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## Supplemental Information for:

# Sky islands as foci for divergence of fig trees and their pollinators in South-West China

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Table S1 The contributions of each climatic factors shaping the geographic distributions of *Ficus tikoua* simulated by Species Distribution Modeling (SDM) in the last interglacial (LIG), last glacial maximum (LGM) and current time. (Top five contribution climate factors were marked as bold).

Time	LIG	LGM	Current
Bio1 (annual mean temperature)	0.5%	<b>15.7%</b>	0.2%
Bio2 (mean diurnal range)	<b>8.4%</b>	<b>9.9%</b>	1.3%
Bio3 (isothermality)	1.2%	3.0%	1.7%
Bio4 (temperature seasonality)	<b>4.4%</b>	<b>10.6%</b>	<b>7.4%</b>
Bio5 (max temperature of warmest month)	0.5%	0.1%	0.7%
Bio6 (min temperature of coldest month)	<b>27.9%</b>	8.5%	<b>23.5%</b>
Bio7 (temperature annual range)	2.8%	0.7%	6.3%
Bio8 (mean temperature of wettest quarter)	3.0%	2.1%	2.2%
Bio9 (mean temperature of driest quarter)	1.3%	<b>18.4%</b>	<b>18.5%</b>
Bio10 (mean temperature of warmest quarter)	0.2%	0.2%	0.3%
Bio11 (mean temperature of coldest quarter)	<b>27.4%</b>	3.2%	<b>16.4%</b>
Bio12 (annual precipitation)	2.0%	5.1%	2.5%
Bio13 (precipitation of wettest month)	1.9%	0.4%	0.1%
Bio14 (precipitation of driest month)	1.6%	<b>16.0%</b>	<b>8.5%</b>
Bio15 (precipitation seasonality)	3.1%	1.2%	1.1%
Bio16 (precipitation of wettest quarter)	0.5%	0.4%	0.2%
Bio17 (precipitation of driest quarter)	<b>9.8%</b>	0.2%	<b>7.4%</b>
Bio18 (precipitation of warmest quarter)	1.7%	0.5%	<b>0.7%</b>
Bio19 (precipitation of coldest quarter)	1.9%	4.1%	1.0%

YKM	YXW	SMH	SXC	YWD	SPZ	YHZ	YQJ	YLD	SYJ	SHS	SLS	QKY	SGL	SJA	SNX	SYJ	SFY	SSP	SSN	SNC	SGJ	SMY	SBZ
0.000																							
0.297	0.000																						
0.273	0.236	0.000																					
0.347	0.319	0.096	0.000																				
0.334	0.372	0.178	0.198	0.000																			
0.233	0.295	0.186	0.180	0.172	0.000																		
0.322	0.277	0.200	0.193	0.302	0.229	0.000																	
0.220	0.272	0.187	0.212	0.302	0.155	0.142	0.000																
0.200	0.206	0.107	0.164	0.233	0.171	0.143	0.119	0.000															
0.328	0.341	0.125	0.062	0.208	0.156	0.236	0.245	0.184	0.000														
0.398	0.388	0.296	0.336	0.380	0.353	0.306	0.309	0.269	0.317	0.000													
0.426	0.410	0.323	0.362	0.400	0.359	0.331	0.331	0.334	0.318	0.203	0.000												
0.501	0.476	0.341	0.377	0.455	0.402	0.349	0.388	0.321	0.340	0.118	0.325	0.000											
0.513	0.499	0.355	0.400	0.475	0.428	0.381	0.407	0.329	0.364	0.128	0.326	0.028 <sup>NS</sup>	0.000										
0.456	0.404	0.337	0.373	0.431	0.389	0.346	0.358	0.318	0.338	0.138	0.119	0.214	0.198	0.000									
0.530	0.550	0.398	0.440	0.500	0.476	0.438	0.443	0.409	0.419	0.109	0.339	0.217	0.232	0.212	0.000								
0.440	0.413	0.310	0.340	0.408	0.350	0.316	0.328	0.274	0.311	0.170	0.230	0.155	0.179	0.155	0.269	0.000							
0.393	0.289	0.275	0.296	0.368	0.314	0.253	0.296	0.263	0.280	0.135	0.226	0.166	0.195	0.175	0.231	0.171	0.000						
0.505	0.434	0.377	0.385	0.433	0.422	0.337	0.393	0.377	0.389	0.326	0.269	0.373	0.387	0.309	0.437	0.319	0.259	0.000					
0.435	0.400	0.315	0.325	0.403	0.335	0.301	0.283	0.314	0.333	0.236	0.230	0.278	0.296	0.224	0.303	0.230	0.182	0.274	0.000				
0.515	0.473	0.385	0.409	0.450	0.444	0.375	0.423	0.400	0.393	0.279	0.283	0.329	0.350	0.314	0.382	0.333	0.249	0.058	0.296	0.000			
0.435	0.404	0.303	0.320	0.403	0.337	0.290	0.323	0.274	0.292	0.153	0.164	0.124	0.129	0.092	0.243	0.077	0.141	0.280	0.197	0.281	0.000		
0.466	0.477	0.333	0.354	0.375	0.390	0.352	0.378	0.341	0.332	0.243	0.171	0.311	0.308	0.190	0.335	0.255	0.253	0.331	0.276	0.332	0.158	0.000	
0.476	0.411	0.357	0.386	0.426	0.414	0.339	0.391	0.365	0.383	0.307	0.263	0.337	0.368	0.303	0.409	0.308	0.252	0.061	0.292	0.047 <sup>NS</sup>	0.276	0.325	0.000

Table S3 Means, standard errors and results of all populations on 19 Bioclimate variables for *Ceratosolen sp.*. Turkey's D was used to conduct multiple comparison of the bioclimatic variables between different region pairs at different time. (Bold characters represent  $P < 0.05$ )

		Bio1 (°C)	Bio2 (°C)	Bio3 (°C)	Bio4 (SD*100)	Bio5 (°C)	Bio6 (°C)	Bio7 (°C)	Bio8 (°C)	Bio9 (°C)	Bio10 (°C)	Bio11 (°C)	Bio12 (mm)	Bio13 (mm)	Bio14 (mm)	Bio15 (CV)	Bio16 (mm)	Bio17 (mm)	Bio18 (mm)	Bio19 (mm)		
SCB	LIG	Mean	15.2	7.8	2.4	738.2	31.4	-0.7	32.1	24.0	5.0	25.9	2.8	667.7	185.0	0.0	112.5	394.0	3.2	326.6	3.4	
		SE	0.3	0.2	0.1	74.9	0.4	0.4	0.5	0.5	0.6	0.5	0.3	43.1	6.7	0.0	3.2	27.5	0.8	40.2	0.8	
	LGM	Mean	13.3	8.3	3.0	624.5	26.8	-0.1	26.9	20.0	4.5	21.0	4.5	994.6	232.2	11.6	89.9	581.8	40.5	554.5	40.5	
		SE	0.2	0.3	0.1	8.5	0.3	0.4	0.4	0.3	0.2	0.3	0.2	34.3	17.1	1.5	4.9	31.8	4.8	29.2	4.8	
	Current	Mean	16.9	7.5	2.7	693.3	30.8	3.3	27.5	24.7	7.5	25.5	7.5	1058.6	213.2	13.5	78.9	561.3	46.2	540.4	46.2	
		SE	0.2	0.2	0.1	10.7	0.4	0.3	0.3	0.3	0.2	0.3	0.2	27.6	9.9	1.6	3.6	19.9	4.9	20.3	4.9	
		P (LIG vs LGM)	<b>0.000</b>	0.269	<b>0.000</b>	0.171	<b>0.000</b>	0.446	<b>0.000</b>	<b>0.000</b>	0.631	<b>0.000</b>	<b>0.000</b>	<b>0.000</b>	<b>0.021</b>	<b>0.000</b>	<b>0.001</b>	<b>0.000</b>	<b>0.000</b>	<b>0.000</b>	<b>0.000</b>	
		P (LIG vs Current)	<b>0.000</b>	0.650	<b>0.015</b>	0.751	0.440	<b>0.000</b>	<b>0.000</b>	0.388	<b>0.000</b>	0.750	<b>0.000</b>	<b>0.000</b>	0.233	<b>0.000</b>	<b>0.000</b>	<b>0.000</b>	<b>0.000</b>	<b>0.000</b>	<b>0.000</b>	
		P (LGM vs Current)	<b>0.000</b>	<b>0.046</b>	<b>0.002</b>	0.514	<b>0.000</b>	<b>0.000</b>	0.586	<b>0.000</b>	<b>0.000</b>	<b>0.000</b>	<b>0.000</b>	0.418	0.507	0.556	0.135	0.853	0.570	0.944	0.570	
	HDM	LIG	Mean	14.1	11.1	3.6	634.5	28.8	(1.7)	30.5	20.2	9.6	21.1	5.6	874.3	243.9	0.0	121.8	635.0	2.0	518.4	11.4
		SE	0.5	0.3	0.1	14.8	0.5	0.4	0.3	0.5	1.0	0.5	0.6	30.5	10.2	0.0	1.6	22.8	0.9	27.6	4.3	
LGM		Mean	12.0	10.9	4.5	466.9	22.3	(1.6)	23.9	17.2	5.4	17.3	5.4	885.2	187.5	9.5	85.3	499.8	32.7	492.2	32.7	
		SE	0.5	0.2	0.1	12.3	0.6	0.4	0.5	0.5	0.5	0.5	0.5	19.1	5.2	0.8	1.5	11.6	2.9	13.9	2.9	
Current		Mean	15.9	10.9	4.4	482.3	26.4	1.8	24.6	21.3	9.0	21.3	9.0	933.5	198.4	9.2	88.4	544.2	31.3	544.2	31.3	
		SE	0.5	0.3	0.1	15.8	0.6	0.5	0.4	0.5	0.6	0.5	0.6	21.0	4.8	0.9	1.6	12.7	2.8	12.7	2.8	
		P (LIG vs LGM)	<b>0.013</b>	0.787	<b>0.000</b>	<b>0.000</b>	<b>0.000</b>	1.000	<b>0.000</b>	<b>0.000</b>	<b>0.001</b>	<b>0.000</b>	0.979	0.945	<b>0.000</b>	<b>0.000</b>	<b>0.000</b>	<b>0.000</b>	<b>0.000</b>	<b>0.000</b>	0.605	<b>0.000</b>
		P (LIG vs Current)	<b>0.040</b>	0.868	<b>0.000</b>	<b>0.000</b>	<b>0.011</b>	<b>0.000</b>	<b>0.000</b>	0.283	0.826	0.982	<b>0.000</b>	0.204	<b>0.000</b>	<b>0.000</b>	<b>0.000</b>	<b>0.001</b>	<b>0.000</b>	0.614	<b>0.001</b>	
		P (LGM vs Current)	<b>0.000</b>	0.987	0.738	0.731	<b>0.000</b>	<b>0.000</b>	0.409	<b>0.000</b>	<b>0.003</b>	<b>0.000</b>	<b>0.000</b>	0.342	0.540	0.971	0.365	0.151	0.913	0.151	0.956	
YGP		LIG	Mean	16.6	9.0	2.9	694.7	32.6	2.2	30.3	23.6	8.1	24.8	7.2	1173.4	287.3	1.9	99.2	736.9	22.2	540.6	34.5
		SE	0.5	0.3	0.1	21.9	0.6	0.6	0.4	0.7	0.8	0.6	0.6	31.4	10.2	0.9	3.7	20.6	5.7	39.6	5.7	
	LGM	Mean	14.6	9.8	4.1	522.4	25.9	2.0	24.0	20.2	8.0	20.8	7.3	1117.6	216.2	17.6	73.4	577.1	71.9	556.7	82.5	
		SE	0.4	0.1	0.1	22.5	0.7	0.4	0.6	0.5	0.6	0.6	0.4	39.7	7.2	1.2	1.4	18.0	5.4	15.3	8.4	
	Current	Mean	18.1	8.9	3.8	541.4	28.9	5.0	23.9	23.8	10.8	24.2	10.4	1268.2	238.3	21.4	74.3	659.4	78.1	644.3	80.8	
		SE	0.4	0.2	0.2	24.0	0.6	0.5	0.5	0.5	0.5	0.6	0.5	43.3	6.2	2.4	1.8	16.5	7.7	16.5	8.9	
		P (LIG vs LGM)	0.010	<b>0.022</b>	<b>0.000</b>	<b>0.000</b>	<b>0.000</b>	0.910	<b>0.000</b>	<b>0.000</b>	0.991	<b>0.000</b>	0.986	0.564	<b>0.000</b>	<b>0.000</b>	<b>0.000</b>	<b>0.000</b>	<b>0.000</b>	<b>0.000</b>	0.902	<b>0.000</b>
		P (LIG vs Current)	0.058	0.955	<b>0.000</b>	<b>0.000</b>	<b>0.000</b>	<b>0.001</b>	<b>0.000</b>	0.965	<b>0.010</b>	0.807	<b>0.000</b>	0.199	<b>0.000</b>	<b>0.000</b>	<b>0.000</b>	<b>0.012</b>	<b>0.000</b>	<b>0.020</b>	<b>0.000</b>	
		P (LGM vs Current)	<b>0.000</b>	<b>0.010</b>	0.166	0.827	<b>0.005</b>	<b>0.000</b>	0.987	<b>0.000</b>	<b>0.007</b>	<b>0.001</b>	<b>0.000</b>	<b>0.021</b>	0.136	0.221	0.966	<b>0.007</b>	0.774	0.057	0.987	

Table S4 Population genetic variation of *Ceratosolen* pollinating fig wasp of *F. tikoua*. Number of individuals ( $N_{SSR}$ ), number of alleles ( $N_A$ ), allelic richness after rarefaction ( $A_R$ ), observed ( $H_O$ ) and expected ( $H_E$ ) heterozygosity with significance for deviation from HWE ( $*P < 0.05$ ,  $**P < 0.01$ ,  $***P < 0.001$ ) after correction for multiple testing, inbreeding coefficient ( $F_{IS}$ ) ( $*P < 0.05$ ), and private allelic richness ( $P_A$ ).

Population	$N_{SSR}$	$N_A$	$A_R$	$H_O/H_E$	$F_{IS}$	$P_A$
YMJ	27	6.89	5.45	0.230/0.735***	0.70*	0.14
YMZ	28	5.33	4.51	0.249/0.559***	0.57*	0.05
YJS	17	4.22	3.64	0.499/0.532	0.10	0.00
YYS	23	6.11	4.8	0.616/0.631	0.05	0.00
YSH	30	6.56	4.92	0.230/0.698***	0.69*	0.06
GTY	29	6.33	4.95	0.196/0.614***	0.69*	0.12
YPZ	15	5.89	5.43	0.274/0.707**	0.63*	0.03
YJY	12	2.22	2.15	0.111/0.276*	0.62*	0.08
GYZ	28	5.33	4.14	0.182/0.551	0.68*	0.02
GLZ	26	5.00	4.20	0.245/0.608**	0.61*	0.01
GDL	23	5.00	4.10	0.250/0.506**	0.51*	0.04
GHC	29	5.56	4.60	0.168/0.627**	0.74*	0.13
YLX	30	5.44	4.32	0.163/0.618**	0.74*	0.00
GLL	26	7.33	5.73	0.356/0.720***	0.52*	0.00
YLP	28	8.67	6.55	0.361/0.734**	0.52*	0.08
YKM	26	2.67	2.28	0.088/0.308	0.72*	0.06
GND	18	5.22	4.33	0.275/0.554*	0.53*	0.02
YQU	17	4.56	3.96	0.210/0.605**	0.67*	0.32
YWD	28	4.22	3.23	0.222/0.381	0.43*	0.04
CSJ	28	6.00	4.57	0.259/0.617***	0.59*	0.00
QGL	28	9.22	6.84	0.408/0.753**	0.47*	0.11
QSD	29	7.78	5.91	0.400/0.727	0.46*	0.19
YXW	11	3.56	3.35	0.242/0.359*	0.37*	0.01
SPZ	27	3.67	3.13	0.137/0.417**	0.68*	0.00
QTL	14	5.33	4.83	0.296/0.630*	0.56*	0.13
YHZ	20	4.11	3.37	0.285/0.508	0.46*	0.00
YQJ	26	3.89	3.16	0.262/0.436	0.42*	0.11
YLD	13	3.89	3.75	0.308/0.486	0.40*	0.05
QKY	13	4.22	3.98	0.181/0.476*	0.65*	0.01
SYY	31	4.56	3.65	0.345/0.492	0.31*	0.01
SXC	25	5.78	4.39	0.271/0.475*	0.45*	0.03
SGL	17	4.44	3.72	0.183/0.409	0.57*	0.01
SMH	24	5.78	4.36	0.239/0.510	0.55*	0.11
SJA	27	5.33	3.58	0.162/0.442	0.65*	0.11
SNX	16	2.67	2.56	0.028/0.312*	0.92*	0.09
SHS	26	5.56	4.36	0.125/0.494**	0.75*	0.07
SLS	24	4.22	3.29	0.153/0.423***	0.65*	0.00
SYJ	30	5.44	4.03	0.160/0.500*	0.69*	0.07
SFY	28	5.67	4.41	0.570/0.587	0.05	0.00
SSP	26	4.22	3.52	0.095/0.475**	0.81*	0.00

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SSN	27	4.33	3.34	0.076/0.445**	0.84*	0.03
SNC	25	4.33	3.75	0.064/0.474**	0.87*	0.06
SGJ	29	5.11	3.94	0.161/0.501	0.69*	0.10
SMY	28	4.00	3.42	0.136/0.426	0.69*	0.01
SBZ	29	5.11	3.96	0.047/0.512***	0.91*	0.22

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Fig. S1 Five demographic scenarios of the first run performed in DIYABC. All individuals in YGP, HDM and SCB were pooled together respectively, and were regarded as one population for each region. Each population was highlighted by different colors.  $t_1$  and  $t_2$  represented the divergent time of each population. The values in square brackets were posterior probability and the 95% credibility interval of each scenario calculated in DIYABC.

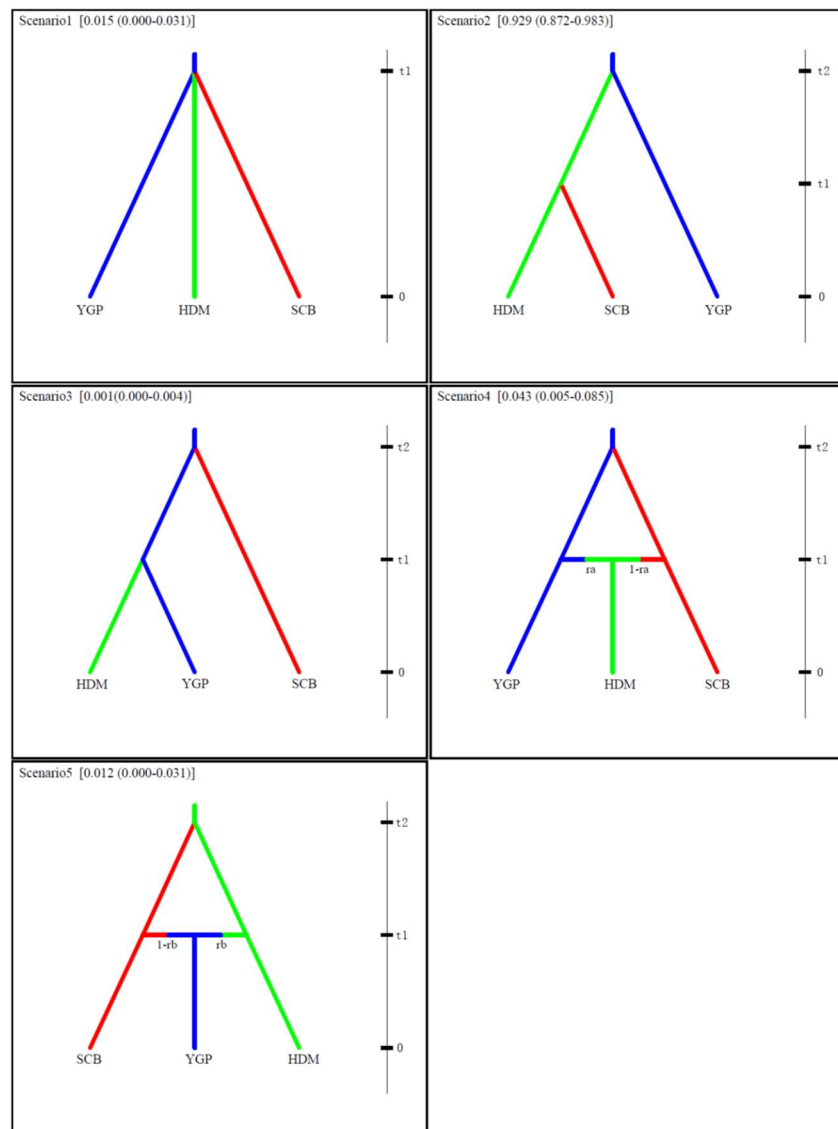


Fig. S2 Two scenarios of the second run performed in DIYABC. All the parameters were the same as Fig S1.

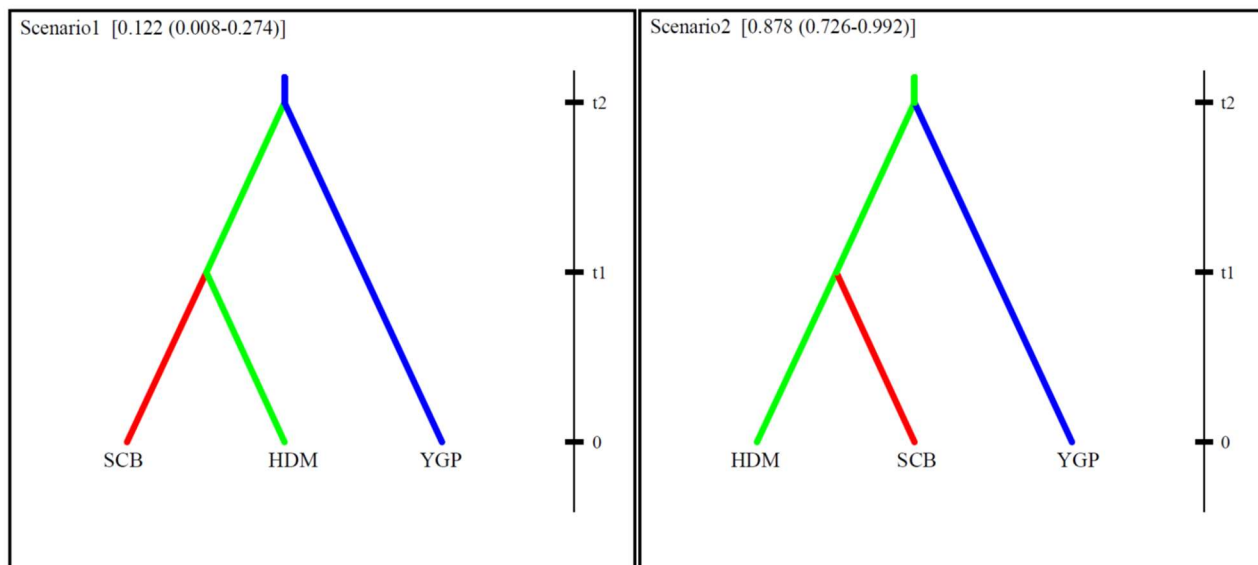




Fig. S3 The phylogenetic trees and network (left, Max Parsimony tree; middle, Bayesian tree; right, network) ITS2 genes of the *Ceratosolen* pollinating fig wasps reared from *Ficus tikoua* populations in Southwest China. In the network, each haplotype was indicated by an ellipse with the frequencies showed by the ellipse sizes. The haplotypes whose frequencies were no less than five were indicated in the network. The color indicated corresponded lineage compositions between phylogenetic trees and network.

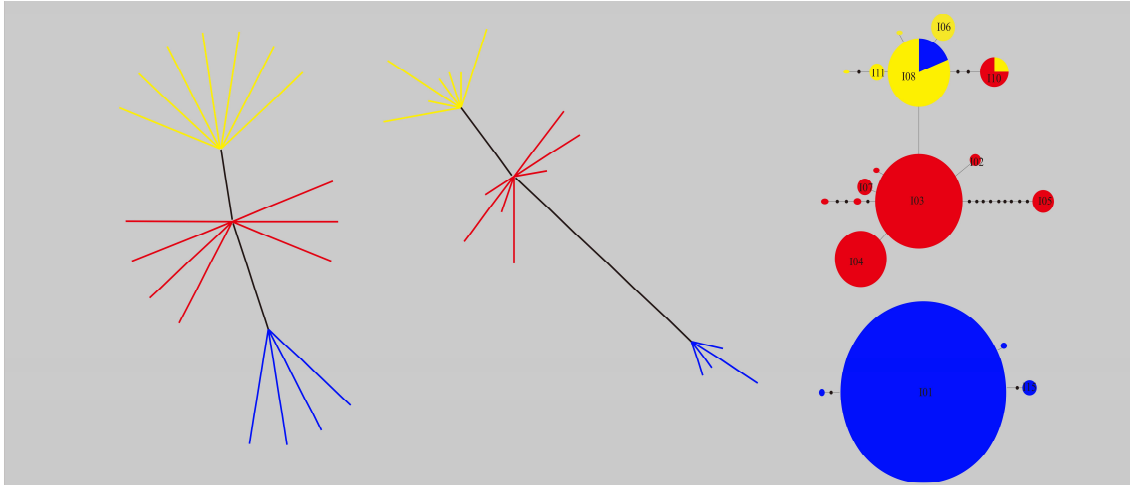


Fig. S4 The mean posterior probability of the data for  $K$ ; (b) the magnitude of delta  $K$  ( $\Delta K$ ) simulated by STRUCTURE.

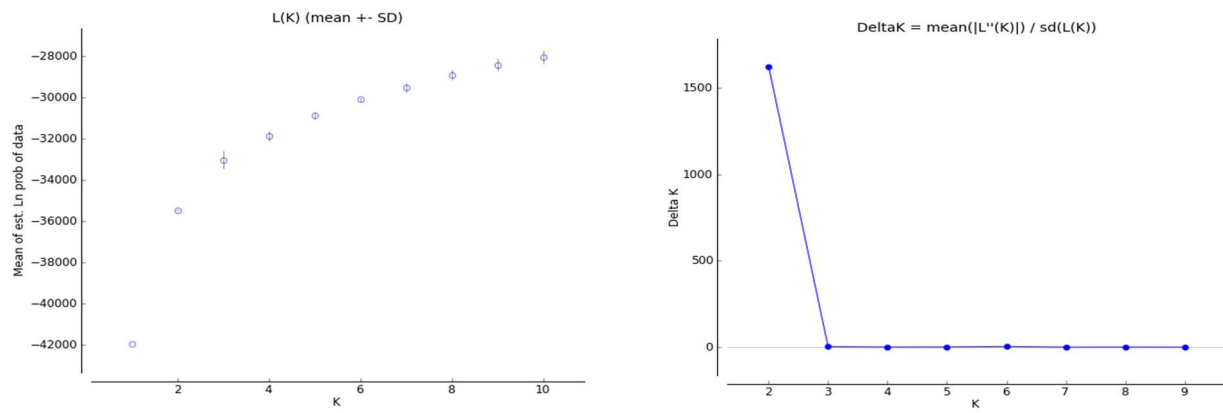


Fig. S5 The geographic distribution and frequencies of two SSR groups of the *Ceratosolen* pollinating fig wasp of *Ficus tikoua* in Southwest China. Red and blue indicated the frequencies of individuals assigned into each of the two SSR groups in the populations, while the yellow showed the frequencies of individuals could not be assigned into either group absolutely. The geneflow barriers of pollinator were highlighted by red lines.

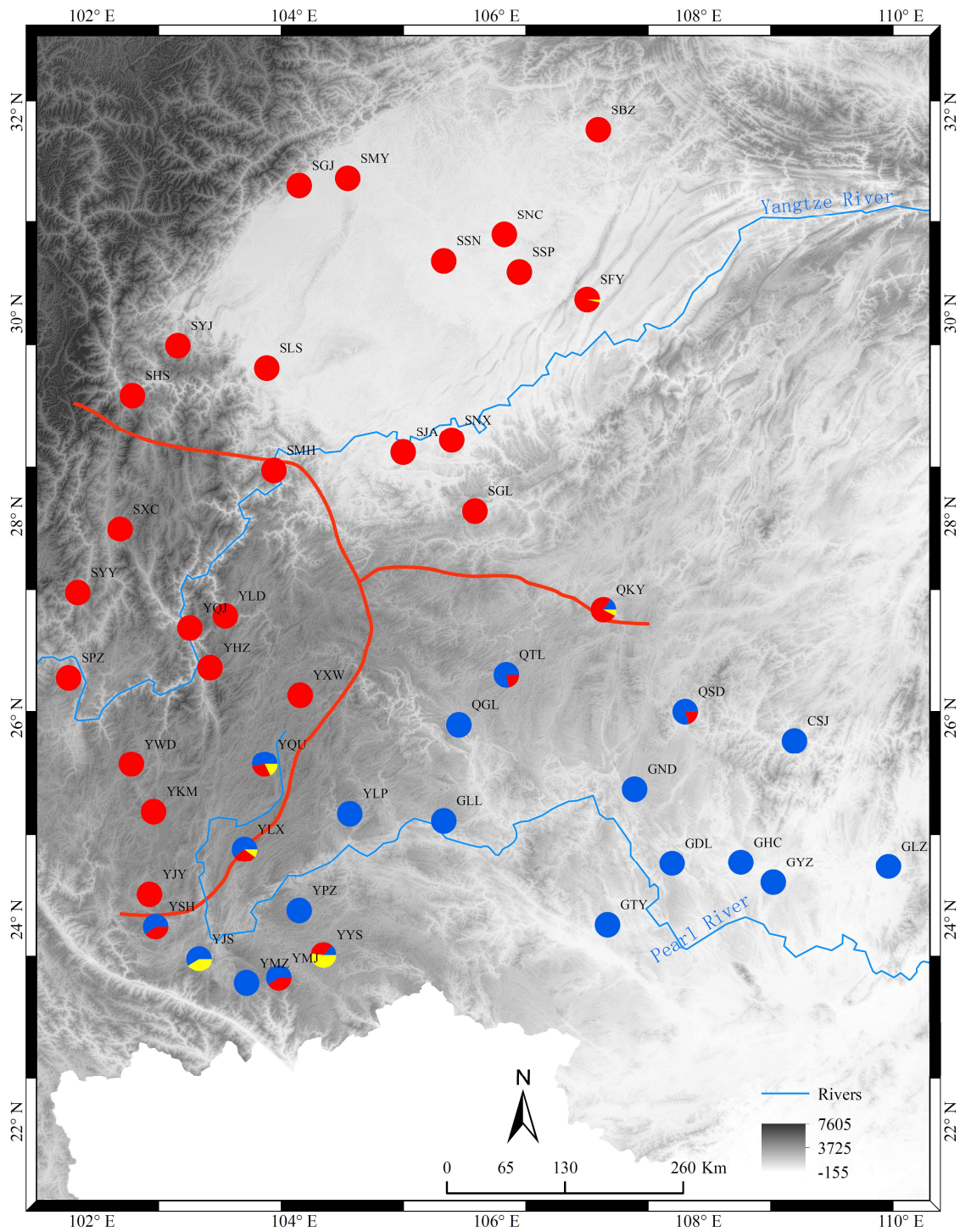


Fig. S6 The relationships of genetic distances and geographic distances between population pairs based on SSR genotypes. All populations were pooled together.

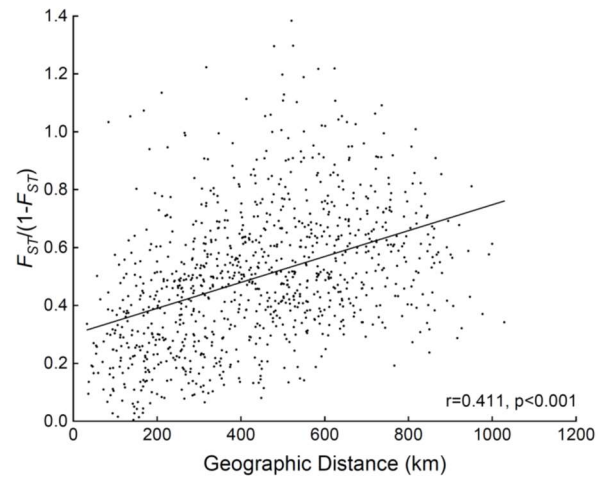


Fig. S7 The relationships of genetic distances and geographic distances between population pairs in each region based on SSR genotypes. Red, yellow and blue color indicate the populations in SBC, HDM, YGP regions were involved respectively.

