

Supporting information

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Supporting Tables

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Figure S1. Bayesian inference analysis of 16 EST-SSR data determining the most likely number of clusters (K) for three *Cerris* oaks (*Q. variabilis*, *Q. acutissima* and *Q. chenii*). The distribution of the likelihood $L(K)$ values (a) and Delta K values (b) are presented for $K = 1-8$ (10 replicates).

Figure S2. Bayesian inference analysis of nuclear data for *Q. variabilis* and *Q. acutissima* separately, STRUCTURE plots are presented for $K = 2$.

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Figure S6. Principal component analysis results obtained along the first three axes for the pre-evaluate models and prior distributions of three oak species demographic models in DIYABC. (a), (b) and (c) representing the species of *Q. variabilis*, *Q. acutissima*, and *Q. chenii*, respectively.

Figure S7. Model checking in DIYABC for the best-supported demographic models.

Figure S8. Predicted distributions of *Q. variabilis* (a, d, j), *Q. chenii* (b, e, h) and *Q. acutissima* (c, f, i) based on ecological niche modelling using Maxent. Predicted distributions are shown for the present time (a, b, c), LGM (d, e, f), and LIG distribution (g, h, i). The results of identity tests (j-l). Bar indicate the null distributions of D and I . Both are generated from 100 randomizations. x-axis indicates values of I and D and y-axis indicates number of randomizations. Red and green solid line indicates values in actual Maxent runs.

Figure S9. (A) Standard principal component analysis (PCA) performed with climatic values for three *Cerris* oaks populations. (B) Climatic space constructed over all background areas and actual niches of all populations in this study, where the solid line represents an occurrence density of 20%, and (C) an occurrence density of 100% is denoted by the thin line and 100% of available climatic background by the thick line.

Figure S10. Contribution of each environmental variable to spatial distribution of the PCA-env

Table S1. Genetic diversity of 44 populations of three *Cerris* oaks (*Q. variabilis*, *Q. acutissima* and *Q. chenii*) estimated based on 16 microsatellite loci.

ID	Location	Longitude (°E)	Latitude (°N)	<i>N</i>	<i>N_a</i>	<i>N_e</i>	<i>I</i>	<i>H_O</i>	<i>H_E</i>	<i>F_{IS}</i>
<i>Q. variabilis</i>										
SPX	Yunnan, Wenshan	105.63	23.63	20	5.188	3.680	1.285	0.143	0.630	0.783
SPY	Yunnan, Kunming	102.66	25.04	20	4.813	3.080	1.130	0.127	0.574	0.789
SPW	Guizhou, Qianxinan	105.44	25.1	20	4.938	3.074	1.167	0.116	0.585	0.811
SPU	Guangxi, Baise	106.23	24.29	20	5.125	3.515	1.253	0.224	0.622	0.655
SPE	Jiangxi, Shangrao	117.99	28.44	17	3.938	2.386	0.968	0.125	0.514	0.771
SPg	Gansu, Longnan	105.69	33.69	20	4.688	2.916	1.160	0.186	0.598	0.702
SPC	Shandong, Linyi	117.98	35.56	20	4.688	2.974	1.088	0.153	0.542	0.729
SPS	Anhui, Hefei	117.18	31.84	10	3.875	2.758	1.023	0.139	0.535	0.764
SPI	Hubei, Xiangyang	112.03	31.99	20	5.063	3.091	1.184	0.169	0.590	0.726
SPF	Hunan, Changsha	112.94	28.19	10	3.375	2.617	0.964	0.112	0.535	0.811
SPM	Jiangsu, Changshu	120.78	31.63	17	4.375	2.906	1.116	0.174	0.577	0.714
SPR	Henan, Zhumadian	113.73	32.79	15	5.063	3.028	1.237	0.128	0.617	0.806
SPA	Henan, Dengfeng	113	34.52	20	4.750	3.172	1.132	0.111	0.565	0.813
SPJ	Jiangxi, Jiujiang	115.59	29.09	20	4.688	2.981	1.141	0.139	0.581	0.771
SPV	Yunnan, Dali	100.27	25.61	20	4.063	2.685	1.034	0.123	0.550	0.786
SPH	Shaanxi, Shangluo	109.89	33.53	11	4.188	3.053	1.123	0.097	0.588	0.850
SPLD	Sichuan, Ganzhi	102.22	29.89	20	4.188	2.767	1.007	0.154	0.515	0.713
SPWS	Chongqing, Wushan	110.08	31.28	17	4.625	3.071	1.152	0.19	0.588	0.694
SPc	Hubei, Yichang	111.29	30.69	19	4.563	3.244	1.149	0.162	0.585	0.736
Mean					4.536	3.000	1.122	0.146	0.573	
<i>Q. acutissima</i>										
A	Yunnan, Wenshan	105.63	23.63	10	2.500	1.671	0.557	0.106	0.318	0.695
B	Yunnan, Kunming	102.66	25.04	20	3.688	2.049	0.758	0.163	0.392	0.602
C	Guizhou, Qianxinan	105.44	25.1	20	4.313	2.629	0.918	0.244	0.458	0.487
E	Guangxi, Baise	106.23	24.29	20	4.125	2.400	0.917	0.242	0.476	0.511
SR	Jiangxi, Shangrao	117.99	28.44	13	4.000	2.465	0.966	0.203	0.502	0.622
J	Gansu, Longnan	105.69	33.69	20	3.813	2.768	0.937	0.241	0.488	0.526
LY	Shandong, Linyi	117.98	35.56	20	4.250	2.529	0.934	0.204	0.472	0.585

HF	Anhui, Hefei	117.18	31.84	20	4.188	2.707	0.977	0.214	0.507	0.596
XY	Hubei, Xiangyang	112.03	31.99	20	4.250	2.584	0.978	0.189	0.509	0.645
CS	Hunan, Changsha	112.94	28.19	10	3.125	2.375	0.825	0.2	0.453	0.596
CY	Jiangsu, Changshu	120.78	31.63	6	2.938	2.525	0.866	0.302	0.501	0.471
QS	Henan, Zhumadian	113.73	32.79	20	3.875	2.473	0.849	0.198	0.455	0.584
P	Sichuan, Meishan	113	34.52	10	4.188	2.704	0.992	0.259	0.521	0.526
T	Shandong, Jinan	115.59	29.09	20	3.688	2.268	0.862	0.224	0.462	0.533
U	Anhui, Huaibei	100.27	25.61	20	3.813	2.225	0.845	0.232	0.449	0.502
YS	Guangxi, Guilin	109.89	33.53	10	3.875	2.979	1.005	0.231	0.518	0.589
YK	Zhejiang, Yongkang	102.22	29.89	20	5.625	3.372	1.259	0.222	0.593	0.641
PS	Guangdong, Shaoguan	110.08	31.28	10	4.313	2.410	0.996	0.36	0.520	0.331
H	Yunnan, Jinghong	111.29	30.69	17	2.688	1.910	0.661	0.081	0.385	0.801
L	Beijing, Miyun	105.63	23.63	10	3.688	2.322	0.892	0.197	0.490	0.614
Mean					3.847	2.468	0.900	0.216	0.474	
<i>Q. chenii</i>										
XA	Jiangxi, Lushan	115.98	29.6	20	6.063	3.831	3.334	0.284	0.627	0.564
XB	Hunan, Xinning	111.1	26.75	14	5.438	3.699	1.279	0.27	0.609	0.583
XC	Anhui, Hefei	117.17	31.84	20	5.063	3.255	1.209	0.274	0.600	0.562
XD	Anhui, Taihu	117.13	30.47	14	4.438	3.045	1.116	0.295	0.573	0.507
XE	Anhui, Yuexi	116.46	30.72	17	5.000	3.543	1.204	0.313	0.583	0.488
Mean					5.200	3.474	1.228	0.287	0.598	

sympatric population; N , sample size; N_a , average number of alleles; N_e , number of effective alleles; I , Shannon's information index; H_o , observed heterozygosity; H_E , expected heterozygosity; F_{IS} , inbreeding coefficient.

Table S2. Primer sequences and characterization of the 16 microsatellite loci used in this study

Locus name	GenBank NO.	Primer sequences(5'-3')	Ta (°C)	Motif
QV1	KP855973	F-AACCTCACAATGAGTGCTCTA R-GAGCTTGGTTGGCTAAAAT	55	(AAC) ₇
QV2	KP856092	F-AAGACAAGCACTTGTTTACCA R-CAGCATCAAAGTCTACTAGG	55	(GA) ₁₁
QV3	KP855993	F-TATCTTTTGTGGGGGAAGATA R-AGAAGGCCTCATCTTTCTTTA	55	(GA) ₁₃
QV4	KP856140	F- ATTCATTTTCTCCACCAAA R- CCATTATGATTGGATTAGGG	55	(AAT) ₈
QV6	KP855682	F- CGCTTGCCACAATAGTAATAA R- AAGTACCAAAAATGACAATG	55	(ATC) ₈
QV7	KP856122	F- TGTCTTCTCTTGTCATTTCTCA R- TGAGTTGTTACTCCATTTGGT	55	(TCT) ₁₂
QV8	KP855892	F- CCTGCTTCCAATATTCTCATA R- GCAAAATCACTCATCAAGAAC	55	(TTC) ₆
QV9	KP855677	F- CCCTAAAATTTCAATCAATC R- TTTATGCTCATTCCTCTTGAA	55	(AG) ₁₃
QV10	KP856035	F- TGCCTTATTGTTGATGCTG R- CAAAATCCAAAAGGCCAAAC	55	(GA) ₁₄
QV11	KP856152	F- ACCAATGTGAAAAGGGAAG R- TGGGTTTGGTTTCTTCTTCT	55	(AAG) ₆
QV12	KP856046	F- CAGCTCTGGATGGATATAATG R- ACATGCATGGAGAGAAATAGA	55	(TC) ₉
QV13	KP856153	F- GTCAAGAAGGAAGCCGTAA R- TCTTTGTCACCCCATCAC	55	(TA) ₁₀
QV14	KP856067	F- AGAGCAATTCCCAACTAACTT R- TAGTTCAAGATCTGAGCCAAA	55	(TC) ₁₀
QV15	KP855752	F- GACCCATTGACTGAACTCAT R- GTGTCTCTGTCCAAAACCTCAA	55	(AG) ₁₇
QV16	KP856019	F- GTCCAAGTAGGTTCTTCATT R- AAAGAAATGGGTCCCAAA	55	(TTC) ₇
QV17	KP856055	F- ACGAGAATGACAGGAAAATA R- TGATCGTCGTGGTAATCTTAG	55	(ACA) ₇

Table S3. Prior distributions for model parameters used in divergence model comparisons

Parameter	Models		
	Prior Distribution	Minimum	Maximum
Effective population size			
NA(ancestral population)	uniform	100	1000000
N1	uniform	100	1000000
N2	uniform	100	1000000
N3	uniform	100	1000000
Time of events			
t1	uniform	5000	200000
t2	uniform	200000	300000
Mean mutation rate	Gamma	1.0×10^{-6}	1.0×10^{-5}
Individual locus mutation rate	Gamma	1.0×10^{-7}	1.0×10^{-4}
Mean coefficient P	uniform	0.1	0.3
Individual locus coefficient P	Gamma	0.01	0.9

N1, effective population size of *Q. variabilis*; N2, effective population size of *Q. acutissima*; N3, effective population size of *Q. chenii*; NA, effective population size of ancestral population.

Table S4. Posterior probability under logistic and descriptions of four scenarios, and prior setting for all parameters used in approximate Bayesian computation (ABC) for demographic analysis of three species (Fig. 3b)

	<i>Q. variabilis</i>		<i>Q. acutissima</i>		<i>Q. chenii</i>	
	Posterior Probability [95% CI]		Posterior Probability [95% CI]		Posterior Probability [95% CI]	
Scenario1	0.1699 [0.1646,0.1752]		0.6182 [0.5982,0.6382]		0.3172 [0.3106,0.3237]	
Scenario2	0.0991 [0.0946,0.1036]		0.0003 [0.0000,0.0110]		0.1198 [0.1146,0.1251]	
Scenario3	0.5177 [0.5108,0.5246]		0.0339 [0.0235,0.0443]		0.2308 [0.2249,0.2367]	
Scenario4	0.2133 [0.2075,0.2191]		0.3476 [0.3276,0.3675]		0.3321 [0.3257,0.3386]	
Best supported scenarios		Scenario 3		Scenario 1		Scenario 4
	prior setting	Posterior parameter		Posterior parameter		Posterior parameter
NA	Uniform [10, 10 ⁶]	3.14E+05 [1.13E+05,7.56E+05]	Uniform [100, 10 ⁶]	1.74E+05 [7.19E+04, 3.88E+05]	Uniform [10, 10 ⁶]	3.26E+05 [1.67E+05,6.64E+05]
N1	Uniform [10, 10 ⁶]	6.74E+05 [2.18E+05,9.86E+05]	Uniform [100, 10 ⁶]	8.84E+05 [9.10E+05, 9.96E+05]	Uniform [10, 10 ⁶]	5.72E+05 [2.71E+05,9.15E+05]
N2	Uniform [10, 10 ⁶]	-	Uniform [100, 10 ⁶]	5.94E+05 [2.65E+05, 9.23E+05]	Uniform [10, 10 ⁶]	-
N3	Uniform [10, 10 ⁶]	-	Uniform [100, 10 ⁶]	-	Uniform [10, 10 ⁶]	-
N4	Uniform [10, 10 ⁶]	5.39E+04 [6.79E+03,3.66E+05]	Uniform [100, 10 ⁶]	-	Uniform [10, 10 ⁶]	-
N5	Uniform [10, 10 ⁶]	-	Uniform [100, 10 ⁶]	-	Uniform [10, 10 ⁶]	8.27E+05 [4.38E+05, 9.93E+05]
N6	Uniform [10, 10 ⁶]	-	Uniform [100, 10 ⁶]	-	Uniform [10, 10 ⁶]	-
t1	Uniform [10,10000]	2.32E+03 [1.67E+02,9.02E+03]	Uniform [10,10000]	5.25E+03 [4.12E+02, 9.36E+03]	Uniform [10, 3000]	1.25E+03 [6.53E+01, 2.88E+03]

t2	Uniform [10, 18000]	1.19E+04 [2.89E+03,1.77E+04]	Uniform [10, 10000]	8.21E+03 [4.09E+03,9.95E+03]	Uniform [10, 6000]	4.02E+03 [9.84E+02,5.90E+03]
Mean mutation rate	Gamma [1.0E-06, 5.0E-06]		Gamma [1.0E-06, 5.0E-06]		Gamma [1.0E-06, 5.0E-06]	
Individual locus mutation rate	Gamma [1.0E-07, 5.0E-04]		Gamma [1.0E-07, 1.0E-04]		Gamma [1.0E-07, 5.0E-04]	
Mean coefficient P	Uniform [1.0E-01,3.0E-01]		Uniform [1.0E-01, 3.0E-01]		Uniform [1.0E-01, 3.0E-01]	
Individual locus coefficient P	Gamma [1.0E-02, 9.0E-01]		Gamma [1.0E-02, 9.0E-01]		Gamma [1.0E-02, 9.0E-01]	

Table S5. 14 bioclimatic variables that were used in Ecological niche modeling

Code	Bioclimatic variable
BIO1	Annual precipitation
BIO2	Mean Diurnal Range (Mean of monthly (max temp - min temp))
BIO3	Isothermality
BIO4	Temperature seasonality
BIO5	Max Temperature of Warmest Month
BIO8	Temperature seasonality
BIO9	Mean temperature of the driest quarter
BIO10	Mean temperature of the warmest quarter
BIO12	Annual precipitation
BIO13	Precipitation of the wettest month
BIO14	Precipitation of Driest Month
BIO15	Precipitation Seasonality (Coefficient of Variation)
BIO17	Precipitation of the driest quarter
BIO18	Precipitation of Warmest Quarter

Table S6. Diversity indices of 16 EST-SSR loci for 759 individuals

Locus	<i>N_a</i>	<i>A_R</i>	<i>H_O</i>	<i>H_E</i>	PIC	<i>H_S</i>	<i>H_T</i>	<i>F_{ST}</i>	<i>G'_{ST}</i>
QV1	11	5.760	0.381	0.862	0.847	0.730	0.832	0.119	0.463
QV2	13	4.915	0.317	0.792	0.773	0.415	0.744	0.447	0.763
QV3	17	6.004	0.471	0.850	0.838	0.616	0.819	0.260	0.655
QV4	8	3.767	0.267	0.722	0.688	0.470	0.661	0.289	0.550
QV6	7	4.050	0.218	0.767	0.737	0.308	0.709	0.570	0.823
QV7	9	4.991	0.374	0.834	0.814	0.542	0.796	0.322	0.704
QV8	6	3.473	0.369	0.736	0.695	0.511	0.669	0.243	0.489
QV9	25	8.557	0.268	0.944	0.940	0.822	0.933	0.119	0.682
QV10	14	5.897	0.224	0.843	0.830	0.665	0.791	0.154	0.483
QV11	10	3.945	0.236	0.731	0.695	0.561	0.676	0.174	0.392
QV12	12	3.980	0.261	0.734	0.698	0.524	0.673	0.229	0.470
QV13	10	4.877	0.250	0.785	0.766	0.567	0.746	0.252	0.561
QV14	16	6.120	0.362	0.874	0.862	0.757	0.845	0.104	0.436
QV15	16	5.323	0.467	0.748	0.733	0.576	0.709	0.185	0.450
QV16	6	2.483	0.389	0.519	0.486	0.286	0.390	0.253	0.375
QV17	7	3.412	0.707	0.645	0.576	0.618	0.647	0.047	0.122
Mean	11.7	4.847	0.348	0.774	0.749	0.561	0.727	0.232	0.529

N_a, number of alleles; *A_R*, allelic richness; *H_O*, observed heterozygosity over all populations; PIC, polymorphic information content; *H_E*, expected heterozygosity over all populations; *H_S*, mean genetic diversity within populations; *H_T*, total genetic diversity; *F_{ST}*, differentiation among-population; *G'_{ST}* standardized genetic differentiation.

Table S7. Diversity indices of 16 EST-SSR loci for three related species

Locus	N_a			N			H_o			H_E			PIC			F_{ST}		
	QV	QA	QC	QV	QA	QC	QV	QA	QC	QV	QA	QC	QV	QA	QC	QV	QA	QC
QV1	8	10	10	336	338	85	0.193	0.456	0.824	0.831	0.827	0.840	0.810	0.803	0.816	0.127	0.149	0.044
QV2	11	12	3	336	338	85	0.253	0.320	0.560	0.789	0.427	0.607	0.761	0.416	0.587	0.154	0.400	0.089
QV3	7	12	16	334	338	84	0.269	0.595	0.774	0.521	0.870	0.934	0.503	0.855	0.924	0.107	0.132	0.070
QV4	4	5	7	319	338	85	0.187	0.285	0.494	0.576	0.716	0.808	0.535	0.666	0.780	0.304	0.352	0.069
QV6	3	5	7	323	332	85	0.158	0.208	0.482	0.345	0.704	0.838	0.329	0.656	0.813	0.193	0.516	0.060
QV7	7	7	4	326	336	85	0.202	0.516	0.471	0.750	0.647	0.606	0.720	0.611	0.565	0.129	0.183	0.161
QV8	4	6	3	332	331	84	0.159	0.546	0.500	0.581	0.773	0.568	0.534	0.739	0.543	0.110	0.172	0.076
QV9	21	22	10	310	323	79	0.145	0.325	0.519	0.916	0.934	0.836	0.909	0.928	0.816	0.137	0.153	0.098
QV10	12	12	8	330	338	85	0.155	0.219	0.518	0.858	0.753	0.863	0.845	0.726	0.844	0.129	0.224	0.067
QV11	6	7	10	336	338	85	0.144	0.216	0.682	0.653	0.698	0.896	0.614	0.648	0.881	0.099	0.281	0.061
QV12	9	9	10	328	338	85	0.162	0.222	0.800	0.655	0.664	0.879	0.625	0.606	0.863	0.131	0.305	0.064
QV13	8	10	6	334	337	85	0.168	0.213	0.718	0.832	0.562	0.822	0.811	0.548	0.796	0.127	0.329	0.074
QV14	15	12	10	331	325	85	0.245	0.400	0.671	0.907	0.818	0.831	0.898	0.794	0.808	0.093	0.186	0.091
Qv15	14	12	13	326	338	85	0.531	0.308	0.859	0.871	0.457	0.859	0.859	0.443	0.839	0.109	0.241	0.032
QV16	3	5	2	322	338	85	0.512	0.251	0.471	0.599	0.382	0.409	0.526	0.368	0.0385	0.040	0.465	0.020
QV17	4	6	6	322	337	85	0.671	0.822	0.244	0.675	0.593	0.677	0.613	0.507	0.625	0.071	0.043	0.082
Mean	8.5	9.5	7.8	327.8	335.2	84.5	0.260	0.369	0.599	0.710	0.677	0.767	0.681	0.645	0.743	0.122	0.258	0.072

QV, *Q. variabilis*; QA, *Q. acutissima*; QC, *Q. chenii*. N_a : number of alleles; N , sample numbers; H_o , observed heterozygosity; H_E , expected heterozygosity; PIC, polymorphic information content; F_{ST} , among-population differentiation

Table S8 Hardy-Weinberg equilibrium (HWE) test in this study

	QV1	QV2	QV3	QV4	QV6	QV7	QV8	QV9
<i>Q. variabilis</i>								
SPX	0.0000	0.0000	0.0003	0.0000	NA	0.0000	0.0000	0.0000
SPY	0.0000	0.0000	0.0023	0.0872	0.0000	0.0000	0.0001	0.0000
SPW	0.0000	0.0000	0.0001	0.0819	NA	0.0000	0.0000	0.0000
SPU	0.0000	0.0000	0.8830	0.0002	0.0029	0.0000	0.0002	0.0000
SPE	0.0000	0.0000	0.0011	0.0001	NA	0.0012	0.0003	0.0000
SPg	0.0000	0.4944	0.0002	0.0000	0.0021	0.0000	0.0000	0.0000
SPC	0.0000	0.0009	0.0001	0.0252	0.6870	0.0002	0.0005	0.0018
SPS	0.0001	0.0041	0.3682	0.0008	NA	0.0135	0.0014	0.0100
SPI	0.0000	0.0003	0.7604	0.0000	0.0000	0.0002	0.0000	0.0002
SPF	0.0715	0.0029	0.0031	0.0002	NA	0.0027	0.0001	0.0012
SPM	0.0000	0.9865	0.6597	0.0000	0.0002	0.0000	0.0000	0.0021
SPR	0.0000	0.1837	0.0042	0.0000	0.0004	0.0000	0.0000	0.0012
SPA	0.0000	0.0000	0.0000	0.0000	NA	0.0000	0.0000	0.0000
SPJ	0.0000	0.0000	0.0002	0.0266	NA	0.0000	0.0000	0.0000
SPV	0.0000	0.0000	0.0000	1.0000	NA	0.0000	0.0000	0.0000
SPH	0.0000	0.0001	0.0011	0.0000	0.0044	0.0355	0.0044	0.0000
SPLD	0.0000	0.0000	0.0029	0.0001	NA	0.0000	0.0002	0.0000
SPWS	0.0000	0.0000	0.1702	0.0000	0.0029	0.0000	0.0000	0.0002
SPc	0.0000	0.0000	0.0002	0.0000	NA	0.0000	0.0000	0.0000
<i>Q. acutissima</i>								
A	0.0043	1.0000	0.0000	0.0007	NA	0.7386	0.0465	0.0014
B	0.0000	0.6870	0.1220	0.0252	0.0000	0.0027	0.9010	0.0000

C	0.0372	0.8284	0.3970	0.0471	NA	0.3333	0.2933	0.0469
E	0.0178	NA	0.5274	0.8476	0.0000	0.8570	0.2807	0.0000
SR	0.2955	0.0834	0.1933	0.0082	0.0000	0.0003	0.0002	0.0908
J	0.0005	1.0000	0.1385	0.0000	0.0000	0.7661	0.6773	0.0663
LY	0.7514	1.0000	0.0294	0.0000	0.0000	0.1978	0.1003	0.0000
HF	0.0217	0.0054	0.0063	0.0000	0.0000	0.0030	0.0042	0.0534
XY	0.2308	0.4962	0.0175	0.0000	0.0000	0.2901	0.0013	0.0000
CS	0.0023	0.9904	0.0559	0.1540	0.0000	0.1901	0.2078	0.0029
CY	0.0042	0.0725	0.4096	NA	0.0030	0.4456	0.00351	0.0172
QS	0.0020	0.9968	0.2791	0.0000	0.0000	0.6642	0.6331	0.0208
P	0.0873	0.1557	0.1209	0.0004	0.0000	0.8179	0.1265	0.7277
T	0.0059	1.0000	0.0987	0.0000	NA	0.9282	0.3277	0.0000
U	0.0000	0.9968	0.1204	0.0023	NA	0.9499	0.5136	0.0001
YS	0.0032	NA	0.1684	NA	NA	0.8161	0.6404	0.0063
YK	0.5147	0.0232	0.0063	0.0002	0.0023	0.0000	0.0019	0.0002
PS	0.1286	0.9998	0.2577	0.0000	0.0003	0.9785	0.0777	0.0343
H	0.0000	NA	0.0000	0.0000	NA	0.3820	0.0005	0.0000
L	0.0005	0.1726	0.4860	0.0000	0.0000	0.5256	0.0101	0.0206
<i>Q. chenii</i>								
XA	0.0808	0.3701	0.9059	0.0000	0.0000	0.0000	0.0000	0.0000
XB	0.3395	0.1207	0.0867	0.0000	0.0004	0.0004	0.0000	0.0017
XC	0.0025	0.0764	0.4589	0.0000	0.0000	0.0000	0.0148	0.0000
XD	0.1243	0.7814	0.7313	0.0000	0.0000	0.0000	0.1277	0.0161
XE	0.9803	0.1764	0.7982	0.0000	0.0000	NA	NA	0.0001

	QV10	QV11	QV12	QV13	QV14	QV15	QV16	QV17
<i>Q. variabilis</i>								
SPX	0.0000	0.0000	0.0000	0.0000	0.0000	0.6408	0.1642	0.5195
SPY	0.0000	0.0000	0.0000	0.0000	0.0000	0.9882	0.0321	0.0643
SPW	0.0000	0.0000	0.0000	0.0000	0.0000	0.3404	0.0183	0.2981
SPU	0.0000	0.0000	0.0000	0.0000	0.5565	0.5483	0.6807	0.6964
SPE	0.0000	0.0000	0.0000	0.0000	0.0000	0.2944	0.2312	0.6798
SPg	0.0000	0.0000	0.0000	0.0000	0.3249	0.3716	0.1151	0.1953
SPC	0.0000	0.0000	0.0004	0.0000	0.0000	0.2899	0.5789	0.0874
SPS	0.0014	0.0014	0.0022	0.0002	0.0001	0.7101	0.1328	0.5255
SPI	0.0000	0.0000	0.0000	0.0000	0.0000	0.4820	0.3638	0.1783
SPF	0.0001	0.0001	0.0135	0.0005	0.0010	0.0146	0.5255	0.2850
SPM	0.0020	0.0001	0.0000	0.0000	0.0000	0.0140	0.6134	0.6725
SPR	0.0003	0.0000	0.0000	0.0000	0.0000	0.7024	0.2297	0.2843
SPA	0.0000	0.0000	0.0004	0.0004	0.0001	0.0528	0.8183	0.8465
SPJ	0.0000	0.0000	0.0000	0.0000	0.0000	0.1692	0.4759	0.2522
SPV	0.0000	0.0000	0.0000	0.0000	0.0000	0.0015	0.5135	0.5475
SPH	0.0009	0.0000	0.0000	0.0011	0.0924	0.0047	0.3860	0.9539
SPLD	0.0000	0.0000	0.0089	0.0000	0.0000	0.2807	0.8406	0.6905
SPWS	0.0000	0.0000	0.0277	0.0000	0.0417	0.2034	0.1368	0.5893
SPc	0.0258	0.0000	0.0000	0.0000	0.4684	0.0065	0.4255	0.2458
<i>Q. acutissima</i>								
A	0.0001	0.0014	0.0050	0.0050	0.0008	NA	NA	0.0050
B	0.0000	0.0000	0.0000	0.0003	0.0005	0.0007	NA	0.0000
C	0.0000	0.0000	0.0000	0.0003	0.0001	0.0273	NA	0.0000
E	0.0000	0.0000	0.0001	0.0002	0.0000	0.0010	NA	0.0053

SR	0.0037	0.0001	0.0000	0.0008	0.0018	0.0072	NA	0.0040
J	0.0000	0.0000	0.0023	NA	0.0000	1.0000	NA	0.0000
LY	0.0000	0.0000	0.0000	0.0023	0.0000	0.0252	NA	0.0016
HF	0.0000	0.0000	0.0000	NA	0.0001	1.0000	NA	0.0000
XY	0.0000	0.0000	0.0000	0.0000	0.0001	0.0005	0.0023	0.0068
CS	0.0050	0.0001	0.0003	0.0050	0.0017	NA	NA	0.0233
CY	0.0091	0.0040	0.0021	0.0637	0.3063	0.0030	NA	0.0070
QS	0.0000	0.0000	0.0000	NA	0.0000	0.1560	NA	0.0000
P	0.0000	0.0000	0.0000	0.0000	0.0112	NA	NA	0.2004
T	0.0000	0.0000	0.0000	0.0001	0.0012	0.0027	0.0001	0.0101
U	0.0000	0.0002	0.0001	0.0000	0.5934	0.8185	0.2133	0.1562
YS	0.0050	0.0001	0.0003	0.0001	0.2098	0.1405	0.0000	0.6537
YK	0.0000	0.0000	0.0041	0.0000	0.0440	0.1446	0.0000	0.0283
PS	0.0085	0.1963	0.0455	0.0003	0.4840	0.4765	0.3572	0.9088
H	0.0000	0.0000	0.0001	0.0000	0.0013	0.0320	NA	0.0948
L	0.0000	0.0023	0.0000	0.0000	0.0000	0.0740	0.0131	0.8183
<i>Q. chenii</i>								
XA	0.0000	0.0013	0.6621	0.0110	0.0035	0.9456	1.0000	0.0508
XB	0.0012	0.0128	0.1320	0.0868	0.0011	0.9228	NA	0.0050
XC	0.0000	0.3480	0.1664	0.3878	0.0006	0.1728	NA	0.0000
XD	0.0004	0.0024	0.0317	0.4319	0.5984	0.0298	NA	0.0066
XE	0.0000	0.0239	0.0102	0.0008	0.0563	0.1530	NA	0.4498

Table S9. Estimation of rates of contemporary gene flow per generation among three species (QV, QA and QC) using the programs BAYESASS v3.0

	<i>Q. variabilis</i> →	<i>Q. acutissima</i> →	<i>Q. chenii</i> →
<i>Q. variabilis</i>	-	0.001	0.004
<i>Q. acutissima</i>	0.002	-	0.004
<i>Q. chenii</i>	0.001	0.024	-

QV, *Q. variabilis*; QA, *Q. acutissima*; QC, *Q. chenii*. →, source populations.

Table S10. Posterior probability of each scenario and 95% confidence intervals (CI) based on the logistic regression approach for approximate Bayesian computation analyses (ABC) for all three related species (*Q. acutissima*, *Q. variabilis* and *Q. chenii*). Type I and type II errors for the best supported scenario (in bold) are indicated

Scenario	Posterior probability	95% CI	Type I error	Type II error
1	0.1645	[0.1057,0.2232]		
2	0.4747	[0.4128,0.5366]	0.160	0.130
3	0.0664	[0.0074,0.1254]		
4	0.2944	[0.2225,0.3664]		

Table S11. Indices of bottleneck test of the three related species

ID(<i>Q. variabilis</i>)		One-tail Wilcoxon test		ID(<i>Q. acutissima</i>)		One-tail Wilcoxon test		ID(<i>Q. chenii</i>)		One-tail Wilcoxon test	
	Model-shift	TPM	SMM		Model-shift	TPM	SMM		Model-shift	TPM	SMM
SPX	L-shaped	0.021	0.084	A	Shift mode	0.936	0.936	XA	L-shaped	0.798	0.894
SPY	L-shaped	0.316	0.490	B	L-shaped	0.992	0.999	XB	L-shaped	0.381	0.661
SPW	L-shaped	0.467	0.835	C	L-shaped	0.954	0.966	XC	L-shaped	0.423	0.661
SPU	L-shaped	0.080	0.232	E	L-shaped	0.914	0.966	XD	L-shaped	0.211	0.319
SPE	L-shaped	0.533	0.640	SR	L-shaped	0.805	0.874	XE	Shift mode	0.040	0.122
SPg	L-shaped	0.490	0.684	J	L-shaped	0.148	0.213				
SPC	L-shaped	0.752	0.874	LY	L-shaped	0.985	0.994				
SPS	Shift mode	0.577	0.719	HF	L-shaped	0.271	0.428				
SPI	L-shaped	0.647	0.752	XY	L-shaped	0.666	0.826				
SPF	Shift mode	0.004	0.008	CS	Shift mode	0.163	0.251				
SPM	L-shaped	0.353	0.490	CY	Shift mode	0.000	0.001				
SPR	L-shaped	0.783	0.920	QS	L-shaped	0.476	0.665				
SPA	Shift mode	0.300	0.489	P	L-shaped	0.251	0.524				
SPJ	L-shaped	0.360	0.756	T	L-shaped	0.773	0.849				
SPV	L-shaped	0.165	0.360	U	L-shaped	0.924	0.964				
SPH	L-shaped	0.202	0.232	YS	Shift mode	0.040	0.040				
SPLD	Shift mode	0.489	0.756	YK	L-shaped	0.942	0.975				
SPWS	L-shaped	0.372	0.470	PS	L-shaped	0.935	0.971				
SPc	L-shaped	0.126	0.180	H	L-shaped	0.271	9.318				
				L	L-shaped	0.736	0.863				

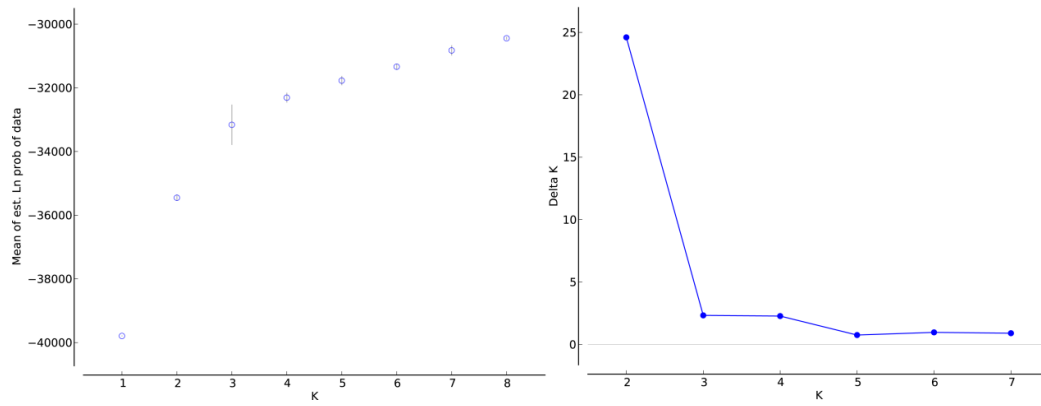


Figure S1. Bayesian inference analysis of 16 EST-SSR data determining the most likely number of clusters (K) for three *Cerris* oaks (*Q. variabilis*, *Q. acutissima* and *Q. chenii*). The distribution of the likelihood $L(K)$ values (a) and Delta K values (b) are presented for $K = 1-8$ (10 replicates).

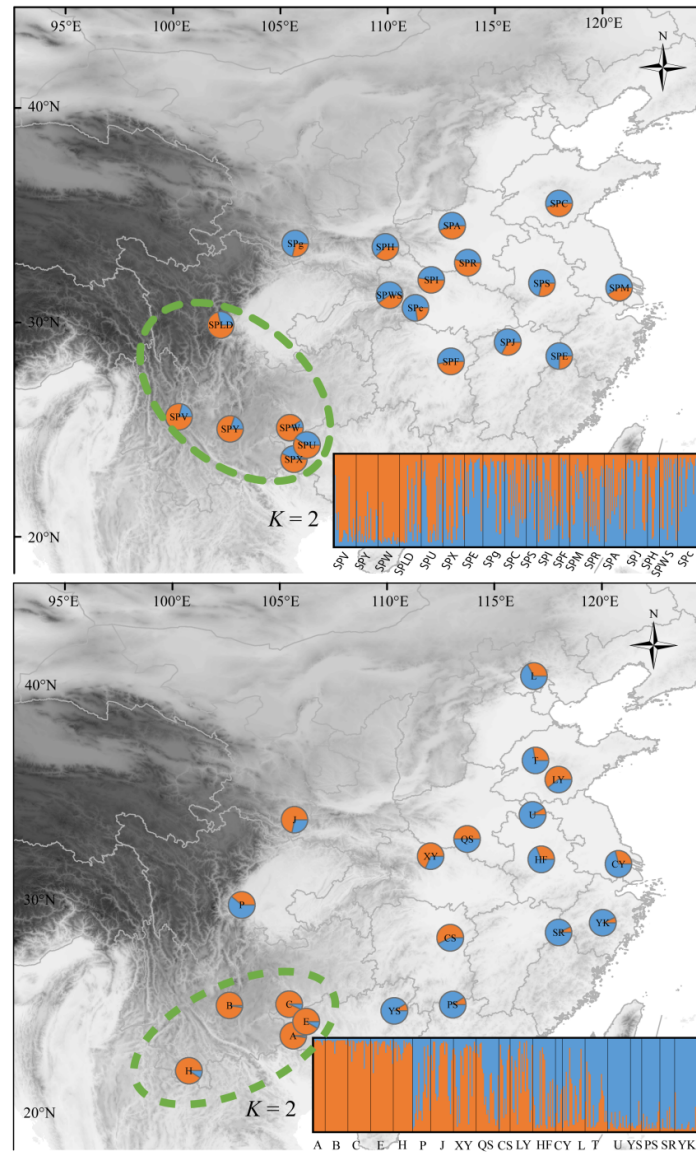


Figure S2. Bayesian inference analysis of nuclear data for *Q. variabilis* and *Q. acutissima* separately, STRUCTURE plots are presented for $K = 2$.

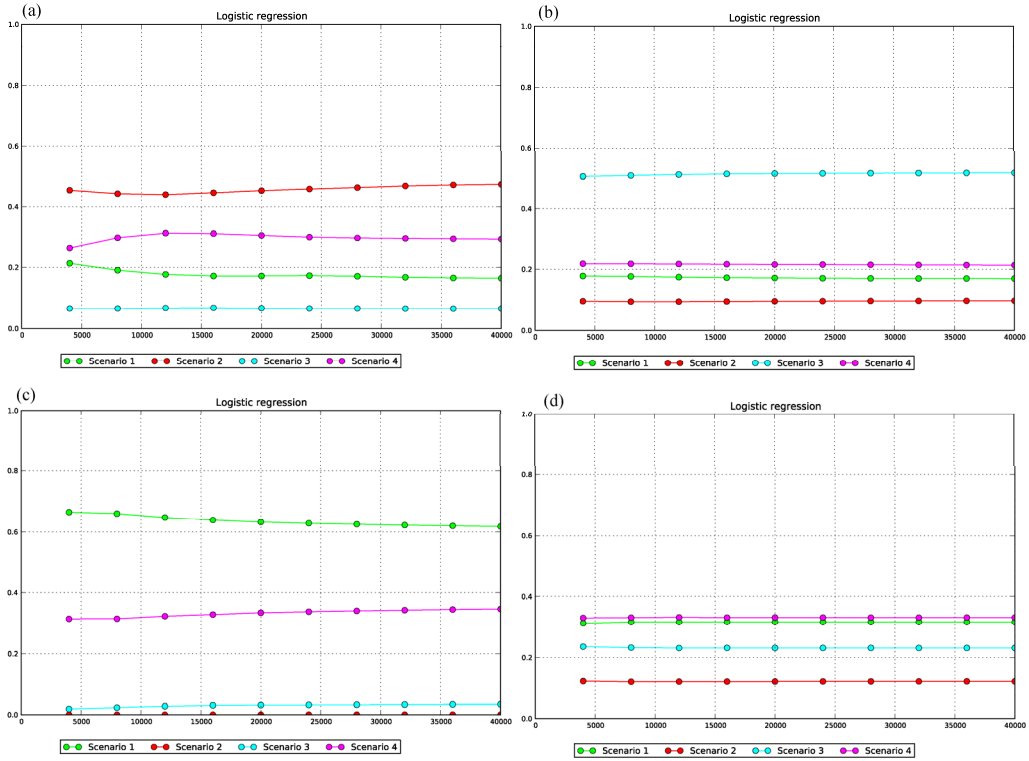


Figure S3. Comparison of posterior probabilities for four simulated scenarios of species differentiation obtained by logistic regression from 1 % of the closest data set in DIYABC.

(a), comparison of posterior probabilities for four simulated scenarios of three oak species (*Q. variabilis* (b); *Q. acutissima* (c) and *Q. chenii* (d)) demographic history obtained by logistic regression from 1 % of the closest data set in DIYABC.

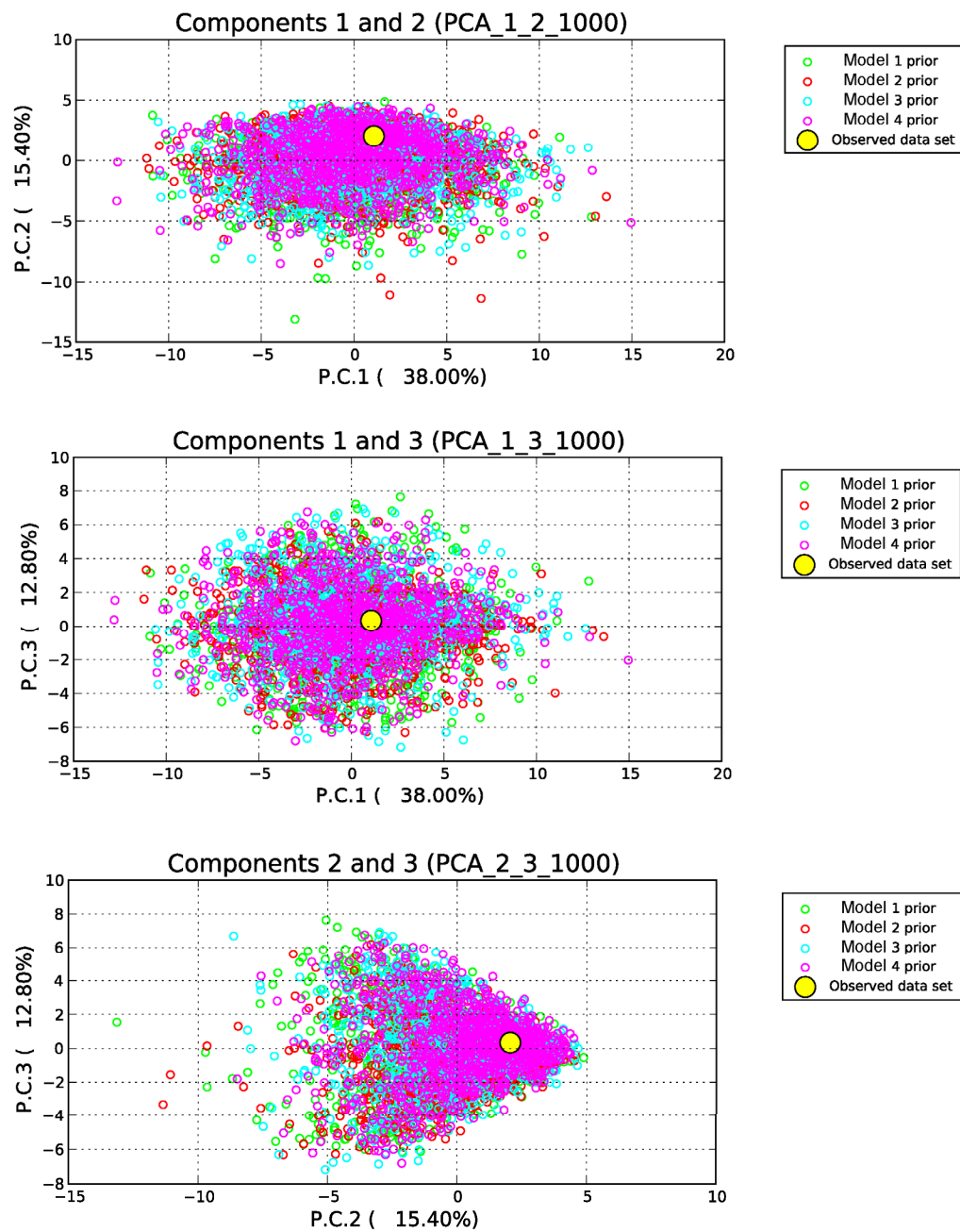


Figure S4. Principal component analysis results obtained along the first three axes for the pre-evaluate models and prior distributions of three oak species divergence in DIYABC.

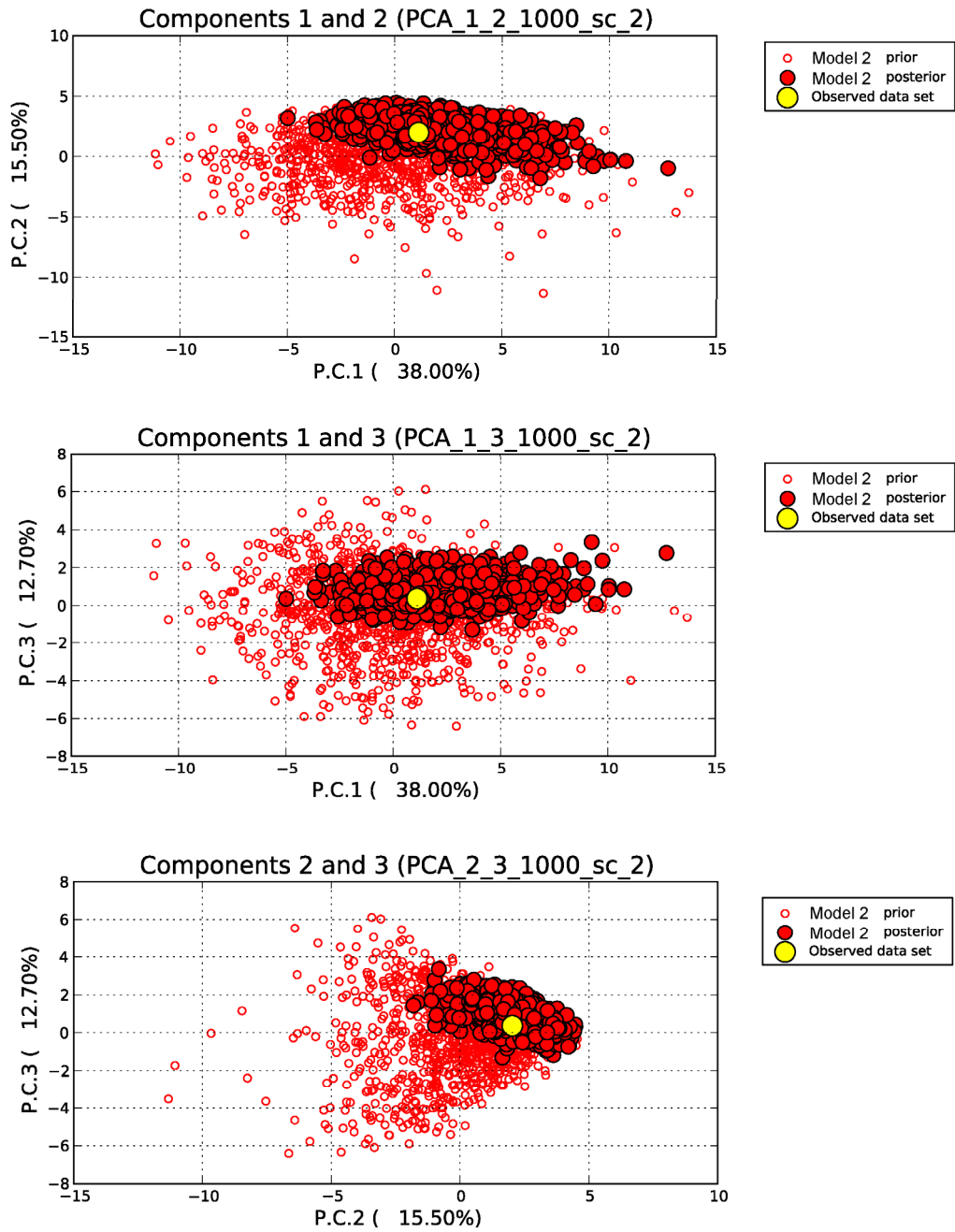


Figure S5. Model checking in DIYABC for the best-supported (species divergence: model 2).

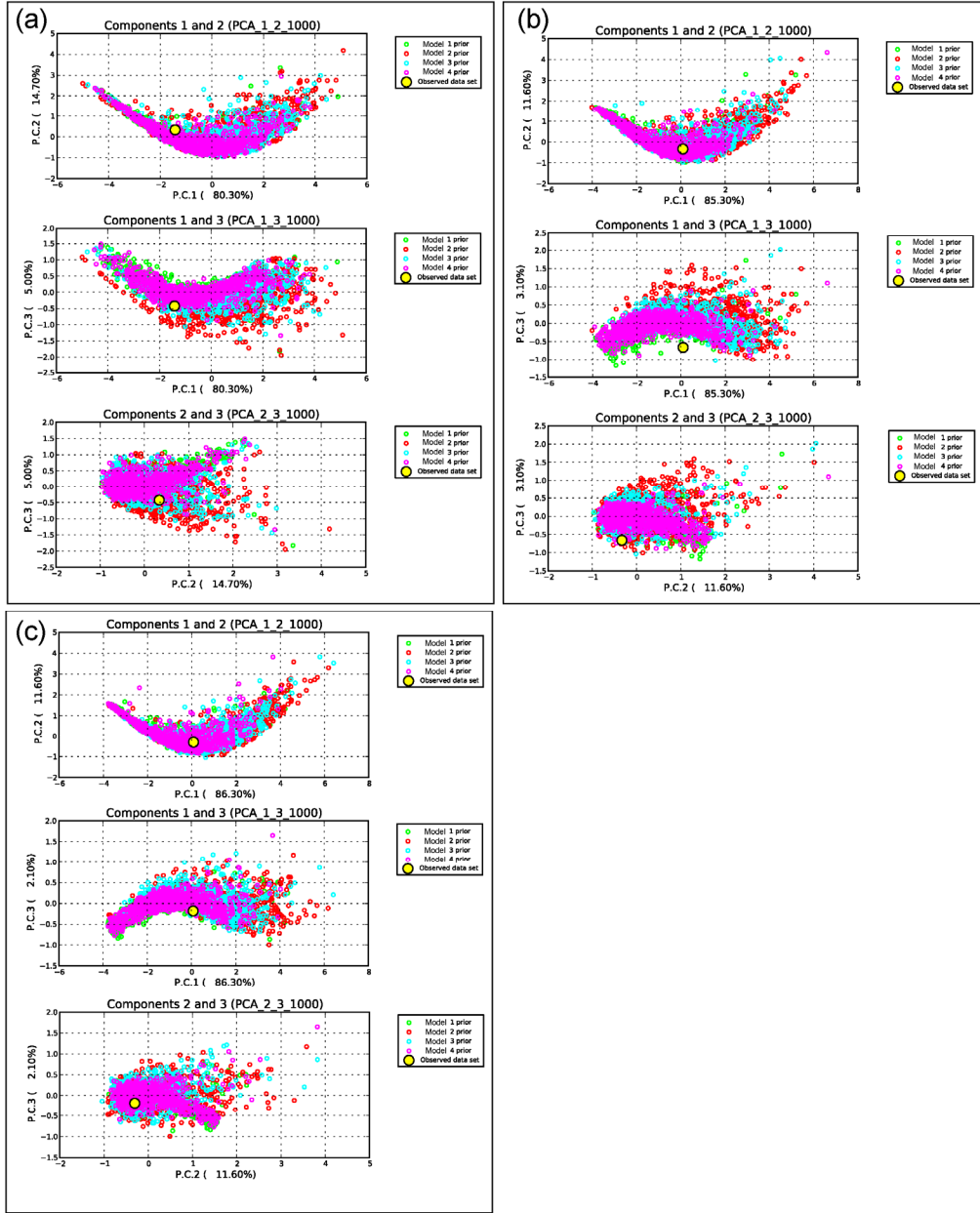


Figure S6. Principal component analysis results obtained along the first three axes for the pre-evaluate models and prior distributions of three oak species demographic models in DIYABC. (a), (b) and (c) representing the species of *Q. variabilis*, *Q. acutissima*, and *Q. chenii*, respectively.

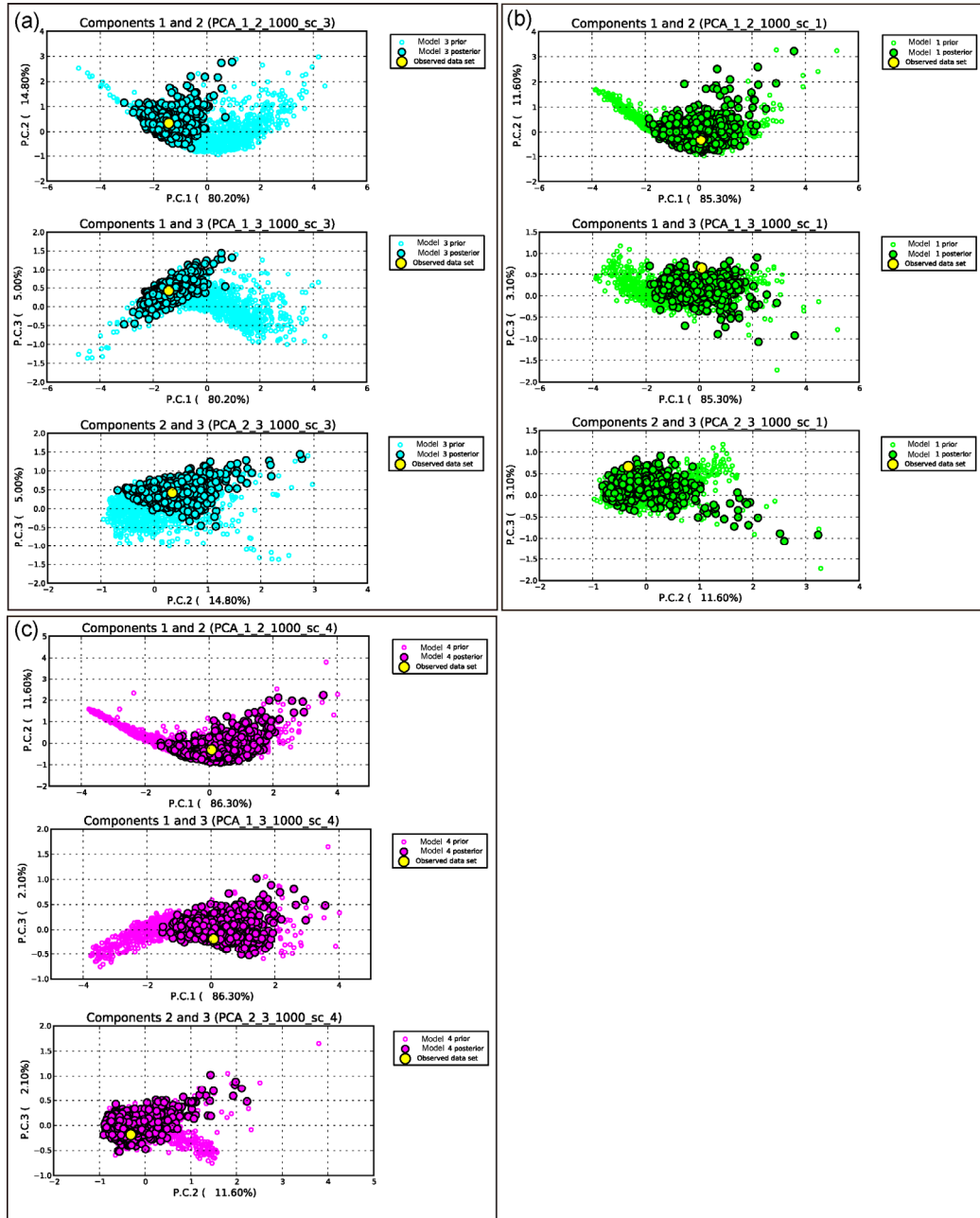


Figure S7. Model checking in DIYABC for the best-supported demographic models. (a), (b) and (c) representing the species of *Q. variabilis* (Model 3), *Q. acutissima* (Model 1), and *Q. chenii* (Model 4), respectively.

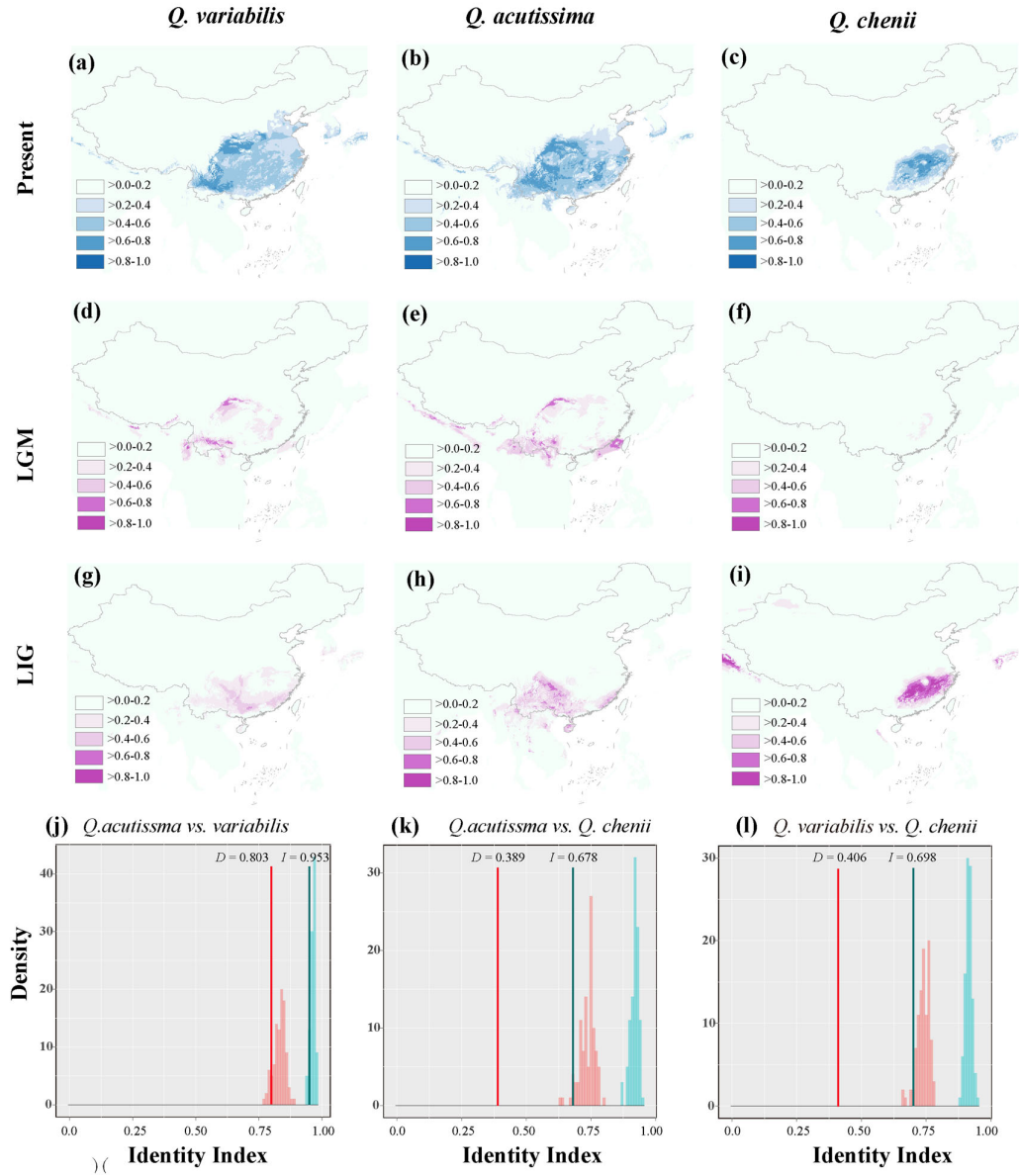


Figure S8. Predicted distributions of *Q. variabilis* (a, d, j), *Q. chenii* (b, e, h) and *Q. acutissima* (c, f, i) based on ecological niche modelling using Maxent. Predicted distributions are shown for the present time (a, b, c), LGM (d, e, f), and LIG distribution (g, h, i). The results of identity tests (j-l). Bar indicate the null distributions of D and I . Both are generated from 100 randomizations. x-axis indicates values of I and D and y-axis indicates number of randomizations. Red and green solid line indicates values in actual Maxent runs.

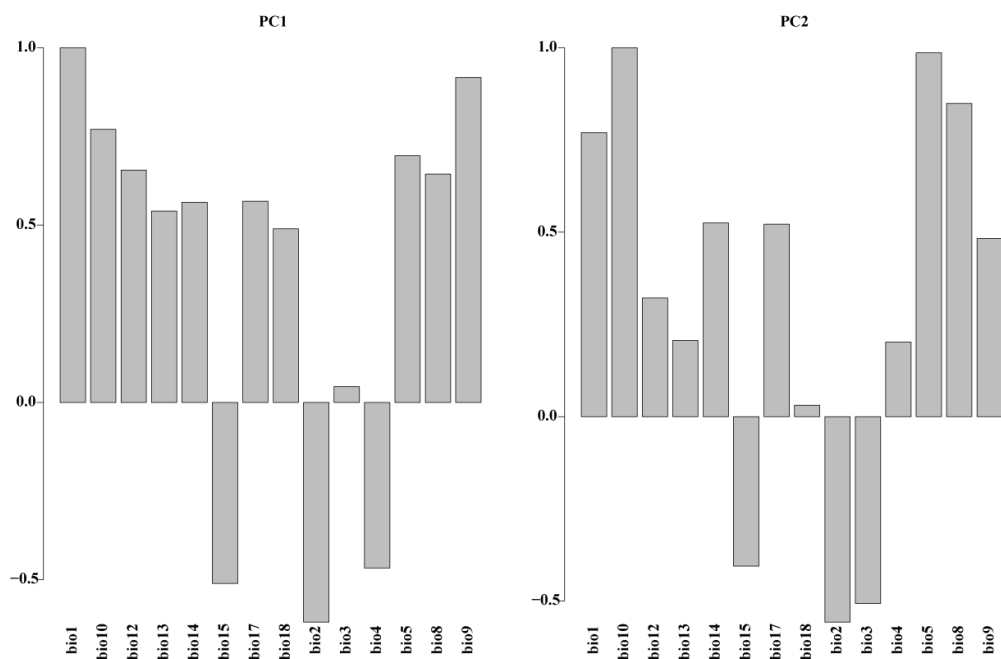


Figure S10. Contribution of each environmental variable to spatial distribution of the PCA-env.