**Supplementary Material**

For

**Transitions in sex determination mechanisms through parental and sexual antagonism**

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# Supplementary Methods

## Model initialization

The model presented here is a modified version of that presented by Schenkel et al. (2021). It features two linkage groups, each of which consists of two loci, being the (potential) sex determination locus and the parentally- or sexually-antagonistic locus. All loci feature two possible alleles, which can be denoted using a 0 or 1. Each linkage group therefore features 4 potential haplotypes, each consisting of an allele at the sex determination locus and an allele at the parentally-/sexually-antagonistic locus. I denote non-sex determining alleles *+* on both linkage groups with a 0 and the sex-determining alleles and with a 1. Similarly, the parentally/sexually-antagonistic alleles and at linkage group are indicated using 0 and 1 respectively, so that e.g. a 11 haplotype consists of a dominant sex-determining allele and an allele , and a 00 haplotype consists of the recessive (non-sex-determining) allele and an allele . I define an array for which each element gives the initial frequency of the th haplotype () on linkage group on the maternal () and paternal () copy. Using , I define the initial population , an array with dimension in which and are arrays wherein each element gives the frequency of a haplotype on linkage group 1 and on linkage group 2; subscripts and are used to distinguish between frequencies of the maternal and paternal copies of these haplotypes. Consequently, each element in gives the frequency of the genotype that consists of haplotypes and for the maternal c.q. paternal copy of linkage group 1, and similarly and for linkage group 2. Per locus (), I define an array that counts the number of focal alleles (, ) in each element of , so that the inner product gives the population frequency of the focal allele at that locus.can be further split up into and , which give the number of the focal alleles on the maternal and paternal copies. Combinations (and where applicable transformations) of different arrays (and possibly the sex-determining arrays ; see details below) can be used to track the frequencies of different haplotypes in different sexes and of different parental origins (e.g., the entrywise product of gives the frequency of a paternally-inherited haplotype with alleles and ).

## Sex determination

Sex is determined by the number of focal alleles at the and loci, and depends on whether is a male-determining allele with identical function to , or a female-determining allele that is dominant to . I define a binary array which denotes whether a genotype in is male (1) or not (0); the binary array indicates whether a genotype is female. If has a male-determining function, then a genotype in is male if , and female otherwise. If has a female-determining function, a genotype in is male if , and female otherwise. The entrywise products and represent the frequencies of genotypes among females () and males (). Similar to the population-level frequency of the focal allele at locus , the frequencies of the focal alleles among females and males are given by the inner products of and .

## Fitness and selection

Fitness is determined by the genotypes at the and loci. For each locus, I define a vector (for both sexes, assuming parentally-antagonistic selection) or for females and for males (assuming sexually-antagonistic selection) that gives the fitness scores of respectively genotypes , , , and (where the initial allele indicates the maternal copy and the second allele the paternal copy). Under parentally-antagonistic selection, is the selective effect of the allele in homozygotes, and and are modifiers that determine the selective cost or benefit of the allele in heterozygotes when maternally- or paternally-inherited. I assume that has a fitness costs in heterozygotes when maternally-inherited (), but a fitness benefit when paternally-inherited (). Under sexually-antagonistic selection, () represents the selective effect of () in females (males), and () represents its dominance in female (male) or heterozygotes. An array contains the fitness scores of each genotype in based on the genotype at , and similarly for the genotype at . These locus-specific fitness scores are assumed to be multiplicative, so that their entrywise product yields an array that gives the total fitness for each genotype in . The entrywise product gives the frequency of each genotype among females after selection has taken place, and similarly for the genotype frequencies among adult males.

## Gametogenesis and reproduction

Reproduction occurs through random fusion of oocytes with sperm. Gametogenesis in males and females occurs in identical ways. To this end, I define an array in which element that defines the probability of sampling a haplotype from a genotype consisting of maternal haplotype and paternal haplotype on linkage group , whilst accounting for recombination between and . Based on , I define an array . The matrix product of withyields the frequency of gametes among oocytes, i.e. , and similarly with males to obtain the gamete frequencies among sperm . Note that and are functionally equivalent to and , as both pairs represent the frequency of maternally- and paternally-inherited haplotypes. The Kronecker product yields an array that denotes the frequency of each genotype among the offspring. has identical dimensions to , and effectively represents its offspring. Redefining represents moving the simulation forward by 1 generation. All simulations are carried out for at least 50,000 generations.

I introduce the novel sex-determining allele at generation 10,000 by manipulating the gamete arrays and . For each, I redefine and , and subsequently and to convert a proportion of 00 and 01 (i.e., and ) gametes into 10 and 11 ( and ).

## References:

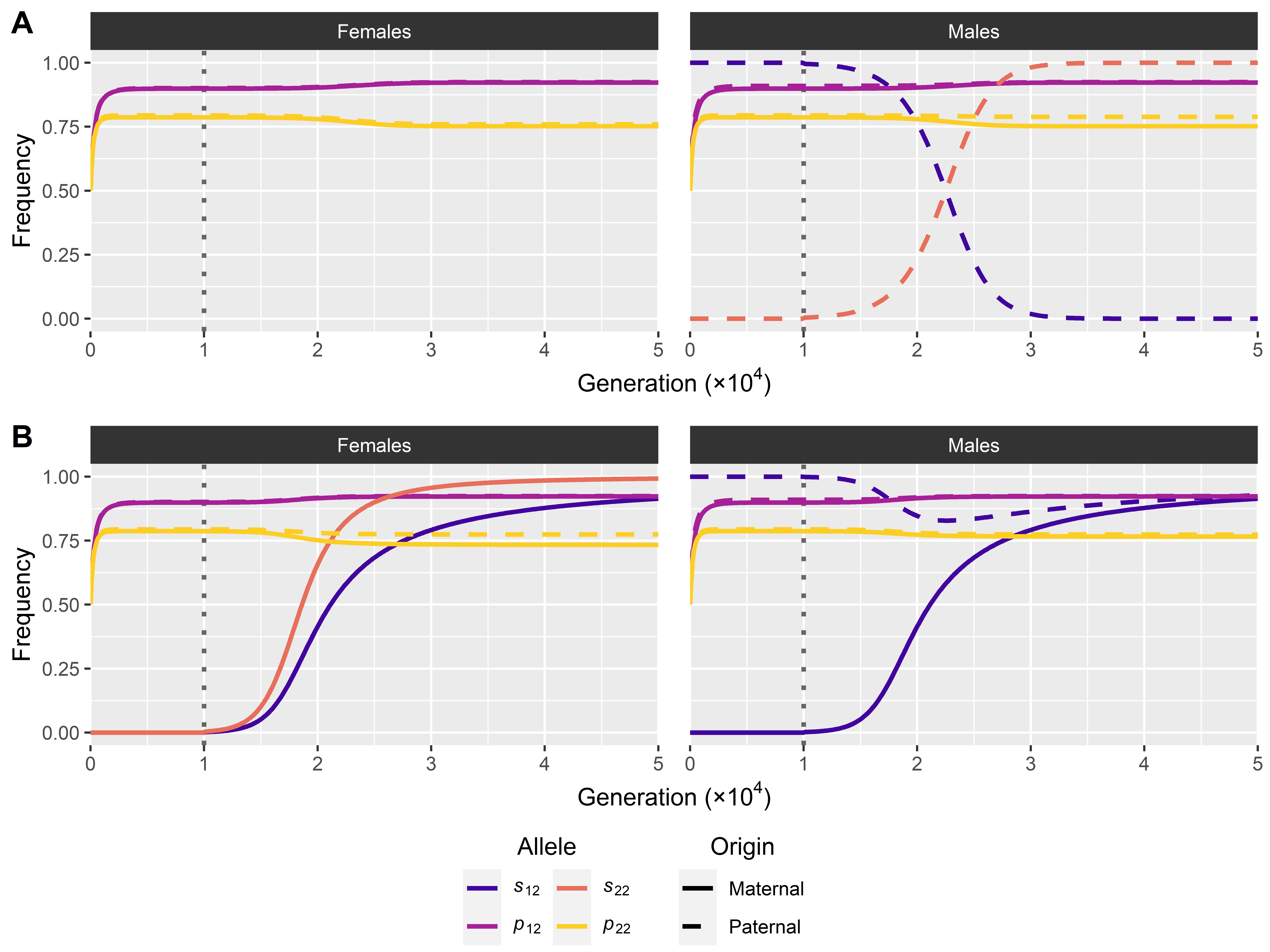
Schenkel MA, Beukeboom LW, Pen I (2021). Epistatic interactions between sex chromosomes and autosomes can affect the stability of sex determination systems. *J Evol Biol* **34**: 1666–1677.

# Supplementary Tables

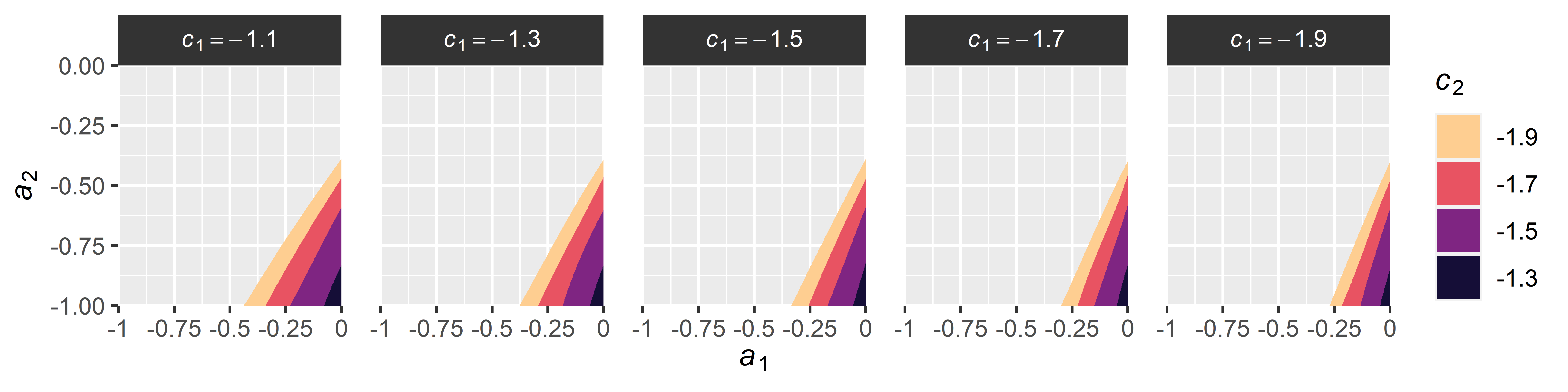
**Supplementary Table S1:** Overview of model variables.

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| --- | --- | --- |
| **Parameter** | **Description** | **Range/standard value** |
|  | Index describing the linkage group that a given variable refers to | {1, 2} |
|  | Sex determination locus on linkage group | - |
|  | Non-sex-determining allele for the sex determination locus on linkage group | - |
|  | Sex-determining allele for the sex determination locus on linkage group | - |
|  | Parentally-antagonistic locus on linkage group | - |
|  | Recombination between and on linkage group | [0,0.5] |
|  | Non-focal allele on linkage group | - |
|  | Focal allele with parentally-antagonistic fitness effects on linkage group | - |
|  | Selection coefficient for allele under parentally-antagonistic selection | [0.01, 0.05] |
|  | Dominance coefficient for heterozygotes under parentally-antagonistic selection | [-1,0] |
|  | Dominance coefficient for heterozygotes under parentally-antagonistic selection |  |
|  | Selection coefficient in females for allele under sexually-antagonistic selection | [0.01, 0.05] |
|  | Selection coefficient in males for allele under sexually-antagonistic selection | [0.01, 0.05] |
|  | Dominance in females of allele under sexually-antagonistic selection | [0.5, 1] |
|  | Dominance in males of allele under sexually-antagonistic selection | [0.5, 1] |
|  | Scaling parameter used to calculate the value of based on |  |
|  | Locus-specific fitness component of genotype |  |
|  | Locus-specific fitness component of genotype under parentally-antagonistic selection |  |
|  | Locus-specific fitness component of genotype under parentally-antagonistic selection |  |
|  | Locus-specific fitness component of genotype under parentally-antagonistic selection |  |
|  | Locus-specific fitness component of genotype under sexually-antagonistic selection in females |  |
|  | Locus-specific fitness component of genotype or under sexually-antagonistic selection in females |  |
|  | Locus-specific fitness component of genotype under sexually-antagonistic selection in females |  |
|  | Locus-specific fitness component of genotype under sexually-antagonistic selection in males |  |
|  | Locus-specific fitness component of genotype or under sexually-antagonistic selection in males |  |
|  | Locus-specific fitness component of genotype under sexually-antagonistic selection in males |  |

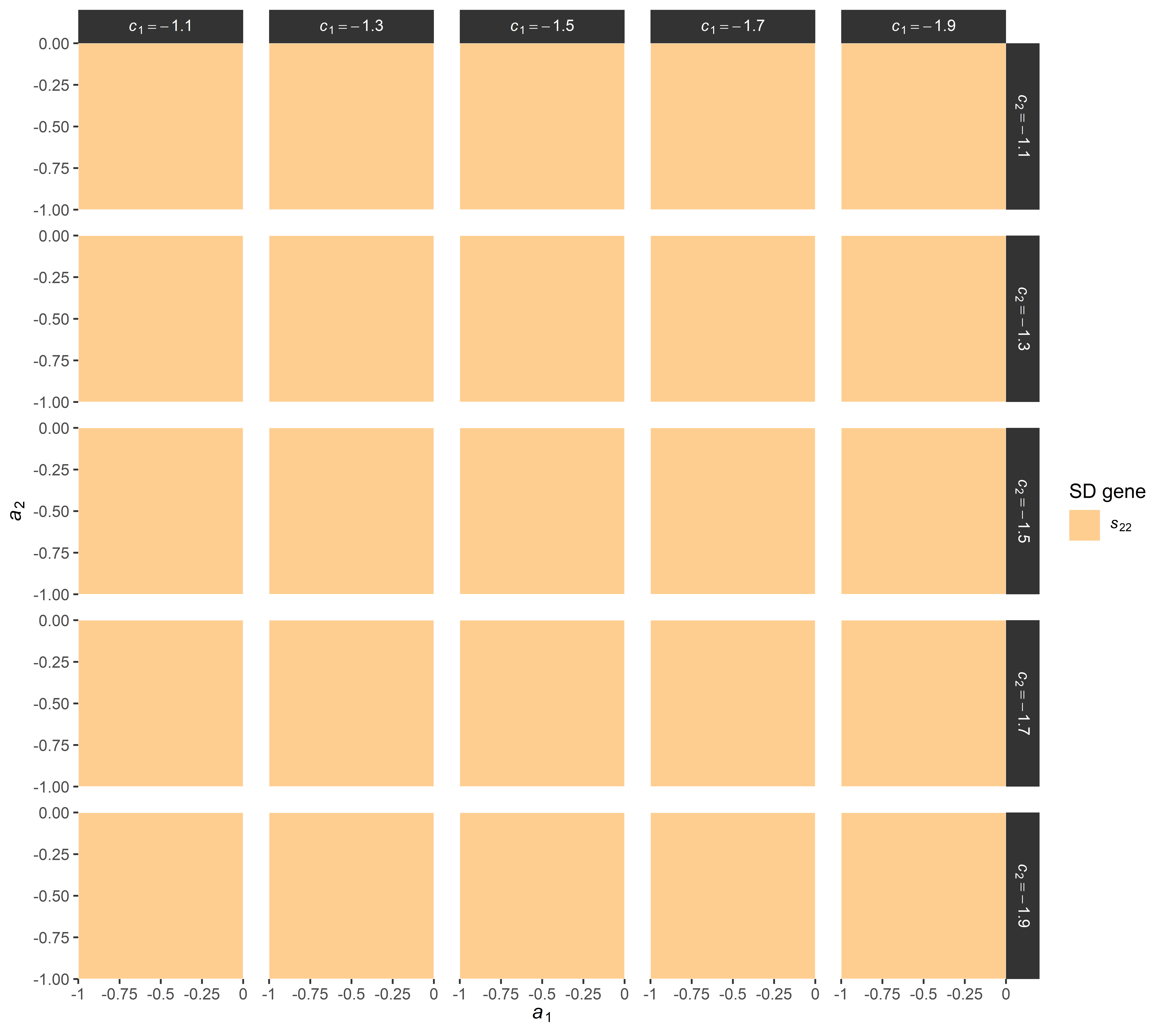
# Supplementary Figures

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**Supplementary Figure S1:** Dynamics of invasion by . (A) Invasion of a male-determining allele and a transition between homologous male heterogametic systems; is lost as invades. (B) Invasion of a dominant female-determining allele and a transition from male to female heterogametic system; approaches fixation as invades. Note that the strength of selection for to increase in frequency drops once approaches fixation, so that is not fully fixed yet at 50,000 generations (40,000 generations after initially evolved). Only alleles with non-zero frequencies for a combination of haplotype and sex are shown. The dashed vertical line indicates the evolution of through mutation in generation 10,000. Parameter values:



**Supplementary Figure S2:** Scope for fixation of a male-determining allele different parentally-antagonistic selection regimes. Shaded areas represent the range of parameter values for which a male-determining can invade. Parameter values: Fitted GAMs used and as predictor variables; separate GAMs were fitted for each combination of and .



**Supplementary Figure S3:** Scope for invasion of a female-determining allele . For the entire parameter range considered here, was able to invade and spread to fixation. Parameter values: Fitted GAMs used and as predictor variables; separate GAMs were fitted for each panel (i.e. combination of and ).