

Supplementary Materials

Table S1. Geographical distribution of 22 *L. chinense* geographic populations and 2 *L. tulipifera* geographic populations.

Species	Population Code	No.	Location	Longitude	Latitude (N)	Altitude (m a.s.l.)	N
<i>L. chinense</i> (Hemsl.) Sarg.	YML	1	Mengla, Yunnan	101°06'E	21°40'	700	13
	YJP	2	Jinping, Yunnan	103°13'E	22°47'	1260	48
	SXY	3	Xuyong, Sichuan	105°50'E	28°20'	800	40
	SHZ	4	Hanzhong, Shaanxi	107°02'E	33°05'	1350	9
	GLP	5	Liping, Guizhou	108°06'E	26°50'	1100	48
	GMN	6	Monan, Guizhou	109°05'E	26°80'	1050	42
	CYY	7	Youyang, Chongqing	108°80'E	28°82'	890	40
	HLC	8	Lichuan, Hubei	108°56'E	30°18'	1200	40
	HHF	9	Hefeng, Hubei	110°02'E	29°54'	1147	48
	HSN	10	Suining, Hunan	110°20'E	26°33'	1500	33
	HCB	11	Chengbu, Hunan	110°19'E	26°22'	1760	40
	HSZ	12	Sangzhi, Hunan	110°20'E	29°15'	1200	20
	HLY	13	Liuyang, Hunan	113°90'E	28°05'	1100	40
	JLS	14	Lushan, Jiangxi	115°59'E	29°41'	1360	48
	JWY	15	Wuyishan, Jiangxi	117°80'E	27°92'	1000	40
	FWY	16	Wuyishan, Fujian	117°37'E	27°27'	1700	40
	FZR	17	Zherong, Fujian	119°54'E	27°15'	480	40
	AHS	18	Huangshan, Anhui	118°01'E	30°01'	1400	31

Species	Population Code	No.	Location	Longitude	Latitude (N)	Altitude (m a.s.l.)	N
<i>L. tulipifera</i> L.	ADB	19	Dabieshan, Anhui	118°20'E	31°13'	1450	20
	ZAJ	20	Anji, Zhejiang	119°41'E	30°38'	1000	40
	ZLS	21	Lishui, Zhejiang	119°55'E	28°27'	1250	40
	ZSY	22	Songyang, Zhejiang	119°29'E	28°27'	1502	48
	LA	23	Louisiana, USA	90°03'W	29°58'	30	31
	MO	24	Missouri, USA	92°23'W	38°87'	240	32
	Total						871

N: Number of samples.

Table S2. Repeat motif, primer sequence, fragment size, Tm and data sources information for 20 EST-SSR loci.

Locus Code	Repeat Motif	Primer Sequence (5'~3')	Fragment Size (bp)	Tm (°C)	Accession
LCEST-41	(TC)11	GTTGTTGGGTTCATGTTTATGG CAGGAGGAAAATCACAGTATCG	237	55	DT583320.1
LCEST-53	(AG)11	ATGATGAGAACACAAGCAGC CACCAAACCAAAGCACTATC	182	56	CV004303.1
LCEST-57	(CTT)8	ATGAAAGAAATGCCCATCC CACCATCACCACCAACACA	226	56	CK750786.1
LCEST-60	(ACA)9	ATGGGGTGTCTAGCAGTGGG TTACGAGATGGGTTCGGAGG	120	58	DT596797.1
LCEST-61	(CT)17	TCTCTCCTTTACAAGTTACTCCGC TCCCATCATTATATCTTCGTCTGA	284	56	CK764846.1
LCEST-62	(TC)10	TCTCTCCTGCGACTCTCCTTA GCCTTCTCGTGCCACTACTAC	137	55	CK754801.1
LCEST-68	(AG)18	GCCCACATCACGAGTCAA TCCAGCAGGTCCCACAGT	239	56	CK765800.1
LCEST-75	(GCT)8	GGCGTCTGGGTCTCTATG GCAACAAGCAGCAACAAT	140	55	CV005000.1
LCEST-80	(AG)34	GGTCCGATTCTCCGTTTC CTGCTTCTGCTGCCATTT	150	55	CK754640.1
LCEST-97	(AAAT)4	ACTGATGCCGAACGATGAT TTGAAGGGAAGAGGGTGAA	206	56	CK750034.1
LCEST-103	(CAG)7	CCCCTGTTTCTTCCCTAA	276	56	CO995544.1

Locus Code	Repeat Motif	Primer Sequence (5'~3')	Fragment Size (bp)	Tm (°C)	Accession
LCEST-104	(AG)14	CGACCCAGATCGTCTTGT CGCCACCCTTTTCTCAAT CCCAAACCTTACCGTCAT	177	54	CK751213.1
LCEST-107	(CCGAAC)5	TCTCTCTCCAAAATCAAGACCCC CATACCAATCACAATCCCAATCG	239	56	CK760956.1
LCEST-119	(CT)23	TCAAAATCTATGGCAGCAGCG GAATGGACGAGAGGAAGCACA	280	56	DT594602.1
LCEST-131	(TC)21	CCATTTTACCAGATTATCCACA ATGAAACAAAGCAATTACACGA	144	55	CK753335.1
LCEST-169	(GAT)8	AATCCCCATTCTACCCTCC TGACTCCTTTGCCCTTGTC	235	56	CK751226.1
LCEST-181	(CA)11	GACGAGTGCTGATGTTGCT AAGTGGTGTTTTGGGTGTG	207	56	DT581093.1
LCEST-184	(TC)19	TGTTTTGTGAGCCTCTGTTTATG AAGATGGGAAGGATGTTGGTTAG	256	56	CK754944.1
LCEST-186	(TC)15	TAGGCTCTATTTACCCCTTGTATT GGATTGACCCACTTGATTATTTAT	148	55	DT595333.1
LCEST-195	(CTTT)6	TGGGGATAAACTACTGGCG ATGGGTGAAAAACGGGAA	160	55	CK763007.1

Table S3. Polymorphism information for 20 microsatellite loci amplified in *L. tulipifera*.

Locus	Na	Ne	He	PIC	I	Fst	Nm
LCEST-41	3	2.029	0.511	0.386	0.733	0.938	0.017
LCEST-53	6	3.040	0.676	0.621	1.315	0.224	0.867
LCEST-57	4	3.226	0.696	0.631	1.248	0.047	5.032
LCEST-60	4	3.650	0.732	0.675	1.335	0.055	4.262
LCEST-61	4	2.095	0.527	0.484	0.997	0.063	3.695
LCEST-62	5	3.279	0.701	0.656	1.382	0.035	6.882
LCEST-68	4	2.997	0.672	0.594	1.127	0.012	21.527
LCEST-75	3	1.617	0.385	0.325	0.636	0.296	0.596
LCEST-80	5	4.350	0.776	0.735	1.539	0.056	4.241
LCEST-97	2	1.171	0.147	0.136	0.277	0.004	62.144
LCEST-103	3	1.844	0.461	0.378	0.735	0.015	16.840
LCEST-104	4	2.536	0.611	0.559	1.131	0.071	3.290
LCEST-107	4	2.224	0.555	0.512	1.049	0.320	0.532
LCEST-119	5	3.852	0.746	0.693	1.408	0.070	3.327
LCEST-131	4	3.351	0.707	0.642	1.262	0.188	1.082
LCEST-169	3	1.154	0.135	0.127	0.282	0.070	3.322
LCEST-181	2	1.446	0.311	0.261	0.487	0.044	5.456
LCEST-184	4	3.397	0.711	0.649	1.280	0.065	3.599
LCEST-186	4	1.390	0.283	0.265	0.573	0.003	94.327
LCEST-195	3	2.124	0.533	0.419	0.811	0.886	0.032
Mean	3.8	2.538	0.544	0.487	0.980	0.173	1.194

Table S4. Analysis of molecular variance (AMOVA) in *L. chinense*.

Source of variance	Variance component	Percentage of total	P-value
Among populations	6.649	38%	0.001
Within populations	10.643	62%	0.001
Total	17.292	100%	

Table S5. Pairwise genetic distances between three regions of *Liriodendron*.

Group	CW	CE	NA
CW	0		
CE	0.076	0	
NA	0.427	0.438	0

CW: Western China; CE: Eastern China; NA: North America.

Figure Captions

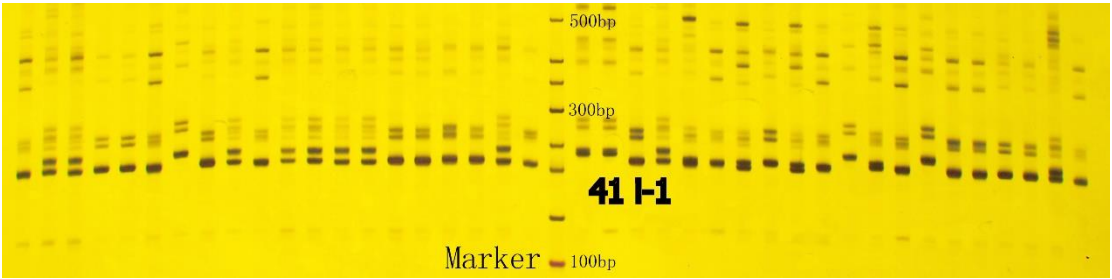


Figure S1. LCEST-41 SSR amplification products of Chengbu, Hunan (HCB) population.

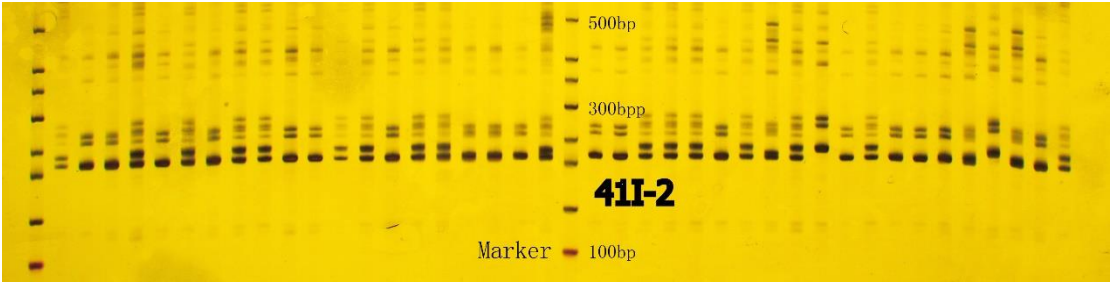


Figure S2. LCEST-41 SSR amplification products of Lichuan, Hubei (HLC) population.

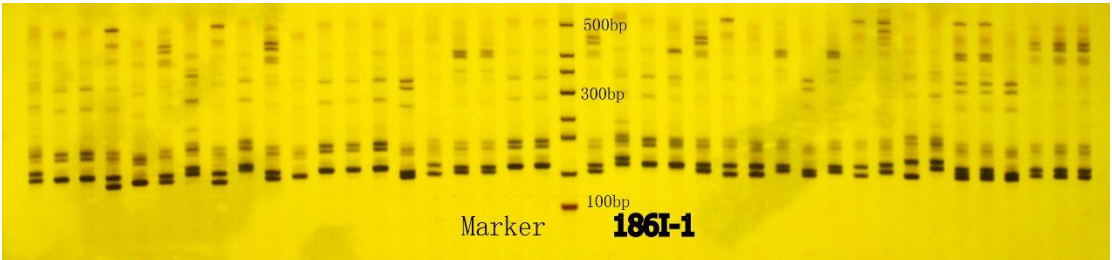


Figure S3. LCEST-186 SSR amplification products of Chengbu, Hunan (HCB) population.

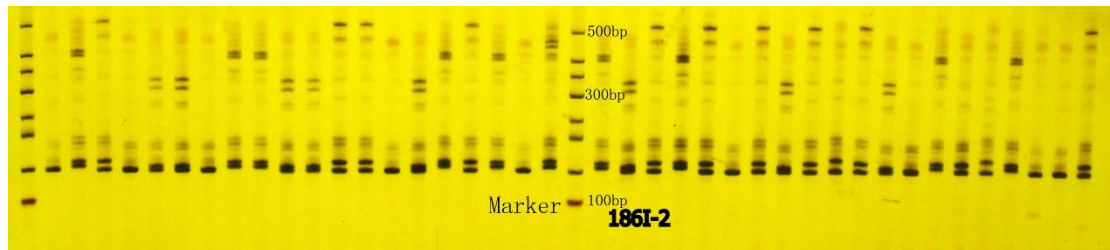


Figure S4. LCEST-186 SSR amplification products of Lichuan, Hubei (HLC) population.

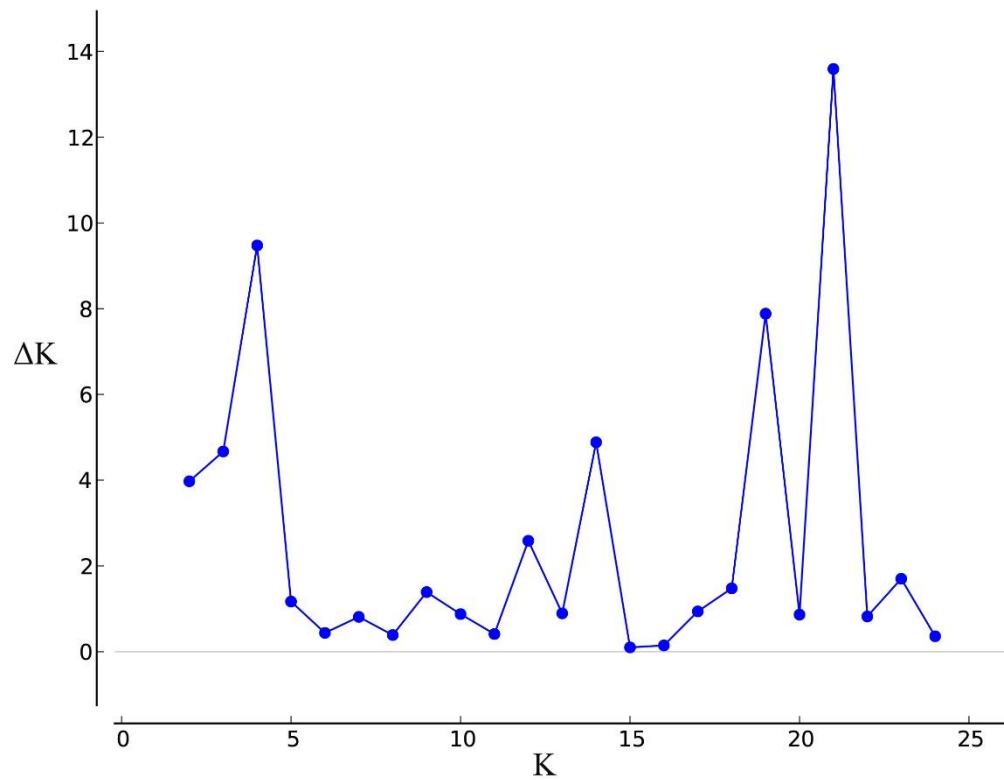


Figure S5. Relationships between the number of clusters (K) and the corresponding ΔK statistics calculated according to ΔK (Evanno et al. 2005) based on STRUCTURE analysis.

$K = 21$

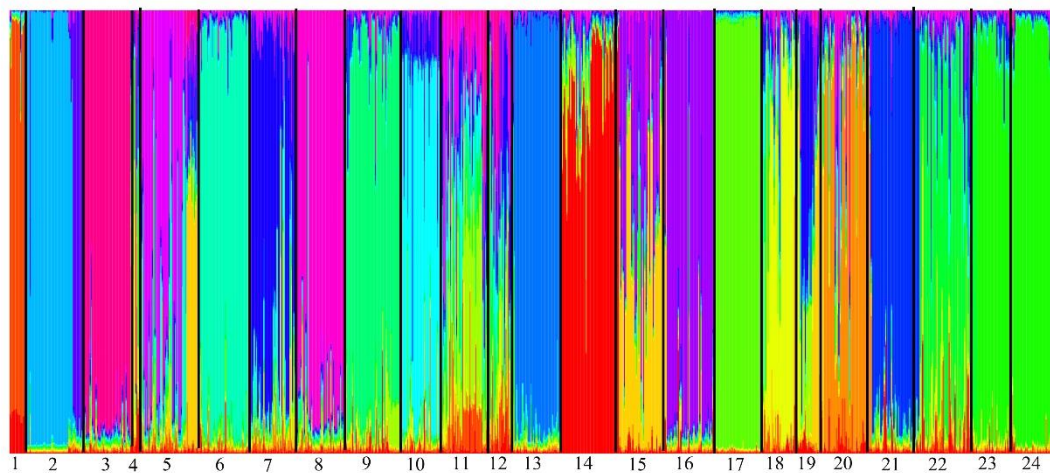


Figure S6. Population genetic structure based on the Bayesian clustering model among 871 samples at $K = 21$. Numbers correspond to the population numbers in Table S1.

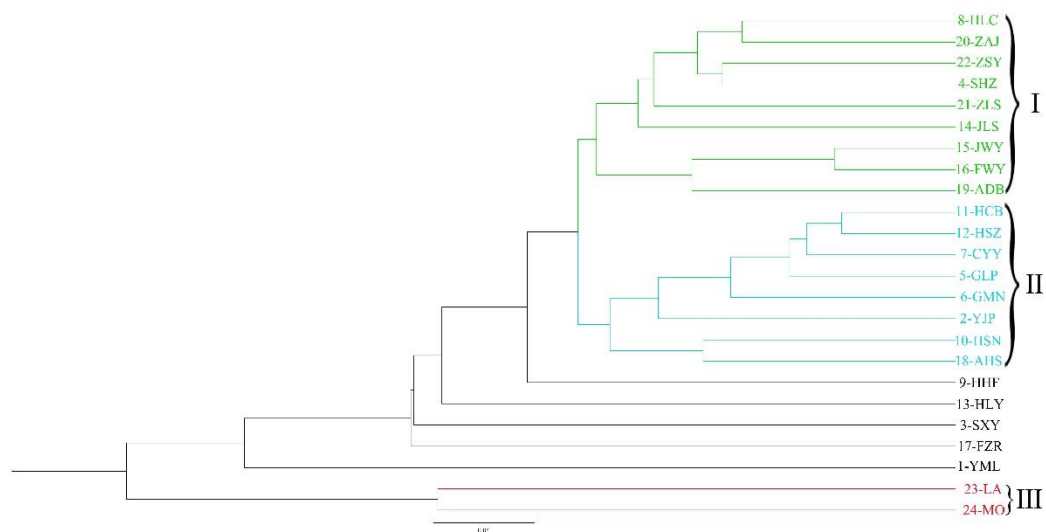


Figure S7. UPGMA tree based on Nei's genetic distances. Numbers correspond to the population numbers in Table S1.

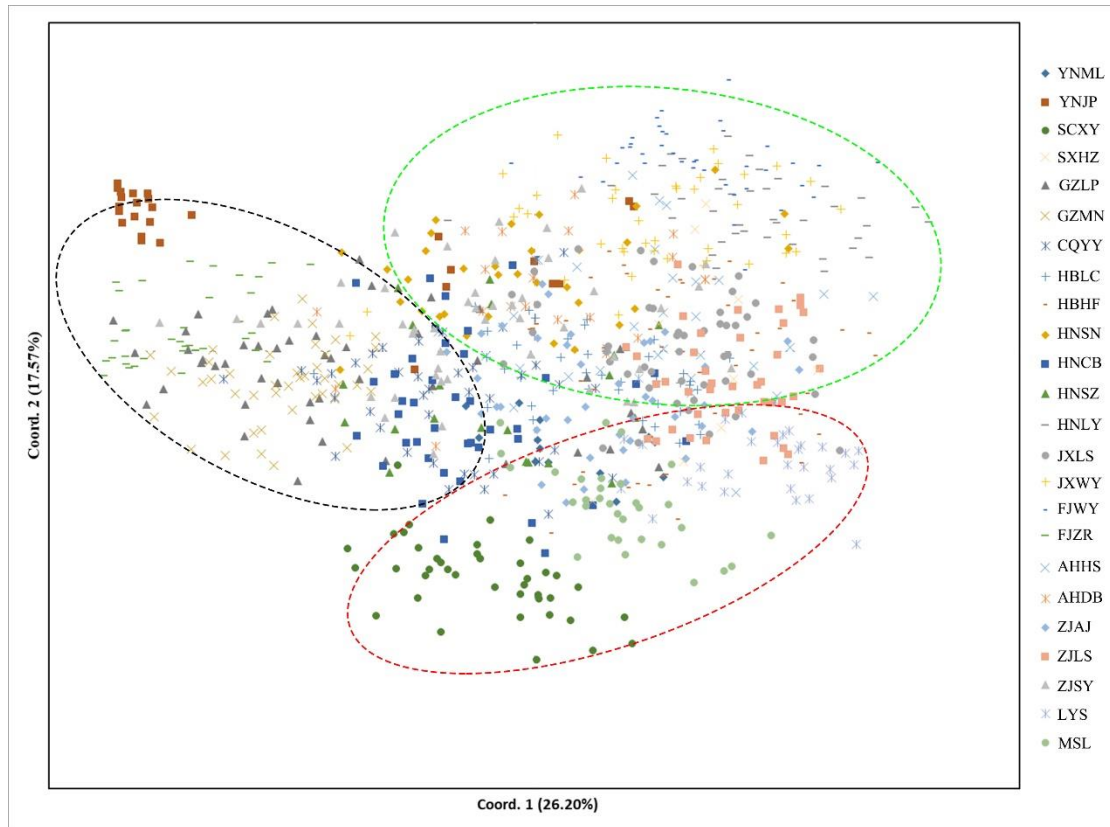


Figure S8. Score plot generated using PCoA.