

# Supporting Information

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## SI Text

**MIMAR Model Assessment.** Mimar simulates samples under a model of isolation with migration, with six parameters, where population 1 is *Capsella grandiflora* and population 2 *Capsella rubella*:  $\theta_1$ ,  $\theta_2$ ,  $\theta_a$ ,  $M_{12}$  (migration rate from population 1 to population 2),  $M_{21}$  (migration rate from population 2 to population 1), and  $\tau$  (divergence time). We considered four nested models of demographic history: model 1 assumed no migration and constrained the ancestral effective population size to be equal to present day *C. grandiflora*, which is population 1 (i.e.,  $\theta_a = \theta_1$ ,  $M_{12} = M_{21} = 0$ ); model 2 allowed for symmetric migration ( $\theta_a = \theta_1$ ,  $M_{12} = M_{21}$ ); model 3 allowed for asymmetric migration ( $\theta_a = \theta_1$ ); and model 4 allowed for both asymmetric migration and free effective population sizes for each population.

**Goodness-of-Fit Tests and Likelihood Ratios.** We performed goodness-of-fit tests by using MIMARgof (1) and a modified version of ms, mspopr, which can simulate a lineage-specific change in population recombination rate (E. Stahl, unpublished data). For each model, we generated 10,000 simulations of 25 loci by using the same number of sites and individuals sequenced per locus as in the original dataset. Another set of 10,000 simulations of 25 loci were run in mspopr, including a lineage-specific change in recombination in *C. rubella*, but with parameter estimates for each model otherwise unchanged. Specifically, we set the population recombination rate to zero in the *C. rubella* lineage at the time of the split of *C. grandiflora* and *C. rubella*. Finally, we also performed goodness-of-fit tests by using the predictive posterior distributions of each model. Model fit was assessed by calculating one-tailed *P* values for observed summary statistics, based on distributions of simulated statistics. In addition to the mean sums over all loci of shared and unique variants used by MIMAR (S1 and S2 for unique polymorphisms in *C. grandiflora* and *C. rubella*, respectively, and Ss and Sf for shared and fixed polymorphisms), we performed goodness-of-fit tests on mean nucleotide diversity estimates ( $\pi_1$  and  $\pi_2$  for *C. grandiflora* and *C. rubella*, respectively), mean  $F_{st}$  and mean Tajima's *D*, to assess how well the model could accommodate aspects of data not directly used by MIMAR. To further assess the fit of the data to a model with no locus-specific positive selection, we also assessed the fit of the data to the variance in  $\pi$  and Tajima's *D* [ $\text{var}(\pi_1)$ ,  $\text{var}(\pi_2)$ ,  $\text{varTajD1}$ ,  $\text{varTajD2}$ ].

Goodness-of-fit tests were performed in two ways: (i) simulating under the Bayesian posterior distribution of parameters (i.e., predictive posterior), and (ii) simulating under the marginal modes of the posterior parameter distributions. The second approach allowed us to assess the degree to which a single demographic model can explain all aspects of the data, whereas the first approach allows a comparison of the overall fit of each inferred posterior distribution. As shown in [supporting information \(SI\) Table S1](#), predictive posterior simulations suggest that all models fit the data equally well under this criterion, suggesting that model 1 is sufficient to explain our data, without the need to invoke migration and changes in effective population size between population 1 and the ancestral population. In other words, we cannot reject the null hypothesis of no migration and equal effective population sizes between population 1 and the ancestral population. Using a likelihood ratio test from maximum likelihood estimates across the MIMAR runs provides a similar conclusion, i.e., the more parameter-rich models do not provide a significant improvement to the likelihood over model 1 ([Table S2](#)). Although the likelihoods in this analysis should be

considered as approximate, the combination of results from the predictive posterior and the likelihood analysis is consistent with the hypothesis that model 1 adequately explains the data.

As shown in [Table S3](#), simulations under the marginal modes provide further evidence in favor of the simpler models over the parameter-rich models. In particular, best-fit parameters under models 1 and 2 are consistent with all tested summary statistics, whereas model 3 fails one goodness-of-fit test, and model 4 fails five tests. Very similar conclusions are obtained when we allow for a lineage-specific change in recombination ([Table S4](#)). One possible explanation for the poor fit of model 4 is that the combination of modes from the marginal posterior distributions is distinct from the best-fitting parameter set. To explore this possibility, we also conducted goodness-of-fit tests under the maximum likelihood parameter estimates for each model. Although these simulations improve the fit considerably, the unconstrained model still shows a poorer fit to the data than the simpler models for parameters not used in estimation ([Tables S3 and S4](#)). In particular, the observed values for nucleotide diversity, Tajima's *D*, and the variance of Tajima's *D* in *C. grandiflora* have low probabilities under this model. This inconsistency is likely because high gene flow and population growth inferred in *C. grandiflora* under this model are not consistent with the patterns consistent with stable equilibrium in this species.

**Exploring the Effects of Positive Selection on Diversity.** If recurrent positive selection reduced diversity in *C. rubella* across the genome, we would predict that these positive selection events would erode any ancestral variation such that the majority of segregating variation would be unique to *C. rubella*. In contrast with this expectation, we found that 84% of variation in *C. rubella* is shared with *C. grandiflora*. To illustrate this expectation, we simulated 10,000 39-gene datasets under (i) the inferred bottleneck model assuming no migration, (ii) the selective sweep model of Thornton and Jensen (2), allowing for only a slight bottleneck of a twofold reduction in effective population size, and (iii) the selective sweep model of Innan and Kim (3) under a slight bottleneck, with positive selection acting on standing variation. All simulations assumed a divergence time of 14,000 years, and an ancestral  $\theta$  equal to  $\theta$  in *C. grandiflora* of 0.03 per base pair.

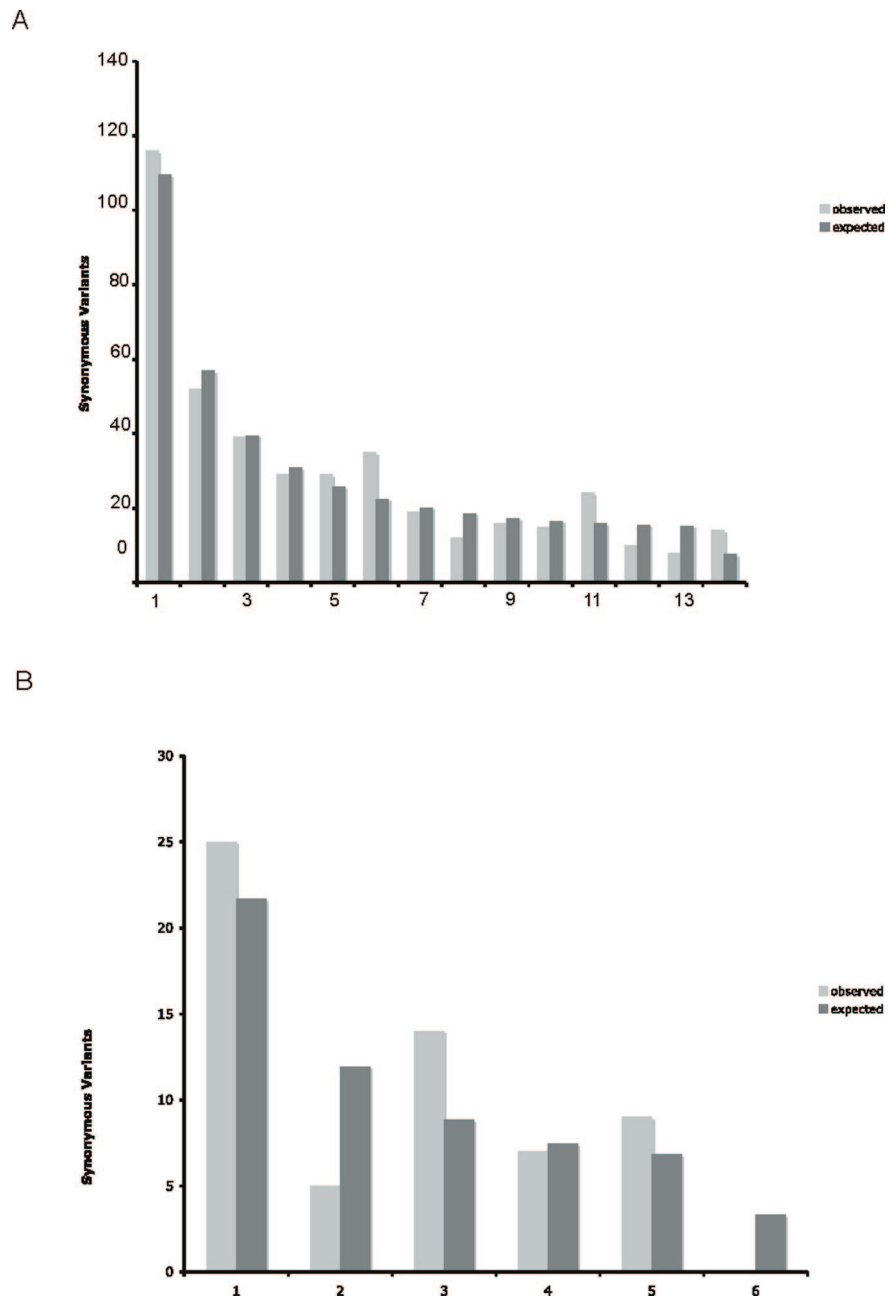
Under the bottleneck model, 60% of 39-gene datasets show 84% or more shared polymorphisms in *C. rubella*, consistent with our observed data ([Fig. S4](#)). In contrast, simulating under a model of selective sweeps, allowing for only a slight bottleneck (reduction of  $N_e$  by half in *C. rubella*) with a selective sweep during the bottleneck ( $4N_s = 6,500$ ), no 39-gene datasets in 10,000 were found to have this high a fraction of shared polymorphisms; the maximum proportion of shared polymorphisms was found to be 0.46 ([Fig. S4](#)). Similarly, the model of selection from standing variation generated no datasets with the observed fraction of shared polymorphism, and the maximum proportion observed was 0.79. Although these simulations are not exhaustive, they illustrate that under reasonable parameter values, we would not expect genome-wide positive selection to lead to the observed maintenance of shared polymorphism.

**Generating Data Summaries and the Use of Ancestral State Inference.** Because MIMAR relies on the inference of derived SNPs, we made every effort to minimize errors associated with ancestral misinference. To determine derived states we used PAML (4) to perform likelihood reconstruction of ancestral states for the

common ancestor of *Capsella* under various substitution models. These likelihood reconstructions were based on sequence data from *A. thaliana*, *A. lyrata*, *B. stricta*, *C. grandiflora*, and *C. rubella*. Given that the phylogenetic position of *Capsella* in relation to *Boecheera* and *Arabidopsis* shows some uncertainty (5, 6), we assumed a star-shaped phylogeny for the three genera. For the purposes of these reconstructions we also assumed that within-*Capsella* genealogies are star shaped. Data reported here are from likelihood reconstructions under the Kimura 2 Parameter (K80) model that distinguishes between transitions and transversions. The reconstructed ancestor of *Capsella* was then used to infer ancestral states for the *Capsella* polymorphism data.

By using the method of Baudry and Depaulis (7) we calculated the rate of ancestral misinference in our dataset as 0.084/base, using transition/transversion ratios estimated directly at synonymous sites. To explore any effect that this residual error may have on demographic inference, we generated a modified version of MIMAR code to use data summaries that do not rely on outgroup inference. In particular, we modified Ss to include only shared polymorphisms, whereas S1 and S2 represent polymorphisms unique to population 1 and 2, respectively, regardless of ancestral vs. derived states. As shown in Table S6, parameter estimates using this approach are very much in line with estimates reported in Table 1 of the text.

1. Becquet C, Przeworski M (2007) A new approach to estimate parameters of speciation models with application to apes. *Genome Res* 17(10):1505–1519.
2. Thornton KR, Jensen JD (2007) Controlling the false-positive rate in multilocus genome scans for selection. *Genetics* 175(2):737–750.
3. Innan H, Kim Y (2008) Detecting local adaptation using the joint sampling of polymorphism data in the parental and derived populations. *Genetics* 179(3):1713–1720.
4. Yang Z (1997) PAML: A program package for phylogenetic analysis by maximum likelihood. *CABIOS* 13:555–556.
5. Koch M, Haubold B, Mitchell-Olds T (2001) Molecular systematics of the *Brassicaceae*: evidence from coding plastidic matK and nuclear Chs sequences. *Am J Bot* 88:534–544.
6. Al-Shehbaz IA, Beilstein MA, Kellogg EA (2006) Systematics and phylogeny of the *Brassicaceae* (*Cruciferae*): An overview. *Plant Systematics Evol* 259:89–120.
7. Baudry E, Depaulis F (2003) Effect of misoriented sites on neutrality tests with outgroup. *Genetics* 165(3):1619–1622.
8. Tajima F (1989) Statistical method for testing the neutral mutation hypothesis by DNA polymorphism. *Genetics* 123:585–595.



**Fig. S1.** Observed and expected [under neutrality as calculated using equation 49, Tajima (8)] minor allele frequency distribution of synonymous SNPs in *C. grandiflor* (A) and *C. rubella* (B) by using *A. thaliana* as an outgroup.

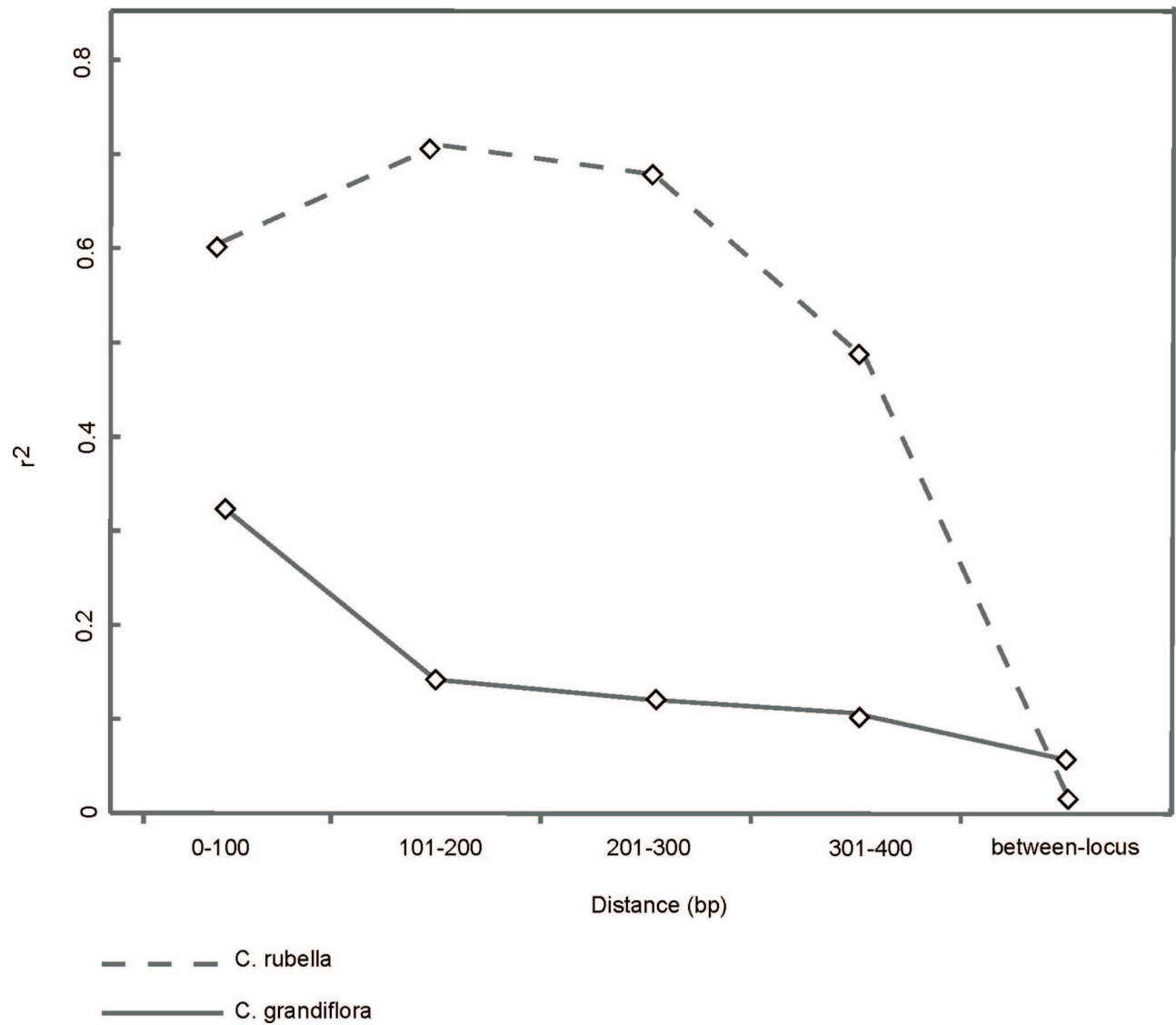


Fig. S2. Average levels of linkage disequilibrium as measured by the squared correlation coefficient  $r^2$  in *C. rubella* and *C. grandiflora* in 100 bp windows.





Table S1. Predictive posterior probabilities from simulations of the posterior distributions (see [SI Text](#) for details)

Model	S1*	S2†	Ss‡	Sf§	Fst¶	$\pi$ 1	$\pi$ 2**	Tajima's D1††	Tajima's D2**
1	0.42	0.25	0.44	0.35	0.47	0.42	0.28	0.34	0.27
2	0.37	0.27	0.42	0.50	0.40	0.37	0.06	0.31	0.47
3	0.44	0.39	0.39	0.38	0.46	0.42	0.25	0.33	0.48
4	0.39	0.34	0.43	0.43	0.45	0.24	0.30	0.16	0.48

Values shown are 1-tailed probabilities of the observed data from simulations under the posterior parameter distributions.

\*Mean number of unique polymorphisms in *C. grandiflora*.

†Mean number of unique polymorphisms in *C. rubella*.

‡ Mean number of shared polymorphisms.

§Mean number of fixed differences.

¶Mean population differentiation.

||Average pairwise differences in *C. grandiflora*.

\*\*Average pairwise differences in *C. rubella*.

††Average Tajima's D in *C. grandiflora*.

\*\*Average Tajima's D in *C. rubella*.





**Table S3. Goodness-of-fit test *P* values based on simulations under the marginal modes (a) and under maximum likelihood parameter estimates (b)**

Model	S1 <sup>c</sup>	S2 <sup>d</sup>	Ss <sup>e</sup>	Π1 <sup>f</sup>	π2 <sup>g</sup>	Tajima's D1 <sup>h</sup>	Tajima's D2 <sup>i</sup>	Fst <sup>j</sup>	Sf <sup>k</sup>	var(π1) <sup>l</sup>	var(π2) <sup>m</sup>	var(Tajima's D1) <sup>n</sup>	var(Tajima's D2) <sup>o</sup>
1a	0.411	0.301	0.372	0.332	0.231	0.319	0.220	0.385	0.456	0.497	0.226	0.278	0.386
1b	0.455	0.492	0.404	0.302	0.190	0.314	0.215	0.332	0.470	0.480	0.206	0.286	0.397
2a	0.196	0.118	0.237	0.202	0.286	0.324	0.150	0.099	0.257	0.413	0.459	0.290	0.385
2b	0.207	0.405	0.486	0.472	0.004*	0.460	0.459	0.004*	0.323	0.428	0.018*	0.312	0.276
3a	0.326	0.125	0.476	0.326	0.017*	0.325	0.468	0.043*	0.420	0.491	0.050	0.294	0.421
3b	0.408	0.201	0.481	0.300	0.048	0.328	0.466	0.113	0.417	0.483	0.092	0.283	0.469
4a	0.442	0.213	0.009*	0.001*	0.008*	0.031*	0.470	0.100	0.468	0.018*	0.026*	0.036*	0.421
4b	0.215	0.343	0.257	0.072*	0.202	0.055*	0.472	0.392	0.315	0.140	0.142	0.045*	0.483

Values shown are 1-tailed *P* values of the observed mean and variances of summary statistics by using coalescent simulations under the various parameter combinations. Significant and marginally significant departures are shown with an asterisk.

<sup>c</sup>Mean number of unique polymorphisms to *C. grandiflora*.

<sup>d</sup>Mean number of unique polymorphisms to *C. rubella*.

<sup>e</sup>Mean number of shared polymorphisms.

<sup>f</sup>Average pairwise differences in *C. grandiflora*.

<sup>g</sup>Average pairwise differences in *C. rubella*.

<sup>h</sup>Average Tajima's D in *C. grandiflora*.

<sup>i</sup>Average Tajima's D in *C. rubella*.

<sup>j</sup>Mean differentiation.

<sup>k</sup>Mean number of fixed differences.

<sup>l</sup>Variance in pairwise differences in *C. grandiflora*.

<sup>m</sup>Variance in pairwise differences in *C. rubella*.

<sup>n</sup>Variance in Tajima's D in *C. grandiflora*.

<sup>o</sup>Variance in Tajima's D in *C. rubella*.



**Table S5. Sequence-based summary statistics as estimated for each locus in both *C. grandiflora* and *C. rubella***

Species	Locus	Sample size	Synonymous sites	Theta synonymous	S synonymous	$\pi$ synonymous	Tajima's D synonymous	Replacement sites	Theta replacement	S replacement	$\pi$ replacement	Tajima's D replacement
<i>C. grandiflora</i>	At1g01040	34	120.1095238	0.012217381	6	0.012481181	0.059785052	419.8904762	0.002912315	5	0.001095269	-1.649659063
<i>C. grandiflora</i>	At1g03560	28	128.1551724	0.006015516	3	0.00487174	-0.456422119	459.8448276	0.007264736	13	0.004245739	-1.392653386
<i>C. grandiflora</i>	At1g04650	32	149.4090909	0.024929075	15	0.020308498	-0.616260234	474.5909091	0.005755263	11	0.006346722	0.326203043
<i>C. grandiflora</i>	At1g06520	28	115.3045977	0.02451511	11	0.022484729	-0.270635841	400.6954023	0.005771862	9	0.004819663	-0.520883643
<i>C. grandiflora</i>	At1g06530	38	111.4188034	0.034178123	16	0.036921937	0.260600475	440.5811966	0.008103115	15	0.006715557	-0.550965203
<i>C. grandiflora</i>	At1g10900	26	139.7407407	0.003750622	2	0.00457991	0.473577154	448.2592593	0	0	0	0
<i>C. grandiflora</i>	At1g11050	32	118.4646465	0.044017205	21	0.052792394	0.689702738	352.5353535	0.004226107	6	0.0035629	-0.440821078
<i>C. grandiflora</i>	At1g15240	30	111.9516129	0.022547226	10	0.011417084	-1.563384883	410.0483871	0.015389637	25	0.009127042	-1.448709834
<i>C. grandiflora</i>	At1g31930	8	108.0925926	0.024976036	7	0.023458724	-0.289096242	317.9074074	0.001213167	1	0.000786392	-1.054819107
<i>C. grandiflora</i>	At1g59720	30	114.3494624	0.077260479	35	0.093502442	0.76792837	419.6505376	0.015639002	26	0.016340909	0.160323884
<i>C. grandiflora</i>	At1g62390	36	124.472973	0.025185881	13	0.021551182	-0.459368216	466.527027	0.003101439	6	0.002534772	-0.499232495
<i>C. grandiflora</i>	At1g62520	28	129.8045977	0.075228311	38	0.079260365	0.199241023	416.1954023	0.00617434	10	0.00359772	-1.342343614
<i>C. grandiflora</i>	At1g65450	22	117.6811594	0.058276411	25	0.067207792	0.580648839	389.3188406	0.004932333	7	0.003891801	-0.6750978
<i>C. grandiflora</i>	At1g68530	36	135.7792793	0.030192862	17	0.033469352	0.358580449	443.2207207	0.001632263	3	0.000605238	-1.409039404
<i>C. grandiflora</i>	At1g72390	40	115.2804878	0.014275502	7	0.006561477	-1.496242606	409.7195122	0.004016618	7	0.00269728	-0.909511059
<i>C. grandiflora</i>	At1g74600	30	121.1236559	0.025007815	12	0.018258153	-0.880694329	406.8763441	0.003722308	6	0.004418299	0.533564216
<i>C. grandiflora</i>	At1g78850	36	103.6621622	0.0604842	26	0.08571801	1.442991383	340.3378378	0.009919885	14	0.007606821	-0.750466787
<i>C. grandiflora</i>	At2g23170	36	123.3648649	0.050824219	26	0.050784957	-0.002671947	407.6351351	0.005915851	10	0.003247535	-1.374013943
<i>C. grandiflora</i>	At2g26730	38	132.1538462	0.052228182	29	0.050471371	-0.116404366	425.8461538	0.0016767	3	0.001299396	-0.496927108
<i>C. grandiflora</i>	At2g28050	32	115.4848485	0.025801691	12	0.025226742	-0.071730967	394.5151515	0.00566462	9	0.001998165	-1.98260169
<i>C. grandiflora</i>	At2g44900	36	123.1711712	0.007831407	4	0.005940887	-0.59129855	386.8288288	0.000623405	1	0.000143618	-1.133212888
<i>C. grandiflora</i>	At2g47430	38	125.5726496	0.005686079	3	0.005290132	-0.153773609	402.4273504	0.000591424	1	0.00067867	0.213763113
<i>C. grandiflora</i>	At3g10340	36	135.3423423	0.040981043	23	0.035535988	-0.454237424	428.6576577	0.004500578	8	0.003036426	-0.948751959
<i>C. grandiflora</i>	At3g23590	26	106.5061728	0.056591271	23	0.042207738	-0.923383112	313.4938272	0.005015551	6	0.002129842	-1.702992442
<i>C. grandiflora</i>	At3g26650	38	93.73504274	0.012695644	5	0.024174554	2.328116714	287.2649573	0	0	0	0
<i>C. grandiflora</i>	At3g44530	38	114.4059829	0.018723218	9	0.018065981	-0.103660344	356.5940171	0.005339525	8	0.003219172	-1.144812013
<i>C. grandiflora</i>	At3g60750	22	145.6086957	0.003767926	2	0.002318971	-0.871247959	448.3913043	0.00061179	1	0.000202745	-1.162402043
<i>C. grandiflora</i>	At3g62890	38	103.8504274	0.022918091	10	0.010738718	-1.601213668	352.1495726	0.007434508	11	0.003728372	-1.527871009
<i>C. grandiflora</i>	At4g08840	28	35.71264368	0.021586739	3	0.009555995	-1.337838808	123.2873563	0.00625303	3	0.004699307	-0.596460285
<i>C. grandiflora</i>	At4g14190	30	91.87096774	0.049455853	18	0.045741315	-0.258696163	301.1290323	0.015926651	19	0.011481694	-0.967102366
<i>C. grandiflora</i>	At4g14370	22	127.0652174	0.034542441	16	0.036930962	0.25117467	451.9347826	0.013960848	23	0.00758643	-1.718251797
<i>C. grandiflora</i>	At4g38160	34	132	0.012969655	7	0.007778318	-1.148619662	429	0.001710284	3	0.001337397	-0.494978031
<i>C. grandiflora</i>	At5g04190	32	127.0707071	0.019540986	10	0.018103332	-0.229741211	412.9292929	0.010824024	18	0.008012189	-0.883634204
<i>C. grandiflora</i>	At5g20280	20	112.9603175	0.044915357	18	0.040815451	-0.343415808	373.0396825	0	0	0	0
<i>C. grandiflora</i>	At5g41920	30	125.0967742	0.048427116	24	0.050627471	0.161166801	390.9032258	0.005165879	8	0.005786775	0.365120611
<i>C. grandiflora</i>	At5g43670	32	112.5656566	0.02205901	10	0.028746664	0.946713864	322.4343434	0.001540212	2	0.000737835	-1.046838824
<i>C. grandiflora</i>	At5g51670	36	129.6936937	0.044625309	24	0.05319004	0.658884766	407.3063063	0.004144439	7	0.001340592	-1.916647035
<i>C. grandiflora</i>	At5g53020	34	64.30952381	0.049439308	13	0.080853398	2.045386197	241.6904762	0.020238335	20	0.033977844	2.310606856
<i>C. grandiflora</i>	At5g66280	30	135.1505376	0.013073857	7	0.010971163	-0.47519625	395.8494624	0.001912999	3	0.000505243	-1.731782748
<i>C. rubella</i>	At1g01040	13	120.047619	0	0	0	0	419.952381	0	0	0	0
<i>C. rubella</i>	At1g03560	12	128.1538462	0.01033568	4	0.012768744	0.82792558	459.8461538	0.001440218	2	0.001779251	0.687881658
<i>C. rubella</i>	At1g04650	14	149.5	0	0	0	0	477.5	0	0	0	0
<i>C. rubella</i>	At1g06520	14	114.7444444	0.002740457	1	0.001245003	-1.155241342	401.2555556	0	0	0	0
<i>C. rubella</i>	At1g06530	14	112.5777778	0	0	0	0	442.4222222	0	0	0	0
<i>C. rubella</i>	At1g10900	12	139.6410256	0	0	0	0	451.3589744	0	0	0	0
<i>C. rubella</i>	At1g11050	13	120.5952381	0.026721361	10	0.038271699	1.726825312	359.4047619	0.001793226	2	0.001712233	-0.126877208
<i>C. rubella</i>	At1g15240	14	113.3777778	0	0	0	0	408.6222222	0	0	0	0
<i>C. rubella</i>	At1g31930	14	108.2111111	0.002905914	1	0.002437238	-0.341438343	317.7888889	0.0009895	1	0.00082991	-0.341438343
<i>C. rubella</i>	At1g59720	14	114.0777778	0.002756472	1	0.00433481	1.212185563	419.9222222	0	0	0	0
<i>C. rubella</i>	At1g62390	13	124.3928571	0.007771674	3	0.003710329	-1.652312061	466.6071429	0.002071851	3	0.000989137	-1.652312061
<i>C. rubella</i>	At1g62520	14	129.7333333	0.048476698	20	0.058446179	0.859675381	416.2666667	0.001510821	2	0.002455104	1.695975145
<i>C. rubella</i>	At1g65450	12	118.3846154	0	0	0	0	388.6153846	0	0	0	0
<i>C. rubella</i>	At1g68530	14	135.7888889	0	0	0	0	443.2111111	0	0	0	0
<i>C. rubella</i>	At1g72390	12	115.6794872	0.005725117	2	0.004060331	-0.849714979	409.3205128	0.002426993	3	0.001998878	-0.578636747
<i>C. rubella</i>	At1g74600	13	121.6309524	0.013246912	5	0.022135054	2.392106459	406.3690476	0.002378972	3	0.003975166	2.121451886
<i>C. rubella</i>	At1g78850	14	105.5444444	0.002979334	1	0.001353526	-1.155241342	344.4555556	0	0	0	0
<i>C. rubella</i>	At2g23170	14	122.6333333	0	0	0	0	408.3666667	0	0	0	0
<i>C. rubella</i>	At2g26730	13	132.202381	0.004875054	2	0.002327434	-1.468005781	425.797619	0	0	0	0
<i>C. rubella</i>	At2g28050	14	115.4222222	0.005448729	2	0.002475384	-1.48074498	394.5777778	0.001593867	2	0.001838103	0.415804348
<i>C. rubella</i>	At2g44900	12	123.6923077	0	0	0	0	386.3076923	0	0	0	0
<i>C. rubella</i>	At2g47430	14	126.4222222	0.002487317	1	0.002086154	-0.341438343	404.5777778	0	0	0	0
<i>C. rubella</i>	At3g10340	13	135.6190476	0	0	0	0	428.3809524	0	0	0	0
<i>C. rubella</i>	At3g23590	11	106.5833333	0.01921973	6	0.024905821	1.171200707	313.4166667	0	0	0	0



**Table S6. Modes of parameter estimates under a range of MIMAR models using summaries of the data that do not rely on outgroup inference, with 90% HPD intervals in parentheses**

Model	$N_{e(Cg)}^*$	$N_{e(Cr)}^*$	$N_{e(A)}^*$	$M_{Cg-Cr}^\dagger$	$M_{Cr-Cg}^\ddagger$	$T^\S$
1. Ancestral size constrained, no migration	503.8 <sup>¶</sup> (442.6, 576.0)	2.4 (0.3, 11.1)	503.8 <sup>¶</sup> (442.6, 576.0)	–	–	9.5 (1.2, 37.8)
2. Ancestral size constrained, symmetrical migration	497.1 <sup>¶</sup> (378.3, 824)	15.2 (5.6, 27.6)	497.1 <sup>¶</sup> (378.3, 824)	3.5 <sup>¶</sup> (1.1, 10.7)	3.5 <sup>¶</sup> (1.1, 10.7)	7.5 (0.6, 3673.0)
3. Ancestral size constrained, asymmetrical migration	493.8 <sup>¶</sup> (421.7, 594.0)	0.4 (0.1, 8.8)	493.8 <sup>¶</sup> (421.7, 594.0)	1.9 (0.011, 5.5)	51.7 (7.7, 376.1)	17.5 (2.5, 3608.8)
4. Ancestral size unconstrained, asymmetrical migration	532.5 (417.6, 893.6)	0.6 (0.138, 8.6)	72.5 (16.7, 584.8)	1.9 (0.01, 8.6)	81.0 (10.5, 400.8)	1362.5 (1.94, 3273.6)

\*Effective population size (effective number of individuals  $\times 10^{-3}$ ) for *C. rubella* (Cr), *C. grandiflora* (Cg), and their ancestor (A).

<sup>†</sup>Migration rate ( $4N_e m$ ) from *C. grandiflora* to *C. rubella*.

<sup>‡</sup>Migration rate ( $4N_e m$ ) from *C. rubella* to *C. grandiflora*.

<sup>§</sup>Time (ka) of the split of *C. rubella* and *C. grandiflora*.

<sup>¶</sup>Constrained.