S1 Appendix

Recursion equations

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

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

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

Denoting the $M$ locus genotype by $b \in \{M M, M m, m m\}$ and the $X$ locus genotype by $c \in \{X X, X Y, Y Y\}$, zygotes develop as females with probability $k_{bc}$. Therefore, the frequencies of $XX$ females are given by $x x_j^b = k_{bc} x x_j$, $XY$ females are given by $x y_j^b = k_{bc} y y_j$, and $YY$ females are given by $y y_j^b = k_{bc} y y_j$. Similarly, $XX$ male frequencies are $x x_j^b = (1 - k_{bc}) x x_j$, $XY$ male frequencies are $x y_j^b = (1 - k_{bc}) x y_j$, and $YY$ male frequencies are $y y_j^b = (1 - k_{bc}) y y_j$. This notation allows both the ancestral and novel sex-determining regions to determine zygotic sex according to an $XY$ system, a $ZW$ system, or an environmental sex-determining system. In addition, we can consider any epistatic dominance relationship between the two sex-determining loci. Here, we assume that the ancestral sex-determining system ($X$ locus) is $XY$ ($k_{MMXY} = 1$ and $k_{MmXY} = 0$) or $ZW$ ($k_{MMZW} = 0$ and $k_{MMZW} = 1$) and epistatically recessive to a dominant novel sex-determining locus, $M$ ($k_{Mmc} = k_{mmc} = k$).

Selection among diploids then occurs according to the diploid genotype at the $A$ locus, $l \in \{AA, A a, a a\}$, for an individual of type $ij$ (see Table 1). The diploid frequencies after selection in sex $\sigma$ are given by $x x_{ij}^a = w_\sigma^a x x_{ij} / \hat{w}_D$, $x y_{ij}^a = w_\sigma^a x y_{ij} / \hat{w}_D$, and $y y_{ij}^a = w_\sigma^a y y_{ij} / \hat{w}_D$, where $\hat{w}_D = \sum_i \sum_j w_\sigma^i x x_{ij} + w_\sigma^i x y_{ij} + w_\sigma^i y y_{ij}$ is the mean fitness of diploids of sex $\sigma$.

Finally, these diploids undergo meiosis to produce the next generation of gametes. Recombination and sex-specific meiotic drive occur during meiosis. Here, we allow any relative locations for the $X$, $A$, and $M$ loci by using three parameters to describe the recombination rates between them. $R$ is the recombination rate between the $A$ and $M$ loci, $\rho$ is the recombination rate between the $M$ and $X$ loci, and $r$ is the recombination rate between the $A$ and $X$ loci (Fig 1). S1 Table shows replacements that can be made for each possible ordering of the loci assuming that there is no cross-over interference. During meiosis in sex $\sigma$, meiotic drive occurs such that,
in Aa heterozygotes, a fraction $a^o$ of gametes produced carry the $A$ allele and $(1 - a^o)$ carry the $a$ allele.

Among gametes from sex $o$, the frequencies of haplotypes (before gametic competition) in the next generation are given by

$$x_1^{o'} = x_{11}^{o,s} + x_{13}^{o,s}/2 + (x_{12}^{o,s} + x_{14}^{o,s})a^o$$
$$- R(x_{14}^{o,s} - x_{23}^{o,s})a^o$$
$$+ (x_{11}^{o,s} + x_{13}^{o,s})/2 + (x_{12}^{o,s} + x_{14}^{o,s})a^o$$
$$- r(x_{12}^{o,s} - x_{13}^{o,s})a^o - \rho(x_{13}^{o,s} - x_{11}^{o,s})/2$$
$$+ \left[ - (R + r + \rho)x_{14}^{o,s} + (R + \rho - r)x_{12}^{o,s} + (R + r - \rho)x_{13}^{o,s} \right] a^o/2$$ \hfill (S1.1a)

$$x_2^{o'} = x_{22}^{o,s} + x_{24}^{o,s}/2 + (x_{22}^{o,s} + x_{23}^{o,s})a^o$$
$$- R(x_{23}^{o,s} - x_{24}^{o,s})a^o$$
$$(x_{22}^{o,s} + x_{24}^{o,s})/2 + (x_{22}^{o,s} + x_{23}^{o,s})(1 - a^o)$$
$$- r(x_{21}^{o,s} - x_{12}^{o,s})(1 - a^o) - \rho(x_{23}^{o,s} - x_{24}^{o,s})/2$$
$$+ \left[ - (R + r + \rho)x_{14}^{o,s} + (R + \rho - r)x_{12}^{o,s} + (R + r - \rho)x_{23}^{o,s} \right] (1 - a^o)/2$$ \hfill (S1.1b)

$$x_3^{o'} = x_{33}^{o,s} + x_{13}^{o,s}/2 + (x_{23}^{o,s} + x_{34}^{o,s})a^o$$
$$- R(x_{23}^{o,s} - x_{14}^{o,s})a^o$$
$$(x_{33}^{o,s} + x_{31}^{o,s})/2 + (x_{23}^{o,s} + x_{34}^{o,s})a^o$$
$$- r(x_{34}^{o,s} - x_{24}^{o,s})a^o - \rho(x_{31}^{o,s} - x_{33}^{o,s})/2$$
$$+ \left[ - (R + r + \rho)x_{14}^{o,s} + (R + \rho - r)x_{12}^{o,s} + (R + r - \rho)x_{23}^{o,s} \right] (1 - a^o)/2$$ \hfill (S1.1c)

$$x_4^{o'} = x_{44}^{o,s} + x_{34}^{o,s}/2 + (x_{24}^{o,s} + x_{14}^{o,s})a^o$$
$$- R(x_{14}^{o,s} - x_{23}^{o,s})a^o$$
$$(x_{44}^{o,s} + x_{42}^{o,s})/2 + (x_{24}^{o,s} + x_{43}^{o,s})(1 - a^o)$$
$$- r(x_{34}^{o,s} - x_{43}^{o,s})(1 - a^o) - \rho(x_{42}^{o,s} - x_{44}^{o,s})/2$$
$$+ \left[ - (R + r + \rho)x_{14}^{o,s} + (R + \rho - r)x_{12}^{o,s} + (R + r - \rho)x_{23}^{o,s} \right] (1 - a^o)/2$$ \hfill (S1.1d)

$$y_1^{o'} = y_{11}^{o,s} + y_{13}^{o,s}/2 + (y_{12}^{o,s} + y_{14}^{o,s})a^o$$
$$- R(y_{24}^{o,s} - y_{34}^{o,s})a^o$$
$$(x_{11}^{o,s} + x_{13}^{o,s})/2 + (x_{12}^{o,s} + x_{14}^{o,s})a^o$$
$$- r(x_{21}^{o,s} - x_{12}^{o,s})a^o - \rho(x_{13}^{o,s} - x_{11}^{o,s})/2$$
$$+ \left[ - (R + r + \rho)x_{14}^{o,s} + (R + \rho - r)x_{12}^{o,s} + (R + r - \rho)x_{23}^{o,s} \right] a^o/2$$ \hfill (S1.1e)
The full system is therefore described by 16 recurrence equations (three diallelic loci in two sexes, $2^3 \times 2 = 16$). However, not all diploid types are produced under certain sex-determining systems. For example, with the $M$ allele fixed and an ancestral XY sex-determining system, there are XX females and XY males ($x_3^0 = x_3^1 = y_3^0 = y_3^1 = y_4^0 = y_4^1 = 0$, $\forall i$). In this case, the system only involves six recursion equations, which we assume below to calculate the equilibria.