

Table S1. Results of neutral test in population division of *Prunus discoidea*

Statistics	BMQ	BYS	DMS	ZJS	HS	LS	YTS	SMS	ZJG	LKY	THC	LCS	YZH
chloroplast DNA fragments													
Tajima'sD	2.53769	0.00000	1.70339	2.13208	2.35898	0.00000	1.50518	1.30634	-0.77806	2.13321	0.17954	2.15610	1.63481
P-value	0.99600	1.00000	0.97100	0.98100	0.99300	1.00000	0.96400	0.92000	0.24200	0.97200	0.61200	0.99300	0.94000
Fu'sFs	6.64627	0.00000	1.19443	-0.79797	2.96257	0.00000	1.40457	1.67306	1.75666	3.67982	1.212661	4.54620	-1.25618
P-value	0.99300	N.A.	0.76800	0.39600	0.92200	N.A.	0.69400	0.85000	0.76600	0.96900	0.77300	0.97400	0.284000
nuclear DNA fragments													
Tajima'sD	-0.59000	1.26352	1.29541	0.00000	1.96274	0.00000	0.00000	0.83775	2.30624	0.00000	0.00000	2.76247	2.54383
P-value	0.28300	0.87000	0.90600	1.00000	0.97700	1.00000	1.00000	0.83500	0.98900	1.00000	1.00000	0.99500	0.99200
Fu'sFs	1.01952	2.83999	6.57871	0.00000	9.40807	0.00000	0.00000	2.17676	5.82751	0.00000	0.00000	9.95939	5.30106
P-value	0.54700	0.89000	0.99500	N.A.	1.00000	N.A.	N.A.	0.81000	0.99600	N.A.	N.A.	1.00000	0.99200

Table S2. Neutral test of geographical grouping of *Prunus discoidea*

Statistics	Central	Eastern	All
	chloroplast DNA fragments		
Tajima'sD	1.84703	0.49778	0.92153
P-value	0.94800	0.67800	0.77500
Fu'sFs	-1.43840	-0.06667	-3.40693
P-value	6.34100	6.53700	0.14700
	nuclear DNA fragments		
Tajima'sD	1.44001	2.71428	1.25492
P-value	0.90400	0.99600	0.82700
Fu'sFs	6.16471	12.46840	7.46592
P-value	0.97400	1.00000	0.98900

Table S3. Mismatch distribution analysis (AMOVA) of *Prunus discoidea*

Statistics	BMQ	BYS	DMS	ZJS	HS	LS	YTS	SMS	ZJG	LKY	THC	LCS	YZH
chloroplast DNA fragments													
Demographic expansion													
SSD	0.49598	0.00000	0.021508	0.01118	0.05453	0.00000	0.02746	0.02339	0.06222	0.18083	0.43848	0.25251	0.01106
P-value	0.00000	0.00000	0.38000	0.10000	0.18000	0.00000	0.09000	0.47000	0.04000	0.08000	0.00000	0.06000	0.12000
Raggedness index	0.74800	0.00000	0.10260	0.06556	0.19370	0.00000	0.27549	0.11111	0.71293	0.53760	0.17324	0.74249	0.05294
P-value	0.91000	0.00000	0.64000	0.14000	0.23000	0.00000	0.04000	0.54000	0.59000	0.01000	1.00000	0.02000	0.43000
Spatial expansion													
SSD	0.17015	0.00000	0.01074	0.01092	0.03506	0.00000	0.02746	0.02366	0.02797	0.13371	0.02402	0.15480	0.00901
P-value	0.02000	0.00000	0.61000	0.07000	0.26000	0.00000	0.02000	0.31000	0.24000	0.01000	0.44000	0.01000	0.33000
Raggedness index	0.74800	0.00000	0.10260	0.06556	0.19370	0.00000	0.27549	0.11111	0.71293	0.53760	0.17324	0.74249	0.05294
P-value	0.19000	0.00000	0.75000	0.19000	0.52000	0.00000	0.07000	0.68000	0.70000	0.14000	0.57000	0.22000	0.58000
nuclear DNA fragments													
Demographic expansion													
SSD	0.04066	0.32171	0.18613	0.00000	0.22771	0.00000	0.00000	0.32000	0.14333	0.00000	0.00000	0.48473	0.06431
P-value	0.03000	0.00000	0.06000	0.00000	0.02000	0.00000	0.00000	0.00000	0.06000	0.00000	0.00000	0.00000	0.13000
Raggedness index	0.74149	0.68043	0.52018	0.00000	0.68388	0.00000	0.00000	0.68000	0.42266	0.00000	0.00000	0.74249	0.08260
P-value	0.68000	1.00000	0.12000	0.00000	0.38000	0.00000	0.00000	0.89000	0.00000	0.00000	0.00000	0.92000	0.39000
Spatial expansion													
SSD	0.01685	0.08780	0.12645	0.00000	0.12932	0.00000	0.00000	0.08734	0.10327	0.00000	0.00000	0.18727	0.04102
P-value	0.24000	0.09000	0.06000	0.00000	0.13000	0.00000	0.00000	0.09000	0.10000	0.00000	0.00000	0.01000	0.18000
Raggedness index	0.74149	0.068043	0.52018	0.00000	0.68388	0.00000	0.00000	0.68000	0.42266	0.00000	0.00000	0.74249	0.08260
P-value	0.57000	0.33000	0.46000	0.00000	0.48000	0.00000	0.00000	0.48000	0.34000	0.00000	0.00000	0.27000	0.85000

Table S4. Mismatch distribution analysis (AMOVA) of *Prunus discoidea*

Statistics	Central	Eastern	All
	chloroplast DNA fragments		
Demographic expansion			
SSD	0.03241	0.00494	0.01938
P-value	0.05000	0.77000	0.18000
Raggedness index	0.08738	0.28830	0.05561
P-value	0.09000	0.93000	0.33000
Spatial expansion			
SSD	0.02578	0.00603	0.01489
P-value	0.07000	0.66000	0.38000
Raggedness index	0.08738	0.02883	0.05661
P-value	0.2000	0.92000	0.53000
	nuclear DNA fragments		
Demographic expansion			
SSD	0.07947	0.45001	0.32821
P-value	0.08000	0.00000	0.00000
Raggedness index	0.45344	0.56042	0.74249
P-value	0.56000	0.94000	0.92000
Spatial expansion			
SSD	0.06239	0.12664	0.18727
P-value	0.25000	0.06000	0.01000
Raggedness index	0.44618	0.56042	0.74249
P-value	0.61000	0.43000	0.27000

Table S5. Statistical parameters of demographic and spatial expansion in *P. discoidea*

Statistics	All_Seqs	Mean	Standard Deviation
Demographic expansion			
Tau	2.94727	2.94727	0
Tau qt 2.5%	0.01563	0.01563	0
Tau qt 5%	0.88867	0.88867	0
Tau qt 95%	5.08594	5.08594	0
Tau qt 97.5%	5.70508	5.70508	0
Theta0	0.00176	0.00176	0
Theta0 qt 2.5%	0	0	0
Theta0 qt 5%	0	0	0
Theta0 qt 95%	0.40781	0.40781	0
Theta0 qt 97.5%	1.31484	1.31484	0
Theta1	5.33203	5.33203	0
Theta1 qt 2.5%	2.77832	2.77832	0
Theta1 qt 5%	3.76709	3.76709	0
Theta1 qt 95%	99999	99999	0
Theta1 qt 97.5%	99999	99999	0
SSD	0.01938	0.01938	0
Model (SSD) p-value	0.13	0.13	0
Raggedness index	0.05661	0.05661	0
Raggedness p-value	0.26	0.26	0
Spatial expansion			
Tau	2.59588	2.59588	0
Tau qt 2.5%	0.49936	0.49936	0
Tau qt 5%	0.74633	0.74633	0

Tau qt 95%	3.72741	3.72741	0
Tau qt 97.5%	4.36392	4.36392	0
Theta	0.00443	0.00443	0
Theta qt 2.5%	0.00072	0.00072	0
Theta qt 5%	0.00072	0.00072	0
Theta qt 95%	1.00528	1.00528	0
Theta qt 97.5%	1.27914	1.27914	0
M	5.92814	5.92814	0
M qt 2.5%	0.30245	0.30245	0
M qt 5%	0.65089	0.65089	0
M qt 95%	99999	99999	0
M qt 97.5%	99999	99999	0
SSD	0.01489	0.01489	0
Model (SSD) p-value	0.4	0.4	0
Raggedness index	0.05661	0.05661	0
Raggedness p-value	0.64	0.64	0

Note: Tau represents the expansion time, Theta represents the effective population size, and M represents the migration rate.

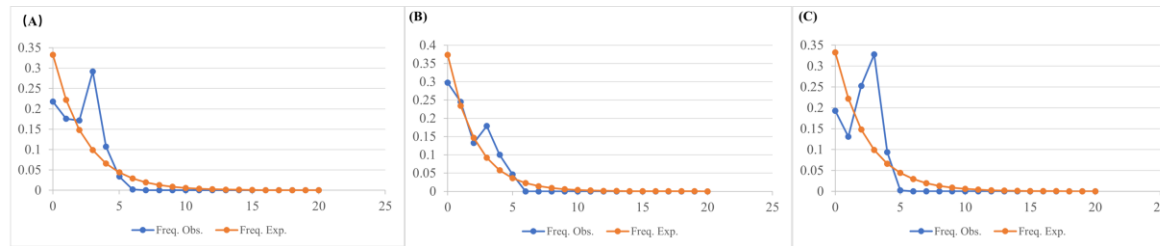


Figure S1. Mismatch analysis of different geographical combinations of *P. discoidea* groups based on the cpDNA (*rpoB*, *rps16*, *trnD-E*) sequences.

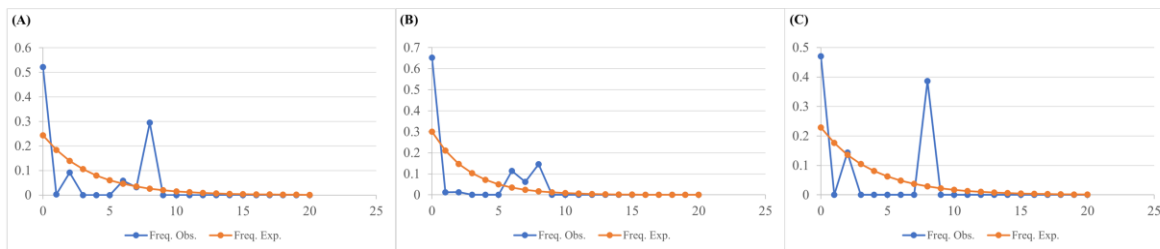


Figure S2. Mismatch analysis of different geographical combinations of *P. discoidea* groups based on the nrDNA (ITS) sequences.