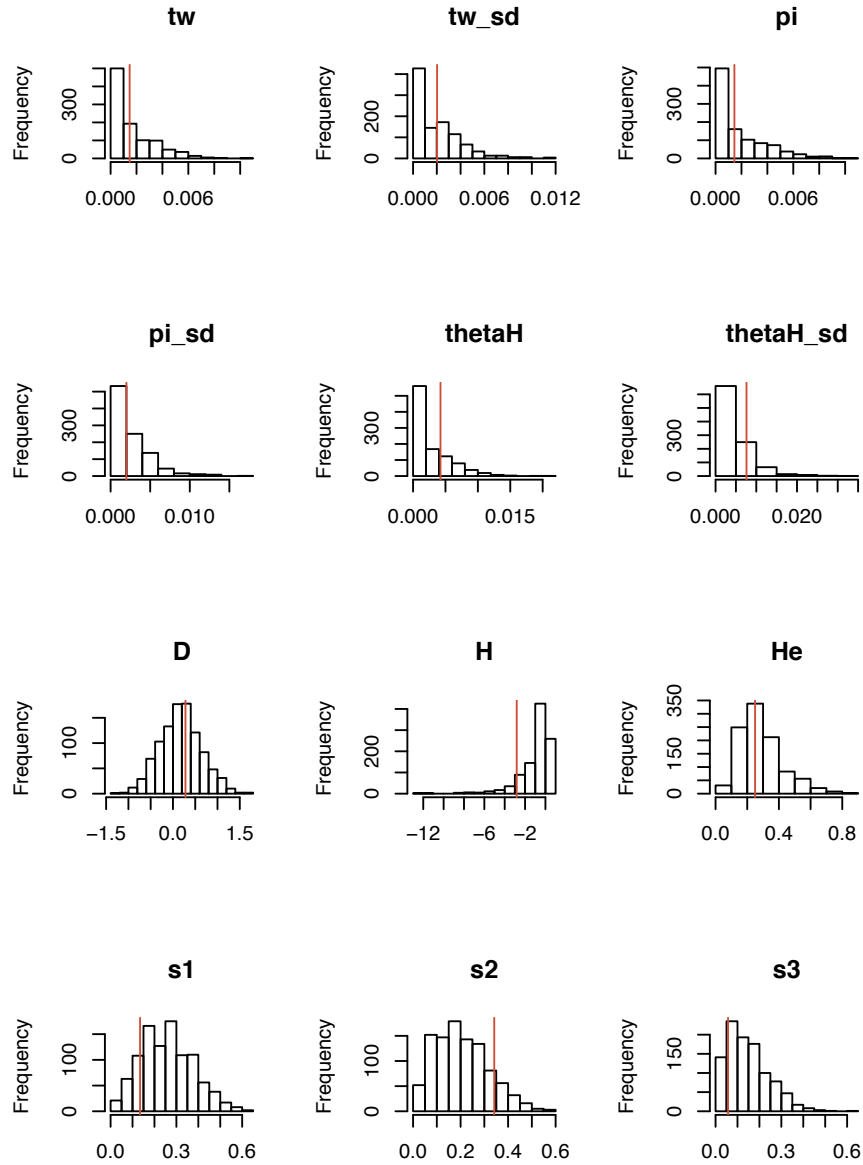
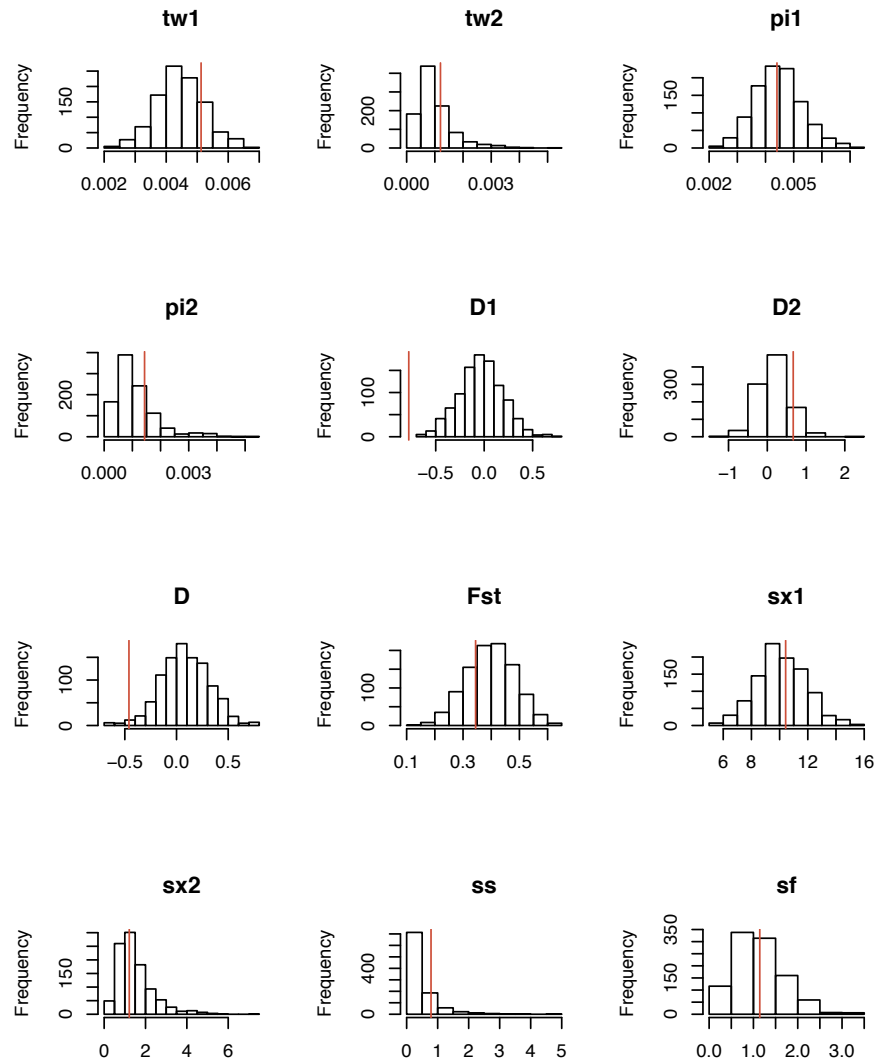


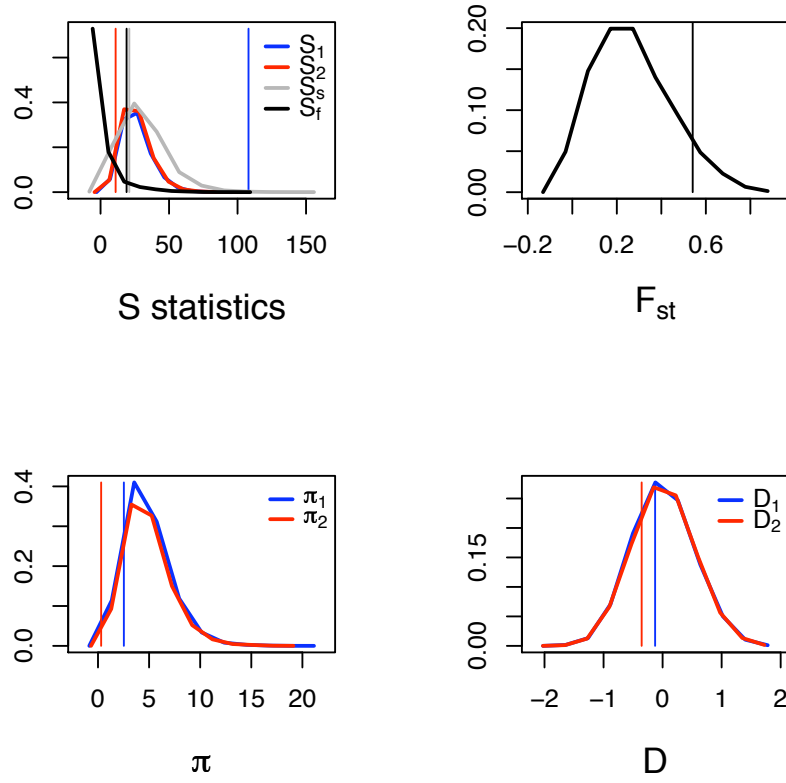
Supplementary tables and figures



Supplementary Figure 1: Posterior predictive distributions simulated under the decline model. The red lines give the observed values for each statistic. Twelve summary statistics were calculated: the mean and standard deviation of Waterson's theta (**tw**, **tw_sd**), the average number of pairwise nucleotide differences (**pi**, **pi_sd**) and Fay & Wu's theta (**thetaH**, **thetaH_sd**), and the mean of Tajima's D (**D**), Fay & Wu's H (**H**), haplotype diversity (**He**) and the relative site frequency spectrum (**s1**, **s2**, **s3**).



Supplementary Figure 2: Posterior predictive distributions simulated under the D_m model. The red lines give the observed values for each statistic. Twelve summary statistics were calculated: Watterson's theta (**tw1**, **tw2**), the average number of pairwise nucleotide differences (**pi1**, **pi2**), Tajima's D (**D1**, **D2**, **D**) and Wakeley & Hey's statistics (**sx1**, **sx2**, **ss**, **sf**). Population 1 is *P. wilsonii* and population 2 is *P. morrisonicola*.



Supplementary Figure 3: Goodness-of-fit for summary statistics in MIMAR. Lines represent the observed values, which can be compared with the simulated distributions. S_1 , S_2 , S_s and S_f denote the number of alleles exclusive to population 1 (*P. wilsonii*) and 2 (*P. morrisonicola*) and the number shared and fixed alleles, respectively. π_1 and π_2 represent the nucleotide diversity in population 1 and 2, F_{st} is the fixation index and D is Tajima's D .

Supplementary Table 1: Sampling locations for Taiwan spruce.

Longitude	Latitude
E121,17,766	N24,12,176
E121,17,841	N24,12,122
E121,18,206	N24,11,412
E121,18,227	N24,11,681
E121,18,231	N24,11,681
E121,18,242	N24,11,922
E121,18,228	N24,11,712
E121,18,278	N24,11,508
E121,18,286	N24,11,476
E121,18,193	N24,11,438
E121,18,086	N24,11,578
E121,18,294	N24,13,013
E121,18,111	N24,11,581
E121,17,737	N24,13,458
E121,18,354	N24,13,065

Supplementary Table 2: Description and references for all statistics calculated for ABC analysis.

	Statistic	Description	Reference
Within-species ABC	tw	Watterson's theta	Watterson, 1975
	pi	Average number of pair-wise nucleotide differences	Tajima, 1983
	thetaH	Fay & Wu's theta	Fay & Wu, 2000
	thetaL	Zeng's theta	Zeng <i>et al.</i> , 2006
	D	Tajima's D	Tajima, 1989
	H	Fay & Wu's H	Fay & Wu, 2000
	Z	Scaled version of Fay & Wu's H	Zeng <i>et al.</i> , 2006
	He	Haplotype Diversity	Nei & Tajima, 1981
	s1-s3	Relative site frequency spectrum binned into 3 classes	-
Between-species ABC	tw1, tw2, tw	Watterson's theta for population 1, 2 and for both populations	Watterson, 1975
	pi1, pi2, pi	Average number of pair-wise nucleotide differences for population 1, 2 and for both populations	Tajima, 1983
	D1, D2, D	Tajima's D for population 1, 2 and for both populations	Tajima, 1989
	thetaH	Fay & Wu's theta	Fay & Wu, 2000
	H	Fay & Wu's H	Fay & Wu, 2000
	He	Haplotype Diversity	Nei & Tajima, 1981
	Fst	Genetic differentiation	Wright, 1951. Calculated as in Hudson <i>et al.</i> , 1992a
	Gst	Genetic differentiation	Nei, 1987
	Kst	Genetic differentiation	Hudson <i>et al.</i> , 1992b
	Hst	Haplotypic measure of genetic differentiation	Hudson <i>et al.</i> , 1992b
	sx1, sx2	Polymorphisms private to populations 1 and 2	Wakeley & Hey, 1997
	ss	Shared polymorphisms	Wakeley & Hey, 1997
	sf	Fixed differences	Wakeley & Hey, 1997
	s1-s9	Relative joint site frequency spectrum binned into 9 classes	-

Supplementary Table 3: Summarized results from the Structure analysis of the five species, where K is the number of clusters considered, $\text{LnP}(D)$ is the natural logarithm of the probability of data averaged over 10 independent runs, SD is standard deviation of $\text{LnP}(D)$ and ΔK is calculated after the method in Evanno et al. (2005).

K	$\text{LnP}(D)$	SD	ΔK
1	-1788	0	NA
2	-1359	0	1436
3	-1253	1	6
4	-1144	21	4
5	-1130	9	5
6	-1160	38	1
7	-1209	113	1
8	-1192	61	1
9	-1255	122	1
10	-1241	69	NA

Supplementary Table 4: Parameters estimated under the within-species population decline model. $\theta = 4N\mu$ and $\rho = 4Nr$ are the population scaled mutation and recombination rates respectively, α is the relative size of *P. morrisonicola* from the present day until t coalescent time units in the past (measured in 4N generations).

	θ	ρ	α	t
Mode	0.0124	0.0051	0.0144	0.0217
Mean	0.02	0.0118	0.0359	0.0521
2.5%	0.005	0.001	0.005	0.005
97.5%	0.06	0.033	0.136	0.142

Supplementary Table 5: Parameters estimated for the D_m model. $\theta = 4N\mu$ and $\rho = 4Nr$ are the population scaled mutation and recombination rates respectively, α is the size of the effective population in *P. morrissonicola* relative to the ancestral population size and t_1 and t_0 are the times of the divergence and bottleneck respectively (expressed in coalescent time units measured in $4N$ generations).

	θ	ρ	α	t_1	t_0
Mode	0.0044	0.0136	0.097	0.2575	0.0854
Mean	0.0045	0.0104	0.1158	0.2684	0.1468
2.5%	0.003	0.001	0.03	0.149	0.016
97.5%	0.006	0.021	0.254	0.424	0.41

Supplementary Table 6: Goodness-of-fit p-values for the parameters simulated by MIMARgof. A significant p-value implies that the distribution of simulated parameter values deviate from the observed. The parameters are the number of alleles private to *P. wilsonii* and *P. morrisonicola* (**s1** and **s2**, respectively), number of shared alleles (**ss**), number of fixed differences (**sf**), fixation index (**fst**), nucleotide diversity in *P. wilsonii* and *P. morrisonicola* (**pi1** and **pi2**, respectively) and Tajima's D in *P. wilsonii* and *P. morrisonicola* (**d1** and **d2**, respectively).

s1	s2	ss	sf	fst	pi1	pi2	d1	d2
1.110223e-16	0.05375	0.2061	0.0448	0.07905	0.1142	5e-05	0.2761	0.25295