Supporting Information

Emerson et al. 10.1073/pnas.1006538107

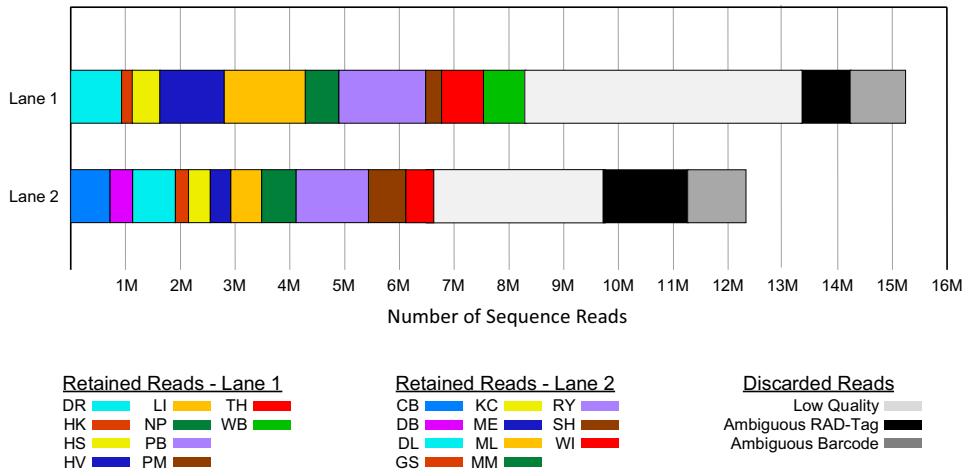

Fig. S1. Distribution of sequence reads among populations of *W. smithii*. Two lanes of an Illumina GAIIX were used to generate the sequence data, each containing a RAD tag library from 10 to 11 populations, identifiable by a 5-bp barcode (*Methods*). Reads were discarded before assembly steps for three reasons: (*i*) low quality—low overall quality scores for a large portion of the sequence, (*ii*) ambiguous RAD tag—at least two low-quality base pairs in the Sbf1 cut site, or (*iii*) ambiguous barcode—at least two low-quality base pairs in the population-specific barcode. Barcodes were separated by at least two mismatches, making the probability of incorrect population assignment very low. Population names are those used in previous publications and are defined by their latitude, longitude, altitude, and state or province of origin as given for each population in Table S1.

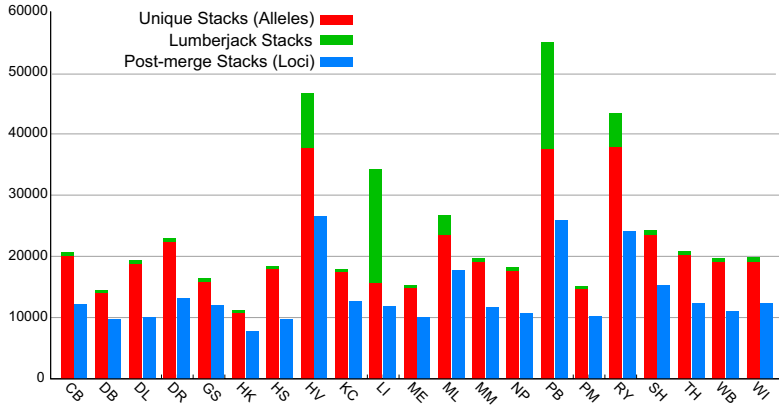

Fig. S2. Frequency distribution of alleles and loci for each population in the *W. smithii* RAD tag dataset. The first step of the RAD tag analysis was to identify all stacks of exactly matching sequences (Fig. 1*B*); these stacks are then merged into loci—sets of stacks such that for each stack, there is another member of the set that differs by at most one nucleotide. Lumberjack stacks can occur when duplicate regions in the genome are within a single nucleotide of one another, resulting in spuriously large sequencing depth. In this analysis, all stacks with a depth of coverage greater than two SDs above the mean stack depth were removed and the remaining stacks were merged into a locus. Population names are those used in previous publications and are defined by their latitude, longitude, altitude, and state or province of origin as given for each population in Table S1.

Table S1. Origin of *W. smithii* populations

Population*	State/province	North latitude, °	West longitude, °	Elevation, m
Northern clade				
WB	MB	54	101	305
DL	ON	50	94	406
RY	WI	46	92	295
ML	WI	46	90	500
DR	ON	46	78	154
KC	ME	46	68	365
ME	ME	46	69	60
TH	PA	41	75	596
Mid-Atlantic clade				
PB	NJ	40	74	10
MM	NJ	40	75	10
HV	NJ	40	75	10
NP	MD	38	75	18
Appalachian clade				
HS†	NC	35	83	1190
HK	NC	35	83	900
DB	NC	35	83	900
CB	NC	35	83	840
NC Coast clade				
SH	NC	35	80	107
PM	NC	35	80	107
GS	NC	34	78	20
Gulf Coast Clade				
WI	FL	30	85	10
LI	AL	30	87	15

*Each two-letter acronym corresponds to a specific population collected within <1 km over the last 30+ y and has been used consistently to denote that population in all previous publications from this laboratory.

†*S. purpurea* at Highlands Biological Station (HS) was transplanted from Horse Cove (HK), ca. 2 km southeast and 270 m lower in elevation around 1900. We included the HS *W. smithii* because the HK locality has been drained and neither pitcher plants nor *W. smithii* were found at HK in 2004. Both HS and HK samples were collected in 1996 when the plants still existed at HK. To our knowledge, HS represents the only transplanted pitcher plants among all localities used in this study.