

Table S1. Sample information of *Asteropyrum*

Region	Location	Population Code	Latitude (° N)	Longitude (° E)	Elevation (m)	N	Hap.
Burma	Grape	PT	27.6635	97.4266	2600	1	H4(1)
Tibet	Mêdog	MT	29.7135	95.5821	2820	24	H7(24)
Yunnan	Fugong	FG	27.1030	98.8190	2106	11	H4(11)
	Gongshan	GS	28.0500	98.5667	2700	9	H4(9)
	Suijiang	SJ	28.3928	104.0658	1217	9	H6(9)
	Jingdong	WLS	24.4156	100.7325	2200	8	H8(7)
	Wenshan	WS	23.3412	103.8684	2200	11	H5(11)
	Yiliang	YL	27.8078	104.3072	1800	21	H9(21)
	Zhenxiong	ZX	27.3756	104.6689	2004	12	H10(10)
	Dujiangyan	DJY	30.9900	103.64	2500	12	H1(8)
Sichuan	Tianquan	ELS	30.0253	102.8603	2079	12	H2(12)
	Emei Shan	EMS	29.5517	103.3623	2296	12	H3(9)
	Ebian	HZG	29.0106	103.0561	1535	13	H3(13)
	Leibo	LB	28.3567	103.4825	1659	12	H6(12)
	Rongjing	LCG	29.6356	102.8847	1346	7	H2(7)
	Mabian	MB	29.0278	103.4789	1150	12	H6(12)
	Majiang	MJ	26.4183	107.335	1611	13	H6(13)
Guizhou	Pingli	PL	32.0027	109.2798	1617	12	H1(12)
Chongqing	Youyang	YY	29.2533	108.9869	1290	8	H5(8)
	Wulong	WL	29.1958	107.3936	1577	12	H5(12)
Hubei	Shennongjia	SNJ	31.4434	110.3045	3057	10	H1(10)
	Xuanen	XE	30.0361	109.7316	1374	12	H1(12)
Hunan	Longshan	LS	29.5814	109.7069	918	12	H5(12)
	Sangzhi	SZ	29.7674	110.0621	1310	12	H1(12)
	Xinning	XN	26.4064	110.9921	946	10	H5(10)
	Yongshun	YS	28.9936	109.8606	1310	12	H5(12)
Guangxi	Longsheng	HP	24.62	109.9205	846	12	H5(9)
	Ziyuan	ZY	25.9117	110.414	1190	12	H5(10)
Total		28				323	

Emei Shan indicates Emei Mountains. N, sample size; Hap., haplotypes of chloroplast *psbA-trnH* region.

Table S2. Description of the prior distribution of parameters from five scenarios in Figure 2 used in Approximate Bayesian Computation.

Parameter	Distribution	Minimum	Maximum
Effective population size			
N_1	Uniform	10	3000000
N_2	Uniform	10	3000000
N_3	Uniform	10	3000000
N_a	Uniform	10	3000000
Time of events (in generations backward in time)			
T_1	Uniform	10	2000000
T_2	Uniform	10	2000000
Admixture rate			
r_a	Uniform	0.001	0.999
Mean mutation rate			
μ	Uniform	1×10^{-10}	1×10^{-7}

N_1 , N_2 , and N_3 , current population sizes; N_a , ancestral population size; T_1 and T_2 , divergence time or admixture time of different clusters, and $T_2 > T_1$.

Table S3. Variable sites of the *psbA-trnH* sequences for each of the haplotypes identified in *Asteropyrum*

Haplotype	9	1	2	4	5	6	7	1	1	1	1	2	2
		5	8	0	7	6	5	2	3	3	9	0	1
								7	2	5	8	5	5
H1	C	C	G	C	T	A	G	A	T	T	T	T	G
H2	T	T	G	C	T	A	G	A	A	T	T	C	G
H3	C	C	G	C	T	A	G	C	A	T	G	T	G
H4	C	C	C	C	T	A	G	A	A	G	T	T	G
H5	C	C	G	C	T	A	G	A	A	T	T	T	T
H6	C	C	G	C	T	A	G	C	A	T	T	T	T
H7	C	C	C	T	T	A	G	A	A	G	T	T	G
H8	C	C	G	C	T	A	G	C	A	G	T	T	G
H9	C	C	G	C	T	A	G	A	A	T	T	T	G
H10	C	C	G	C	C	G	A	A	A	T	T	T	G

Table S4. Results of *t*-tests on elevation and 19 bioclimatic variables between the two groups of *Asteropyrum*

Group		Elevation	Bio1	Bio2	Bio3	Bio4	Bio5	Bio6	Bio7	Bio8	Bio9	Bio10	Bio11	Bio12	Bio13	Bio14	Bio15	Bio16	Bio17	Bio18	Bio19
		(m)	(°C)	(°C)	(°C)	(SD*100)	(°C)	(°C)	(°C)	(°C)	(°C)	(°C)	(°C)	(mm)	(mm)	(mm)	(CV)	(mm)	(mm)	(mm)	(mm)
1	Mean	2190.00	12.15	8.99	35.39	609.62	24.04	-1.64	25.68	18.96	4.51	19.25	4.21	1275.14	269.64	11.86	88.05	718.50	43.57	693.00	46.50
	SE	135.87	1.04	0.47	2.21	28.12	0.94	1.15	0.52	0.93	1.22	0.95	1.18	139.51	33.89	1.36	3.10	92.32	4.60	81.10	5.25
2	Mean	1246.73	13.94	7.84	28.63	719.16	27.50	0.03	27.47	20.47	5.16	22.38	4.63	1361.18	234.73	29.36	66.99	634.91	99.55	580.82	104.73
	SE	84.75	0.67	0.22	0.98	18.94	0.74	0.62	0.40	0.88	0.78	0.72	0.67	77.83	12.94	4.44	3.91	26.70	15.79	16.29	17.94
	P	0.00	0.19	0.06	0.02	0.01	0.01	0.25	0.02	0.26	0.68	0.02	0.78	0.62	0.39	0.00	0.00	0.44	0.00	0.24	0.00

SE, standard errors.

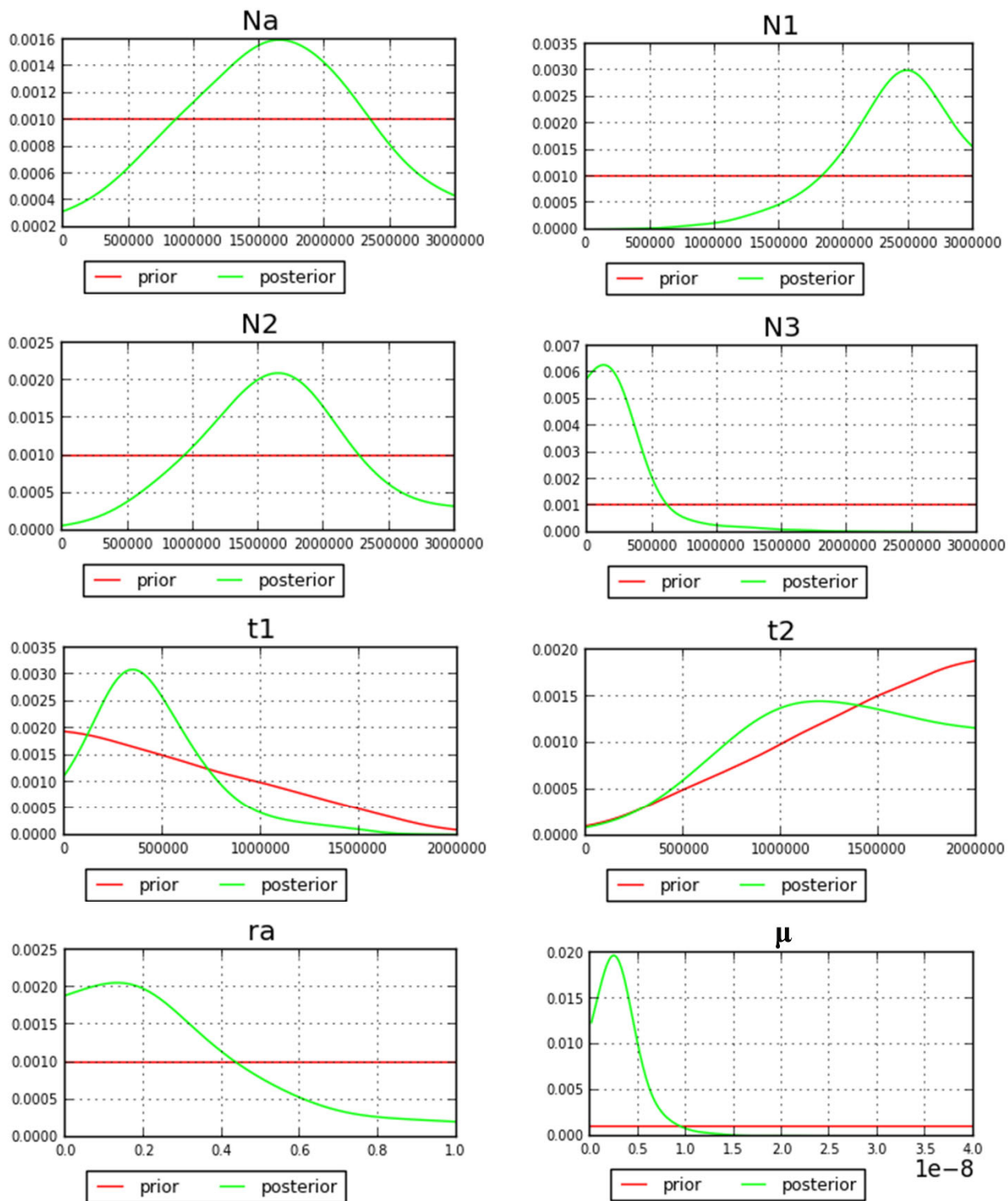


Figure S1. Prior and posterior distributions of demographic parameters under scenario 5 in Figure 2 estimated by DIYABC