Supporting Information

Hough et al. genetics.XXXXXXXXXX

Supporting Information (SI)

All supporting information can be obtained from https://github.com/houghjosh/XYdiversity.

SI Tables

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

| Population ID	Location	Altitude	Latitude	Longitude
Texas				
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, Lousiana	67	30.8941	93.3143
TX-ATH	Athens, Texas	145	32.18471	95.8032
OK-WIL	Willis, Oklahoma	211	33.89663	96.83533
North Carolina				
SC-PRO	Prosperity, South Carolina	126	34.10792	81.43711
GA-BEL	Belfast, Georgia	15	31.84293	81.28405
GA-STA	Statesboro, Georgia	78	32.45237	81.84849
SC-BRA	Branchville, South Carolina	34	33.25082	80.80761
FL-HAM	Hammock, Florida	3	29.06816	82.64664
GA-GLA	Gladys, Georgia	97	31.48198	83.23783

SI Figures
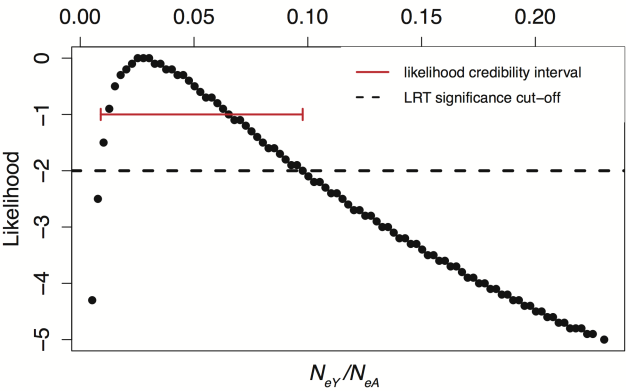
Figure S1. MLHKA likelihood estimation of Y/A ratio. Explain more.
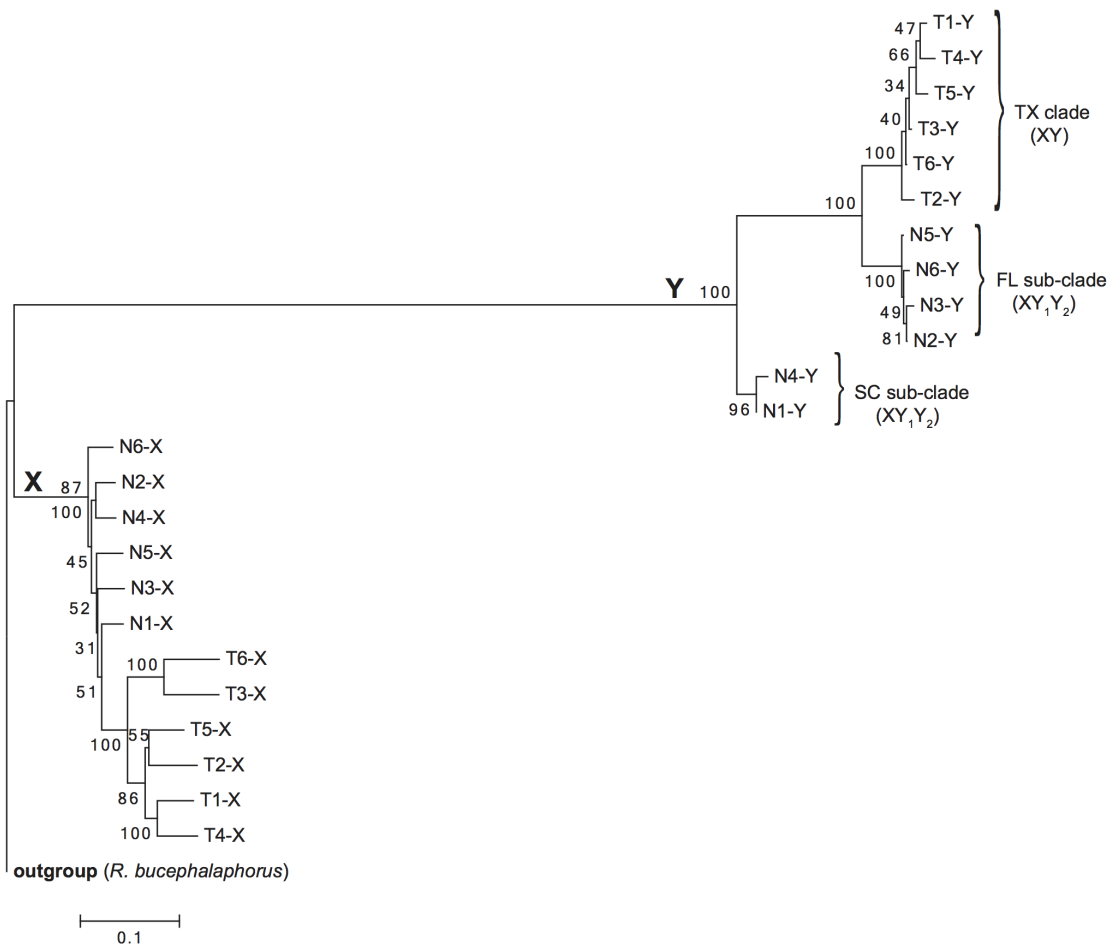
Figure S2. Evolutionary relationships of sex chromosome races in *Rumex hastatulus*, inferred using the Neighbor-Joining method (Saitou and Nei 1987). The percentage of replicate trees in which the associated sequences clustered together in the bootstrap test (1000 replicates) is shown next to branches (Felsenstein 1985). The phylogeny is drawn to scale, with branch lengths in the same units as those of the evolutionary distances used to infer the tree. The evolutionary distances were computed using the Maximum Composite Likelihood method (Tamura et al. 2004) and are in the units of the number of base substitutions per site. The analysis was conducted on an alignment of X- and Y-linked genes from *R. hastatulus*, with orthologous autosomal sequences from the non-dioecious but closely related outgroup species *Rumex bucephalophorus* used to root the tree. 'N' designates the North Carolina race, and 'T' the Texas race, with numbers 1-6 corresponding to each of the 6 populations sampled. The inferred SC (South Carolina), and FL (Florida) sub-clades are indicated.
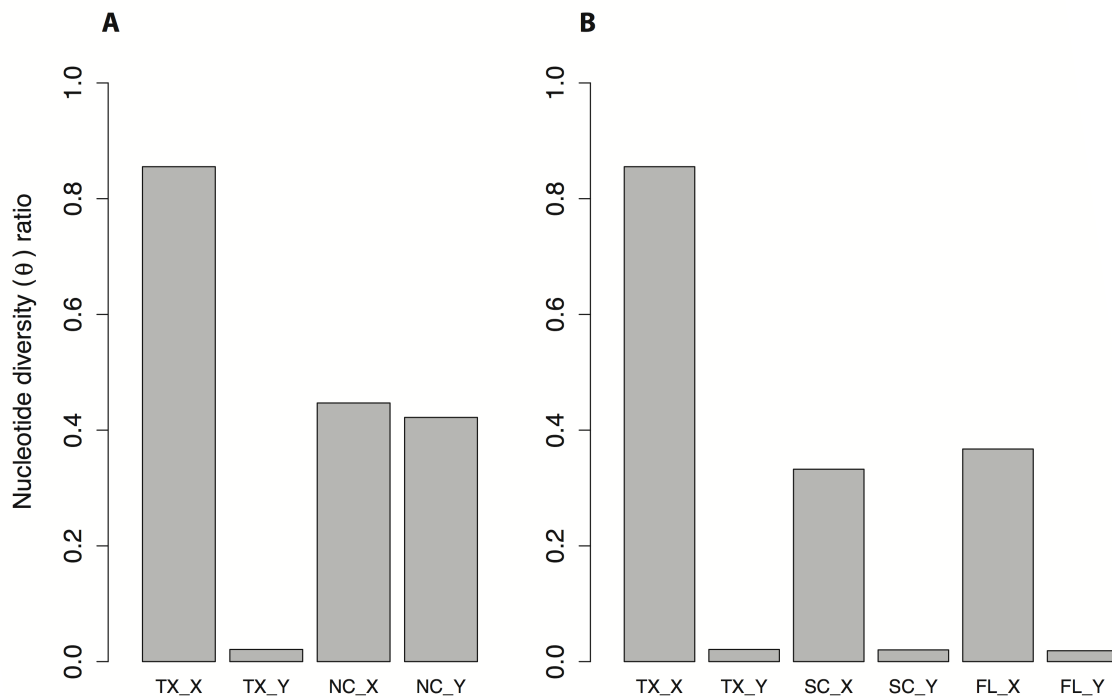
Figure S3. Normalized X/A and Y/A nucleotide diversity ratios for XY and XY_1Y_2 races of *Rumex hastatulus*. In **A**, the South Carolina and Florida sub-clades are collapsed into a single race ('NC'), and in **B**, they are separated into the inferred 'SC' and 'FL' sub-clades.

Simulation code

```
#!/bin/bash

#purifying selection
sfs_code 1 50 -r 0 -t 0.001375 -P 1 -TE 0.3 -L 2 500000 800000 \
-a N -W L 1 2 0 1 1 0.184 0.003 -n 8 -N 500 -A

#positive selection
sfs code 1 2000 -n 20 -N <N> -Td 0 -TE <> -W <type> [args]
```