# **Methods**

## Model Description

We developed a forward time diploid two-locus biallelic model with non-overlapping generations and viability selection. The first locus is the sex determining region which is represented by an X and Y allele. Individuals homozygous for the X allele are females while heterozygous individuals are males. The second locus is Sexually Antagonistic (Brathwaite *et al.*) and has two alleles one is beneficial to females (A1) and one is beneficial to males (A2). Because females are homozygous at the sex determining locus we can ignore recombination in females. In males, recombination between the sex-determining locus and the SA locus occur as a function of the genetic distance (*rd*). When *rd* is less than 0.5 an SA locus in the recombining region of the sex chromosomes is simulated while and *rd* value of 0.5 leads to a simulation where the SA locus is on an autosome. When rd is set to 0.0 the model represents an SA locus in the non-recombining portion of the sex chromosomes. The fitness of an individual is a function of its sex and the genotype at the SA locus (**table 1**).

Simulations were started with a selected number of males and females. One sex is chosen was the common sex and the number of the rare sex was a function of the parameter representing the level of operational sex ratio bias in the system. An equal frequency of the two alleles at the SA locus. Alleles at the SA locus were assigned equally to X and Y chromosomes so that at the start of the simulation there is no linkage disequilibrium and allele frequency in males and females was equal. In each cycle of the simulation fitness was assessed for all individuals. Based on their fitness females were drawn to contribute eggs to the gamete pool. In females since recombination can be ignored, haplotypes for eggs were drawn at random from each selected female. In males, sperm haplotypes were drawn accounting for recombination between the sex-determining locus and the SA locus (double recombination events were not allowed in the model.) To reconstitute the next generation (including any bias in the number of males and females present) eggs were drawn at random and paired with randomly drawn sperm that contained either an X or Y allele at the sex-determining locus as appropriate for the number of offspring needed for each sex. This process was repeated until a specified number of generations was reached or until one of the alleles at the SA locus fixed in the population.

Haplodiploidy requires some modifications to this model. In this case we used a single locus biallelic model, where one of the alleles was male-beneficial, and the other was female-beneficial. Our simulations started with a given population with diploid genotypes for females and haploid genotypes for males. We then run a generation using our starting population with a selection coefficient of 0.5 and a dominance factor of 0.5. Each generation that is simulated goes through selection based on a fitness function, gamete production based on relative fitness, and fertilization of the next generation recapitulating the approach described above for a total of 500 generations and 1000 replications for each variation of the conditions we looked at.

## Simulation Scenarios

In our simulation, we evaluated 56 different pairings of numbers of males and females. In each simulation the population was made up of 50, 100, 500, or 1000 individuals of the common sex. For the second sex the number of individuals was the same as in the common sex or reduced by a factor of 0.8, 0.6, 0.4, 0.2, 0.1, or 0.05. Simulations with 50 of the common sex and an OSR of 0.05 would result in 2.5 individuals of the rare sex. For simulations with this pairing of parameters we used 3 individuals of the rare sex. These pairings were repeated with both males and females as the rarer sex. For each of these scenarios, we varied three other factors: recombination distance *rd* (0.1, 0.2, and 0.5), selection strength *s* (0.1, 0.2, 0.5, and 0.9), and dominance *h* (0.0, 0.5, 1.0). We also evaluated the case for sex specific dominance in which an allele that benefits a sex is dominant in that sex. This condition requires a different fitness function rather than simply a different *h* value (**Table 1**). Under each simulation scenario 1000 replicates were performed. This simulation design yielded a total of 2016 scenarios and over two million individual simulations.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
|  | Additive  dominance  recessive | |  | Sex-specific  dominance | |
|  | Male | Female |  | Male | Female |
| A1A1 |  |  |  |  | 1 |
| A1A2 |  |  |  |  |  |
| A2A2 | 1 | 1 |  | 1 |  |

**Table 1:** Fitness function. The first column represents all the possible genotypes at the SA locus where A1 is male beneficial and A2 is female beneficial. The columns are divided between genetic architecture: additive, dominance, recessive and sex specific dominance in males versus females. The selection coefficient is represented by s and the dominance factor of the male benefit allele is indicated with an h.

In our haplodiploid simulation we followed the same conditions we used above for the number of the common sex and the factor by which the rare sex was reduced, applying the same procedure to both males and females. The selection coefficients considered were also the same as above as were the dominance factors. However, since we were considering a single locus recombination distance did not need to be factored into these scenarios. A total of 672,000 simulations were carried out encompassing all of the relevant scenarios.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | **female** |  |  | **male** |
| A1A1 |  |  | A1 |  |
| A1A2 |  |  |  |  |
| A2A2 |  |  | A2 |  |

**Table 2:** Fitness function for haplodiploid simulations. The first column contains all the genotypes females can exhibit. The third column has the male genotypes. The selection coefficient is denoted by *s* and the dominance factor by *h*.