasion ($\lambda_{W',XY} > 1$) even when the neo-sex-determining
 272 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
 274 favourable in one sex and that sex will be weakened. Therefore, mean fitness can
 decrease (Figure 2B,D).

276 We find that neo-W alleles can invade an XY system for a large number of
 selective regimes. To clarify the parameter space under which $\lambda_{W',XY} > 1$, we
 278 consider several special cases. Firstly, if the \mathbf{A} locus is unlinked to the ancestral
 sex-determining region ($r = 1/2$), a more closely linked neo-W ($R < 1/2$) can
 280 always invade because $(\hat{p}_Y^{\phi} - \hat{p}_X^{\phi}) = 0$ such that the second term in equation (2)
 disappears and invasion depends only on the sign of $(r - R)$. Indeed, invasion
 282 typically occurs when the neo-W is more closely linked to the selected locus than
 the ancestral sex-determining region (Figure 3). Secondly, we can simplify cases

284 where invasion occurs despite $R > r$ using the special case where $R = 1/2$ and $r <$
 286 $1/2$ (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
 occurs when we further assume that haploid selection only occurs in one sex (e.g.,
 288 during male meiosis only) and dominance coefficients are equal in the two sexes,
 $h^{\varphi} = h^{\delta}$. Where there is no gametic competition and meiotic drive in one sex
 290 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 3B). When there
 292 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
 294 selection and there are sex differences in selection of one type (e.g., $s^{\varphi}(s^{\delta} - s^{\varphi}) > 0$,
 see Figure 3C,D). These special cases indicate that neo-W invasion can occur for
 296 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	$h^{\delta} = h^{\varphi}, t^{\varphi} = t^{\delta} = \alpha_{\Delta}^{\varphi} = 0$	$s^{\varphi}s^{\delta} > 0$
female drive only	$h^{\delta} = h^{\varphi}, t^{\varphi} = t^{\delta} = \alpha_{\Delta}^{\delta} = 0$	$s^{\varphi}s^{\delta} > 0$
sperm competition only	$h^{\delta} = h^{\varphi}, t^{\varphi} = \alpha_{\Delta}^{\varphi} = \alpha_{\Delta}^{\delta} = 0$	$s^{\varphi}(s^{\delta} - s^{\varphi}) > 0$
egg competition only	$h^{\delta} = h^{\varphi}, t^{\delta} = \alpha_{\Delta}^{\varphi} = \alpha_{\Delta}^{\delta} = 0$	$s^{\delta}(s^{\varphi} - s^{\delta}) > 0$

298 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-
 300 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-
 302 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
 304 **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, $\alpha^{\delta} \neq 1/2$,
 306 $\alpha^{\varphi} = 1/2$). We will also disregard gametic competition ($t^{\varphi} = t^{\delta} = 0$) such that

zygotic sex ratios are only biased by meiotic drive in males. In this case, the zy-
 308 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
 310 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
 312 zygotic sex ratio is crucial to the evolution of new genetic sex-determining sys-
 tems, invasion into ZW and XY systems will be distinct. However, we find that
 314 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) oc-
 316 cur 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
 318 1A,B to Figure 1C,D).

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

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

324 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 invest-
 326 ment 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
 328 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
 330 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.
 332 However, we find that the growth rate of a rare, dominant offspring-controlled
 neo-ESD allele that produces males or females with equal probability ($k = 1/2$)
 334 is

$$\lambda_{ESD',XY} = 1 + \frac{1}{2} \frac{(\lambda_{Y',XY} - 1) + (\lambda_{W',XY} - 1)}{2} \Big|_{R=1/2} + O(\epsilon^3), \quad (4)$$

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

Equation (4) shows that invasion by a novel 'perfect' ESD (equal sex ratio,
 340 $k = 1/2$) mutation is the same for an ancestrally XY or ZW system (since $\lambda_{Y',XY} =$
 $\lambda_{W',ZW}$, $\lambda_{W',XY} = \lambda_{Y',ZW}$). Thus, by the same argument as above (if drive occurs
 342 in males only then the sex ratio is only biased when the ancestral sex-determination
 system is XY), Fisherian sex ratio selection does not explain invasion by an offspring-
 344 controlled neo-ESD locus. Rather, the neo-ESD gets half of the fitness of a femi-
 nizing mutation (neo- W) and half of the fitness of a masculinizing mutation (neo- Y),
 346 but only has an effect one half of the time (the other half of the time it produces
 the same sex as the ancestral system would have, to leading order). The net result
 348 can be that perfect ESD will not invade, even if current sex ratios are biased. For
 example, if there is haploid selection in males (either drive or pollen/sperm com-
 350 petition) but the conditions in table 3 are not met, perfect ESD will not invade,
 even though it would equalize the zygotic sex ratio from an initially biased case
 352 (assuming $r < 1/2$).

Fisherian sex ratio selection is sometimes considered in terms of balancing
 354 parental investment in male versus female offspring (Charnov 1982). In addition,
 under environmental sex-determination, the proportion of males/females is some-
 356 times controlled by the mother, e.g., the proportion of eggs laid in warm versus
 cold environments could determine the sex ratio of offspring. We therefore also
 358 considered the invasion of a neo-sex-determining allele (m) in a model in which
 mothers that have at least one m allele produce daughters with probability k . As

360 with offspring-controlled ESD, for all $k \in \{0, 1/2, 1\}$, we find that invasion into
an ancestrally XY system is the same as invasion into an ancestrally ZW system (at
362 least up to order ϵ^3), implying transitions between genetic sex determination and
maternally controlled environmental sex determination are not driven by Fisherian
364 sex ratio selection on biased zygotic sex ratios.

Discussion

366 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;
368 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
370 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
372 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
374 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
376 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
378 same inheritance pattern as the non-mutant allele. The mutations we consider
here, neo-sex-determining alleles, break this assumption. For example, the suc-
380 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-
382 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
384 to be found in males or females, such as an environmental sex determination mu-
tation (equation 4), are not strictly autosomal if they determine sex. Thus, despite
386 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

388 (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-
390 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).

392 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
394 is local mate competition, where all matings are between siblings and assuming
one male can inseminate many females (Hamilton 1967). Therefore, with local
396 mate competition, feminizing mutations can spread because they bias the sex ratio
towards females (Wilson and Colwell 1981, Vuilleumier et al. 2007). Secondly,
398 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-
400 location to males/females depends on the environment (Trivers and Willard 1973,
Charnov and Bull 1977, Charnov 1982). In such cases, flexible sex determination
402 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
404 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,
406 West 2009).

It has previously been demonstrated that new sex-determining systems can
408 evolve if there is genetic variation maintained by sexually-antagonistic selection
(van Doorn and Kirkpatrick 2007; 2010). In particular, transitions to new sex-
410 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
412 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
414 are linked with a locus under haploid selection and the ancestral sex-determination
locus is not. However, with haploid selection, heterogametic transitions (XY to
416 ZW or ZW to XY) can also occur when the new sex-determining region is less
closely linked to the locus under selection.

418 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
420 system. With sexually antagonistic selection (between diploid sexes) only, linkage
between a selected locus and the sex-determining region strengthens associations
422 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,
424 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
426 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-
428 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
430 neo-W (neo-Y) alleles can invade, see figure 2.

We assume that sex-determining alleles do not experience direct selection ex-
432 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
434 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
436 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
438 that all individuals have YY or WW genotypes (Figure 1). Any recessive delete-
rious alleles linked to the Y or W will therefore be revealed to selection during a
440 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
442 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
444 very rare recombination events around the ancestral sex-determining region can
allow these heterogametic transitions to complete. While not explicitly studied,
446 we also predict that Y or W degeneration would prevent fixation of the new sex-
determiners considered here.

448 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-
450 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
452 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-
454 duced recombination between sex chromosomes (Hurst and Pomiankowski 1991).
Furthermore, in some cases, a driving allele may act by killing any gametes that
456 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.
458 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
460 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
462 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
464 evolution of new sex determination system could be influenced by these dynam-
ics. How the evolution of new sex-determining mechanisms could be influenced
466 by two-locus meiotic drive and/or by ecological feedbacks under different mating
systems remains to be studied.

468 The hypotheses presented here can be empirically investigated in a similar
manner to the idea that transitions between sex-determining systems are favoured
470 by linkage to sexually antagonistic variation. In the case of sexually antagonis-
tic variation, one supporting observation is that genes that appear to experience
472 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,
474 it is possible that sexually antagonistic variation accumulated after sex chromo-
some transitions because linkage with the sex-determining regions allows sexu-
476 ally antagonistic selection to maintain polymorphisms under a larger parameter
space (Rice 1987, Jordan and Charlesworth 2011). We note that linkage with sex

478 chromosomes is not, a priori, more permissive to the maintenance of ploidy an-
tagonistic variation (Immler et al. 2012). However, as with sexually-antagonistic
480 variation, a comparison between closely related clades could indicate whether
a polymorphism pre-dates a transition in sex-determination or arose afterwards.
482 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
484 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
486 sex chromosome turnover.

Taken at face value, our results indicate that transitions in heterogamety (XY
488 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
490 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
492 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
494 after spermatogenesis because transcripts shared during spermatogenesis may be-
come depleted, revealing the haploid phenotype of the sperm (Immler et al. 2014).
496 Given the caveats mentioned above about the form of meiotic drive modelled, we
would also expect that heterogametic transitions in sex determination would be
498 more common in clades where there is meiotic drive.

We have shown that haploid selection can drive transitions between sex de-
500 termination systems, such that haploid selection should be incorporated into the
factors that influence the evolution of sex determination. However, the particular
502 way in which transitions are affected by haploid selection is not intuitively obvious.
Firstly, sex-specific haploid selection affects turnovers between sex determination
504 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
506 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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702 **Figures**

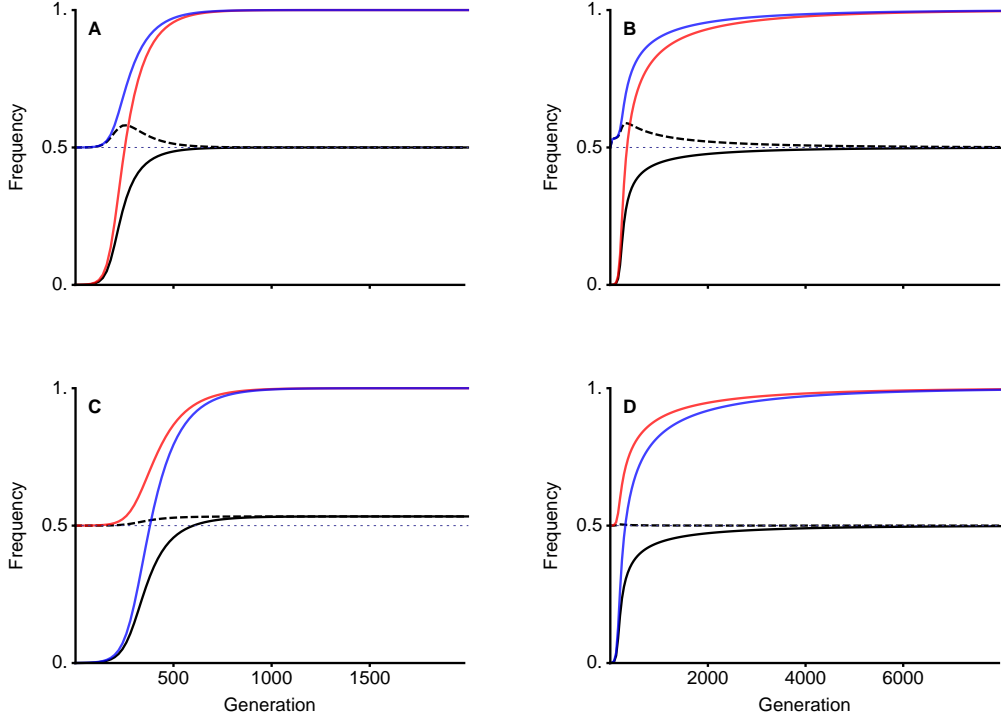


Figure 1: Heterogametic transitions from XY to ZW sex determination (neo-W frequency shown by black lines, panels A and B) or from ZW to XY (neo-Y frequency shown by black lines, panels C and D) occur similarly regardless of sex ratio biases present before (B versus D) or after (C versus A, dashed lines 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 ($r^{\text{f}} = r^{\text{d}} = 0$) and meiotic drive occurs during male meiosis only ($\alpha_{\Delta}^{\text{f}} = 0$, $\alpha_{\Delta}^{\text{d}} = -1/5$). 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 (2) 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, $s^{\text{f}} = s^{\text{d}} = 1/5$, $h^{\text{f}} = h^{\text{d}} = 7/10$.

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).

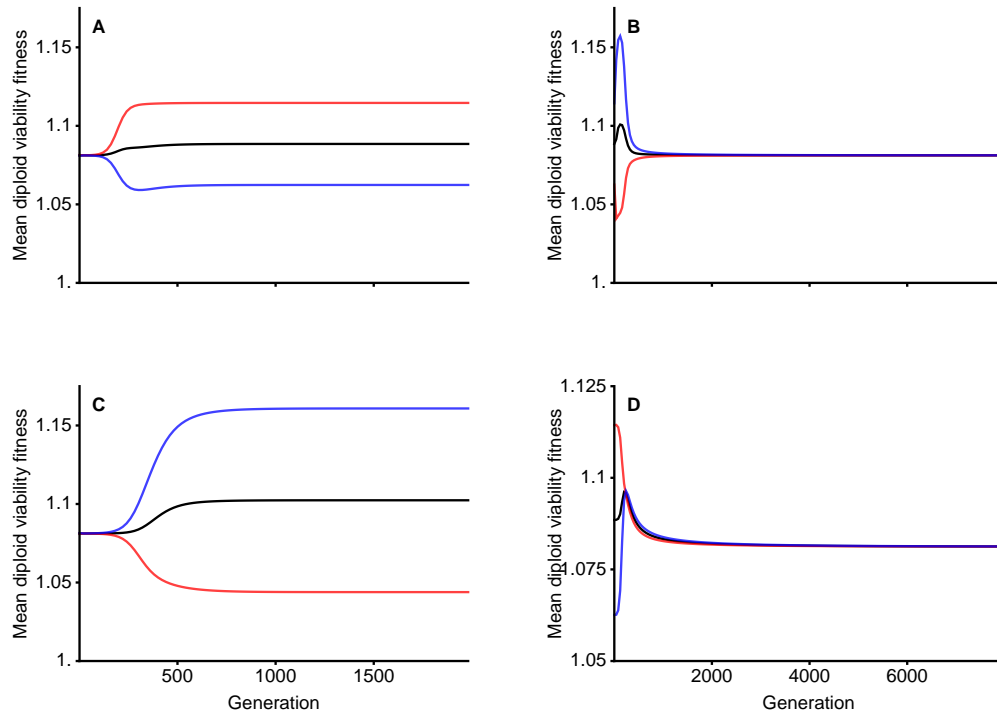


Figure 2: Here, we plot how male mean fitness (blue lines), female mean fitness (red lines), and population mean fitness (male mean fitness plus female mean fitness, black lines) changes during the transitions between sex-determination systems shown in Figure 1. Here we multiply male mean fitness and 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).

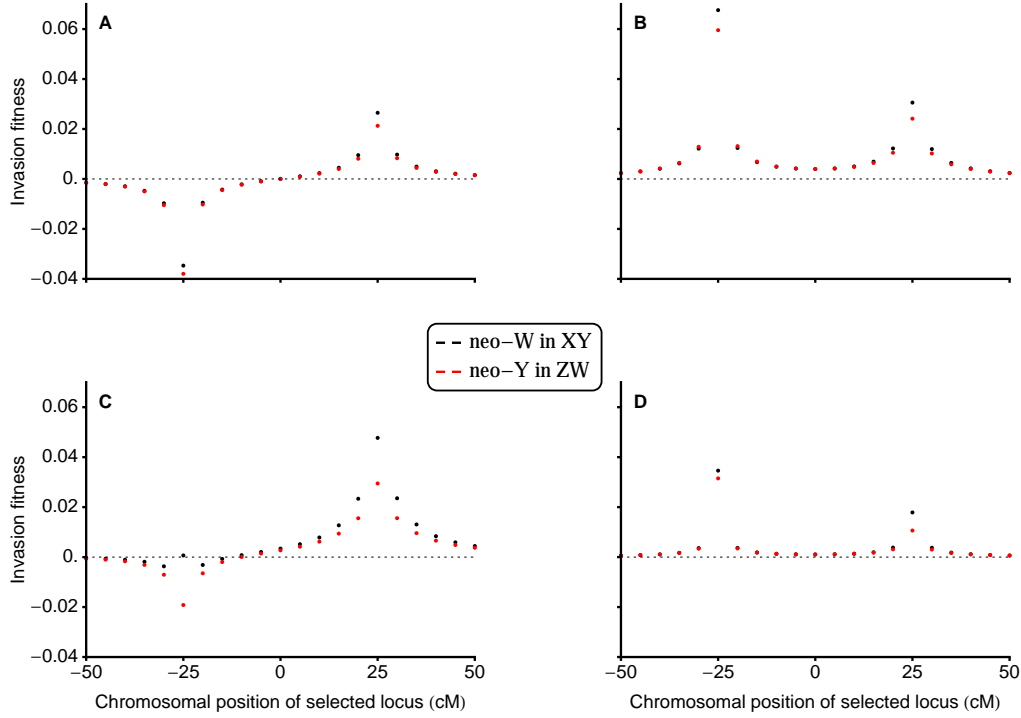


Figure 3: The invasion fitness of a neo-W allele plotted against the relative location of a locus under direct selection, **A**, for various selective regimes. We assume that the ancestral sex-determining locus is located at -0.25, the novel sex-determining locus is located at 0.25 and that there is 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**

Appendix

704 Recursion Equations

In each generation we census the genotype frequencies in male and female gametes/gametophytes (hereafter, gametes) after meiosis (and any meiotic drive) and immediately before gametic competition. At this stage, the frequencies of X-bearing male and female gametes are given by X_i^δ and X_i^φ and the frequencies of Y-bearing gametes are given by Y_i^δ and Y_i^φ where the index i specifies genotypes $MA = 1$, $Ma = 2$, $mA = 3$, and $ma = 4$ ($\sum_{i=1}^4 Y_i^\delta + X_i^\delta = 1$ and $\sum_{i=1}^4 Y_i^\varphi + X_i^\varphi = 1$). Competition then occurs among gametes of the same sex (e.g., among eggs and among sperm separately) according to the **A** locus allele, g ($g \in A, a$, see Table 1), carried by individuals with genotype i . The genotype frequencies after gametic competition are $X_i^{\delta,s} = w_g X_i^\delta / \bar{w}_H^\delta$ and $Y_i^{\delta,s} = w_g Y_i^\delta / \bar{w}_H^\delta$, where $\bar{w}_H^\delta = \sum_{i=1}^4 w_g X_i^\delta + w_g Y_i^\delta$ is the mean fitness of male ($\delta = \delta$) or female ($\delta = \varphi$) gametes. Random mating then occurs between gametes to produce diploid zygotes with genotype ij at the **A** and **M** loci, such that XX zygotes are denoted xx_{ij} , XY zygotes are xy_{ij} , and YY zygotes are yy_{ij} . In XX and YY zygotes, individuals with genotype ij are equivalent to those with genotype ji ; for simplicity, we denote the frequency of genotype ij to 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 $yy_{ij} = (Y_i^{\varphi,s} Y_j^{\delta,s} + Y_j^{\varphi,s} Y_i^{\delta,s})/2$.

722 Denoting the **M** locus genotype by b ($b \in MM, Mm, mm$) and the **X** locus 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 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 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

732 that the ancestral sex-determining system (**X** locus) is XY ($k_{MMXX} = 1$ and
 $k_{MMXY} = k_{MYY} = 0$) and epistatically recessive to a dominant novel sex-
734 determining locus, **M** ($k_{Mmc} = k_{mmc} = k$).

Selection among diploids then occurs according to the diploid genotype at the
736 **A** locus, h , for an individual of type ij ($h \in AA, Aa, aa$, see Table 1). The
diploid frequencies after selection in sex ϕ are given by $xx_{ij}^{\phi,s} = w_h^{\phi}xx_{ij}/\bar{w}^{\phi}$,
738 $xy_{ij}^{\phi,s} = w_h^{\phi}xy_{ij}/\bar{w}^{\phi}$, and $yy_{ij}^{\phi,s} = w_h^{\phi}yy_{ij}/\bar{w}^{\phi}$, where $\bar{w}^{\phi} = \sum_{i=1}^4 \sum_{j=1}^4 w_h^{\phi}xx_{ij} +$
 $w_h^{\phi}xy_{ij} + w_h^{\phi}yy_{ij}$ is the mean fitness of individuals of sex ϕ .

740 Finally, these diploids undergo meiosis to produce the next generation of ga-
metes. Recombination and sex-specific meiotic drive occur during meiosis. Here,
742 we allow the relative locations of the SDR, **A**, and **M** loci to be generic by using
three parameters to describe the recombination rates between them. R is the re-
744 combination rate between the **A** locus and the **M** locus, χ is the recombination rate
between the **M** locus and the **X** locus, and r is the recombination rate between the
746 **A** locus and the **X** locus. Table S.1 gives substitutions for χ for defined relative
locations of these loci. During meiosis in sex ϕ , meiotic drive occurs such that, in
748 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	$\chi = (R - r)/(1 - 2r)$

750 Among gametes from sex ϕ (sperm/pollen when $\phi = \sigma$, eggs/ovules when
 $\phi = \varphi$), the frequencies of haplotypes (before gametic competition) in the next
752 generation are given by

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

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

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

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

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

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

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

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

754 The full system is therefore described by 16 recurrence equations (three loci, each
 with two alleles, and two gamete sexes yields 16 combinations). However, some
 756 diploid types are not produced under a given sex determination system. For exam-
 ple, with the M allele fixed and ancestral XY sex determination, there are no XX
 758 males, XY females, or YY females ($xx_{11}^{\phi}, xx_{12}^{\phi}, xx_{22}^{\phi}, xy_{11}^{\phi}, xy_{12}^{\phi}, xy_{22}^{\phi}, yy_{11}^{\phi}, yy_{12}^{\phi}$,
 and yy_{22}^{ϕ} are all 0). In this case, the system only involves six recursion equations
 760 because there is only one M locus allele and no Y-bearing female gametes. This
 six-equation system yields equilibrium (S.3).

762 **Resident equilibrium and stability**

In the resident population (allele M fixed), we follow the frequency of A in female
 764 gametes (eggs) from an XX female, p_X^{ϕ} , and in X-bearing, p_X^{ϕ} , and Y-bearing,
 p_Y^{ϕ} , male gametes (sperm). We also track the total frequency of Y among male
 766 gametes, q , which may deviate from 1/2 due to meiotic drive in males. Within this
 resident population (when m is absent) we can then describe frequencies among
 768 different gamete types, which are given by $X_{MA}^{\phi} = p_X^{\phi}$, $X_{Ma}^{\phi} = (1 - p_X^{\phi})$, $X_{MA}^{\delta} =$
 $(1 - q)p_X^{\phi}$, $X_{Ma}^{\delta} = (1 - q)(1 - p_X^{\phi})$, $Y_{MA}^{\phi} = qp_Y^{\phi}$, and $Y_{Ma}^{\phi} = q(1 - p_Y^{\phi})$. Mean
 770 fitnesses in this resident population are given in table S.2.

Various forms of selection can maintain a polymorphism at the A locus, includ-
 772 ing sexually antagonistic selection, overdominance and conflicts between diploid
 selection and selection upon haploid genotypes (ploiddally antagonistic selection,

774 Immler et al. 2012) or a combination of these selective regimes.

Table S.2: mean fitnesses in resident (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}^\varnothing)	$\frac{\{p_X^\varnothing w_A^\varnothing p_X^\delta w_A^\delta w_{AA}^\varnothing + (1 - p_X^\varnothing) w_a^\varnothing p_X^\delta w_A^\delta w_{Aa}^\varnothing + p_X^\varnothing w_A^\varnothing (1 - p_X^\delta) w_a^\delta w_{Aa}^\varnothing + (1 - p_X^\varnothing) w_a^\varnothing (1 - p_X^\delta) w_a^\delta w_{aa}^\varnothing\}}{\{\bar{w}_H^\varnothing \bar{w}_H^\delta\}}$
males (\bar{w}^δ)	$\frac{\{p_X^\varnothing w_A^\varnothing p_Y^\delta w_A^\delta w_{AA}^\delta + (1 - p_X^\varnothing) w_a^\varnothing p_Y^\delta w_A^\delta w_{Aa}^\delta + p_X^\varnothing w_A^\varnothing (1 - p_Y^\delta) w_a^\delta w_{Aa}^\delta + (1 - p_X^\varnothing) w_a^\varnothing (1 - p_Y^\delta) w_a^\delta w_{aa}^\delta\}}{\{\bar{w}_H^\delta \bar{w}_H^\varnothing\}}$

Recombination weak relative to selection

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

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

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

782 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
784 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
786 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
788 (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
790 a allele. If there is no haploid selection ($\alpha^\delta = 1/2$, $w_g^\delta = 1$), these equilibria are
equivalent to those found by [Otto \(2014\)](#) and [Lloyd \(197?, see Otto for reference\)](#).

792 We next calculate when (A) and (B) are locally stable for $r = 0$. According to
the ‘small parameter theory’ (??), these stability properties are unaffected by small

794 amounts of recombination between the SDR and **A** locus, although equilibrium
frequencies may be slightly altered. For the *a* allele to be stably fixed on the Y
796 requires that $\bar{w}_{Ya}^\delta > \bar{w}_{YA}^\delta$ where $\bar{w}_{Ya}^\delta = w_a^\delta(2p_X^\varnothing(1 - \alpha^\delta)w_A^\varnothing w_{Aa}^\delta + (1 - p_X^\varnothing)w_a^\varnothing w_{aa}^\delta)$
and $\bar{w}_{YA}^\delta = w_A^\delta(p_X^\varnothing w_A^\varnothing w_{AA}^\delta + 2(1 - p_X^\varnothing)\alpha^\delta w_a^\varnothing w_{aa}^\delta)$. That is, *Ya* haplotypes must
798 have higher fitness than *YA* haplotypes. Substituting \hat{p}_{Xf} from above, fixation of
the *A* allele on the Y requires that $\gamma_i > 0$ where $\gamma_{(A)} = w_a^\delta(2(1 - \alpha^\delta)w_{Aa}^\delta \Phi +$
800 $w_{aa}^\delta \Psi) - w_A^\delta(2\alpha^\delta w_{Aa}^\delta \Phi + w_{aa}^\delta \Psi)$ 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 polymorphism on the X chromosome
802 (equilibrium *A'*) further requires that $\Phi > 0$ and $\Psi > 0$. Fixation of the *a* allele
on the X (equilibrium *B*) is mutually exclusive with (*A*) and requires that $\Psi < 0$
804 and $w_A^\varnothing w_{AA}^\varnothing > (1 - \alpha^\varnothing)w_a^\varnothing w_{Aa}^\varnothing$.

Selection weak relative to recombination

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

$$\begin{aligned} 0 &< -((1 - h^\varnothing)s^\varnothing + (1 - h^\delta)s^\delta + t^\varnothing + t^\delta + \alpha_\Delta^\varnothing + \alpha_\Delta^\delta) \\ \text{and } 0 &< (h^\varnothing s^\varnothing + h^\delta s^\delta + t^\varnothing + t^\delta + \alpha_\Delta^\varnothing + \alpha_\Delta^\delta). \end{aligned} \quad (\text{S.2})$$

which indicates that a polymorphism is maintained under various selective regimes.
810 In particular special cases, e.g., no sex-differences in selection or meiotic drive
($s^\delta = s^\varnothing, h^\delta = h^\varnothing$, and $\alpha^\delta = \alpha^\varnothing = 1/2$), the equilibrium allele frequency and
812 stability can be calculated analytically without assuming weak selection. How-
ever, here, we focus on weak selection in order to make fewer assumptions about
814 fitnesses.

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

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

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

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

820 where $V_A = \bar{p}(1 - \bar{p})$ is the variance in the frequency of A and $D^{\varphi} = (\bar{p}s^{\varphi} + (1 - \bar{p})h^{\varphi}s^{\varphi}) - (\bar{p}h^{\delta}s^{\delta} + (1 - \bar{p}))$ corresponds to the difference in fitness between A and
822 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
824 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
826 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 ($\alpha_{\Delta}^{\varphi} = t^{\varphi} = 0$), these results reduce to those of van Doorn and Kirkpatrick
828 (2007).

Invasion conditions

830 Here, we determine whether a rare neo- Y or neo- W allele spreads when rare, which occurs when $\lambda > 1$. If the average change in frequency of the two haplotypes that
832 carry the m allele (Am and am) is positive, invasion will always occur (i.e., if $\{(\lambda_{mA} - 1) + (\lambda_{ma} - 1)\} / 2 > 0$ then $\lambda > 1$, see table 2 for λ_{mi}). If neither haplo-
834 type increases in frequency ($\lambda_{mA}, \lambda_{ma} < 1$), the m allele will not invade. Otherwise, the new sex-determining allele increases in frequency on one A background and

836 declines on the other, and invasion requires

$$R \left[\frac{p_X^\varphi w_A^\varphi w_a^\delta (1 - \alpha^\delta)}{\bar{w}_H^\varphi \bar{w}_H^\delta (\lambda_{mA} - 1)} + \frac{(1 - p_X^\varphi) w_a^\varphi w_A^\delta \alpha^\delta}{\bar{w}_H^\varphi \bar{w}_H^\delta (\lambda_{ma} - 1)} \right] \frac{w_{Aa}^\delta}{q \bar{w}^\delta} < 1, \quad (\text{S.5})$$

838 for the neo- Y , and

$$R \left[\frac{\bar{p}^\delta w_A^\delta w_a^\varphi (1 - \alpha^\varphi)}{\bar{w}_H^\delta \bar{w}_H^\varphi (\lambda_{mA} - 1)} + \frac{(1 - \bar{p}^\delta) w_a^\delta w_A^\varphi \alpha^\varphi}{\bar{w}_H^\delta \bar{w}_H^\varphi (\lambda_{ma} - 1)} \right] \frac{w_{Aa}^\varphi}{(1 - q) \bar{w}^\varphi} < 1, \quad (\text{S.6})$$

for the neo- W .