

Supporting Information

Hill-Robertson Interference Reduced Genetic Diversity on a Young Plant Y-chromosome

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SI Tables

Table S1. Population identities (ID) and location information for *R. hastatulus* samples

Population ID	Location	Altitude	Latitude	Longitude
TX-MTP	Mount Pleasant, Texas	130	33.17453	94.98799
OK-RAT	Rattan, Oklahoma	138	34.15755	95.41325
TX-LIV	Livingston, Texas	83	30.69947	94.79981
LA-DER	De Ridder, Louisiana	67	30.8941	93.3143
TX-ATH	Athens, Texas	145	32.18471	95.8032
OK-WIL	Willis, Oklahoma	211	33.89663	96.83533

SI Figures

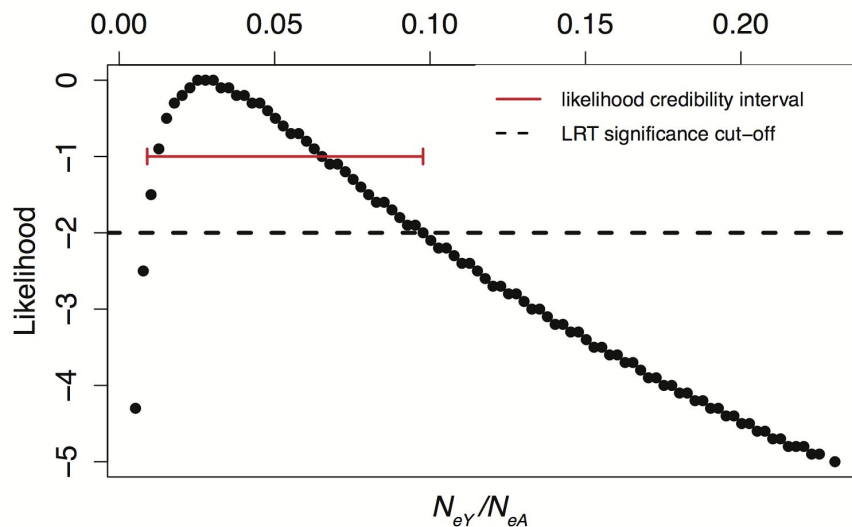


Figure S1. Likelihood estimation of the Y/A ratio

Simulation code

To study the effects of purifying selection on expected levels of Y-chromosome diversity, we conducted forward-time simulations of haploid Y chromosomes using the software SFS_CODE (Hernandez 2008). The SFS_CODE source code was obtained from: http://sfscode.sourceforge.net/SFS_CODE/index/index.html. Simulation commands for purifying selection and purifying + positive selection are given below.

purifying selection alone

```
./sfs_code 1 50000 -r 0 -t 0.0011 -P 1 -TE 1 -L 2 45331 $L -a N -W L
1 2 0 1 1 0.258 0.002 -n 6 -N 500 -A
```

Where we varied $\$L$, the number of sites under selection, over a grid of values from 50000 to 5000000. We ran 50,000 replicate simulations per parameter set.

purifying and positive selection

```
./sfs_code 1 20000 -r 0 -t 0.0011 -P 1 -TE 1 -L 2 45331 $L -a N -W L
1 2 $p 0.258 0.002 0.258 0.002 -n 6 -N 500 -A
```

Where we varied $\$L$, the number of sites under selection, over a grid of values from 50000 to 1300000, and $\$p$, the proportion of sites subject to positive selection, from 0 to 0.005 (see Figure 5) and we ran 20,000 replicate simulations per parameter set.