

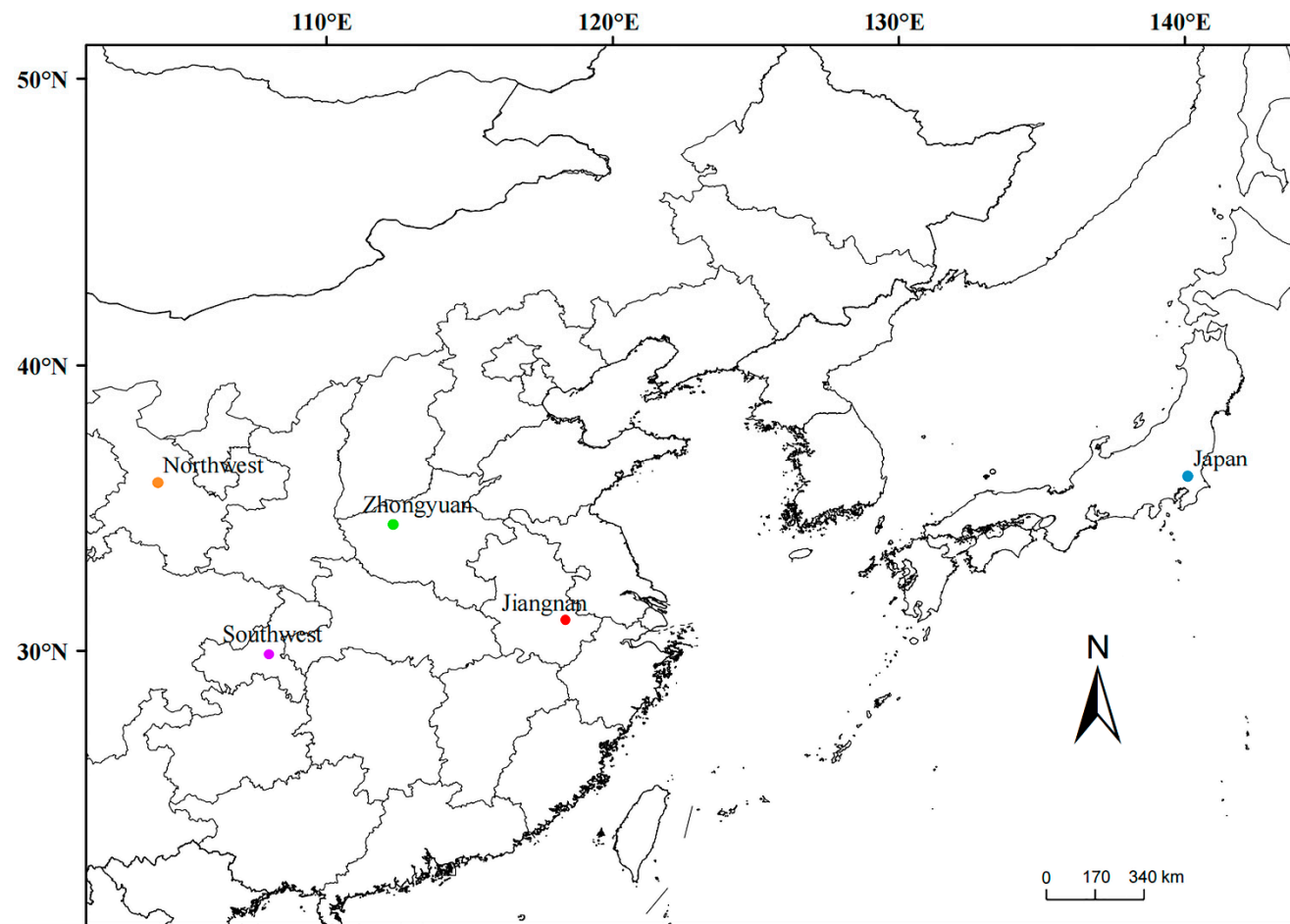


Figure S1. The original geographical sources of the tree peony population samples in this study.

Table S1. Ninety-five EST-SSR markers information on the genetic linkage map in tree peony.

Primer ID	Linkage Group	Genetic Distance(cM)	Primer Sequence (5'-3')	Primer Sequence (3'-5')	Annealing temperature (°C)	Expected size (bp)	Repeat Motif	Segregation type	F1 genotype
PS001	LG1	0	AAACACCCAAGCAAATCG	AATGAAACGCCGTCCTCT	52	475	(CT) ₆	<hkxhk>	(hh,hk,kk)
PS371	LG1	18.7	CATTGAGCCACCCATAGA	GCAACAATCCTGGTAGTGA	58	219	(CAC) ₅	<hkxhk>	(hh,hk,kk)
PS095	LG1	34	TCCCAAGACCTCAAACAAC	CCATCAATACGAGCCAAC	55	394	(CCA) ₅	<lmxll>	(lm,ll)
PS134	LG1	39.7	CATCAACTTCGGCTAACA	CAAACTACCCGATCCTAC	55	387	(CAC) ₅	<hkxhk>	(hh,hk,kk)
PS364	LG1	48.7	GGAGCAAACCTAAGCAC	ATAGCGAGGACCGTGAAT	53.5	205	(CTT) ₅	<hkxhk>	(hh,hk,kk)
PS119	LG1	53.2	GCAAAGACAACAGCCTCG	CTCACCATCCAATCCCAC	57	289	(CAG) ₆	<lmxll>	(lm,ll)
PS202	LG1	63.2	GTGGTGGTCCATCTTGAAG	TTGCTTGAGCGAGTGTTATC	57	163	(TC) ₇	<hkxhk>	(hh,hk,kk)
PS053	LG1	72.3	ATTGCCAGATTTGTTCAAG	CACCACTATTATTCCTTG	50.5	407	(AG) ₇	<lmxll>	(lm,ll)
PS111	LG1	80.5	GCAGATCATGGCGACAAAAC	TGCTGAGGCGAAAGAACAG	57.5	372	(CAA) ₅	<nnxnp>	(nn,np)
PS240	LG1	83.5	AGTAGAATACGAAGAGGCATC	CAAGACCGTGAACAAATATC	55	251	(GAA) ₅	<hkxhk>	(hh,hk,kk)
PS147	LG1	84.9	TCTGGCAAATACCGTGAA	AGCGGAGAAGGATAAATAAG	53	480	(TTC) ₅	<hkxhk>	(hh,hk,kk)
49A	LG1	101.8	TCTGGGTGATAGGTGGAGCTGGTGC	GGAAGACGCCACAATGAAATCACA	55	314	(TGC) ₅	<hkxhk>	(hh,hk,kk)
PS308	LG1	104.8	ACTACTCTATTGCGAAACC	GTCTTATGGCGGCTATGT	53	189	(TC) ₇	<lmxll>	(lm,ll)
PS005	LG1	120.9	GAGACCACCGAGTCACAG	TCAGAGCATGTCCGAAAC	57.5	480	(GA) ₉	<nnxnp>	(nn,np)
PS228	LG2	0	TGAGGCGTGGTAGAGGTT	TCAAGGAGGTGAGGGAGT	57.5	121	(TCT) ₅	<hkxhk>	(hh,hk,kk)
21A	LG2	3.2	CAACTTTGCCAACTTCGTCCACTTC	CCCGTCATGAACAAGAAGAAGGAAA	55	-	-	<hkxhk>	(hh,hk,kk)
PS186	LG2	14	GAGGTGACGGATGGAGTT	CCTAAAGAAGGTTGTGGC	56	356	(GT) ₈	<hkxhk>	(hh,hk,kk)
L72	LG2	15.7	CGCCAAATAAAAGTCTAAACCC	GGGTTAATTTGAGGAGATGGAG	54	-	-	<hkxhk>	(hh,hk,kk)
53	LG2	18.1	ACTGGAAGCAGACCACCTCG	GCATGTAAGAATGCAACAAAATGTA	57	213	(CT) ₁₃	<hkxhk>	(hh,hk,kk)
PSESP2	LG2	27.2	GACGGAGAGAAAGAGAGCATA	GACAAAGACTGACACAGCGAT	54	-	-	<hkxhk>	(hh,hk,kk)
P05	LG2	48.1	TCGCCAACCTGTCGTGGAGAT	TTGAATAGAGCGGAATGGAAAA	54	123-437	(AG) ₉	<hkxhk>	(hh,hk,kk)
PSESP7	LG2	51	GGCTAATCTTGTGCTCAG	AACCCCTCTTCTCCTCA	55	-	-	<hkxhk>	(hh,hk,kk)

PS363	LG3	0	TTCAACCACATCTCCCTC	CTACCACCATAAGGTGAAGAG	52.5	457	(TTG) ₇	<nnxnp>	(nn,np)
PS094	LG3	2.5	GCTGCTTGCTTACTCATC	TTCTTGTA CTCTGCCTCC	55	363	(AGC) ₆	<nnxnp>	(nn,np)
51A	LG3	6.7	TATTGGACCCAGTCGATGATGTTG	GTGTGTGTGCGTGTGTGTAGTG	54.5	-	-	<nnxnp>	(nn,np)
PS074	LG3	41.1	TGCCTTGCTCCTCCTTGT	CGGTAGCCATGAATCCC	57	236	(CT) ₇	<nnxnp>	(nn,np)
PS099	LG3	46.7	GGGTCCAACAACCAAACT	GGTCAGCAAGAGCCAAAAG	56	330	(TGG) ₅	<nnxnp>	(nn,np)
PS052	LG3	55.7	CAAACTCTGCTAATTAAGAC	GATAGAAGGGAAAGGAAG	49	235	(CT) ₇	<nnxnp>	(nn,np)
PS135	LG4	0	ACTTCTTTCTCCCATTC	TTGTCGTCCTATCTTT	51.5	329	(AGC) ₅	<hkxhk>	(hh,hk,kk)
PS083	LG4	37.5	TCCAACCTCTCTACCAG	AAAGTGTCGCAAAATGTAAT	52	218	(GA) ₆	<hkxhk>	(hh,hk,kk)
PS118	LG4	53.5	CGTAGCCGTGCTTCTTTC	CCCATCAACCCATAATCC	54.5	199	(TGG) ₅	<hkxhk>	(hh,hk,kk)
PS129	LG4	80.8	CAATCAACGATGCCTTAG	TCTTTCGGGAAATCTGTC	52.5	225	(ACT) ₅	<hkxhk>	(hh,hk,kk)
SSR12	LG5	0	CGGAAGTTTTCTTTGAC	ATCCTTTTGTAACCTCTGATT	48	151	(AG) ₅	<hkxhk>	(hh,hk,kk)
PS068	LG5	17.9	CTTTGGCATTCTCATTCA	GGTGGTATTGGGCTTCTT	52.5	174	(TC) ₇	<hkxhk>	(hh,hk,kk)
L56	LG5	29.8	CAACCGAAACTATTACATTTT	GAGCAAATATATTCGGTGTCAGC	57	-	-	<hkxhk>	(hh,hk,kk)
PS180	LG1	29.951	CCCCGAAATGGAGGAGTC	CCTAGAACC GTTAGCAACT	60	188	(CT) ₆	<nn×np>	(nn,np)
PS276*	LG1	42.436	CTGTATCCTATCGGTTCTT	ACCTCTTCTTGCTGCTC	52.5	447	(CCGGTG) ₄	<lm×ll>	(lm,ll)
PS321	LG1	51.386	TGCTACCAGCTCCTCCAT	ACGGGCTCCTTACCACAT	53	249	(ATCA) ₅	<nn×np>	(nn,np)
PS337*	LG1	69.217	ATCCTCTTCA CGGCAATC	CATCTCCTCCTAAACAT	53.5	448	(ACTGCC) ₃	<ef×eg>	(nn,np)
PS318*	LG1	77.136	ATCTACTCCCTATCCGTCAC	CTGTTGTCTCTCCACCT	55	369	(CCACA) ₄	<ab×cd>	(nn,np)
PS089*#	LG1	87.03	ACTGGACTGAAGGTGGAT	AACTCCTCCTCGTTGTCT	56.5	333	(ATA) ₆	<ef×eg>	(nn,np)
PS257*#	LG1	89.148	GGCAAAAGAACGAGAAAAC	TCGCCAACTTCTTCTTTC	54	234	(CTCGTA) ₄	<nn×np>	(nn,np)
PS026*#	LG1	105.978	TTCCCTCCATTCTAACAC	ACCCTAGCCTCTGACATT	54	187	(AG) ₆	<nn×np>	(nn,np)
PS339	LG1	110.177	TGAGGACGCCAAAGAATT	CTCCTCTTAACTCCTCCAT	50	175	(ACAGCA) ₃	<nn×np>	(nn,np)
PS159	LG1	134.196	CCTCCATTCA TCTCTGTC	CGGCAAAATAATAAGTAAAGAG	52	124	(CT) ₇	<nn×np>	(nn,np)
PS205*	LG1	134.196	ATTCAAATAGTCTTCGTGC	TGTCTGTCTCATCGTCCC	55	316	(AAAT) ₄	<lm×ll>	(lm,ll)
PS221*#	LG1	173.579	GATACAAGGCGGAAAGTG	ATGGGTCGGTAAACAACAG	56	301	(AAT) ₅	<nn×np>	(nn,np)
PS108*	LG1	206.757	GCTAAGGCGGTCTTCAGG	TGTTTCCTGTTGTCCTC	58.5	434	(CAA) ₅	<nn×np>	(nn,np)

PS273*#	LG1	212.892	CCCTCAGATGGGATGGAA	GGTGCCCAATTCAGGTAG	58.5	314	(GCCGCT) ₄	<nn×np>	(nn,np)
PS345	LG1	219.257	TGAAGTGAATCGAAGCAT	CATTGGTAGGCGGTCTTT	48	366	(TGGTTG) ₃	<nn×np>	(nn,np)
PS271*#	LG2	0	AGAATCCACCTCCTGTCAC	GATTCTTTCTGTTGTGGG	56.5	406	(GGAGAA) ₃	<lm×ll>	(lm,ll)
PS242	LG2	40.128	TCTAAGCCAGAGCCCAAGT	ATTGTTTGGTCGTCCTTT	57.5	199	(TCTCGT) ₃	<nn×np>	(nn,np)
PS299	LG2	61.053	ATCTAACACCTTCCTCC	CACCTGAACACCTCTCC	54	261	(CATCTC) ₃	<hk×hk>	(hh,hk,kk)
PS336	LG2	69.218	GACCACGGTGAGCTTATT	CTCCAACCATTGTCCCT	50	339	(ACCCAT) ₃	<nn×np>	(nn,np)
PS073	LG2	87.281	GTCGGTGAATGAAGGGTT	ACATTTTCAGCCAACACTC	53.5	269	(AG) ₆	<nn×np>	(nn,np)
PS263	LG2	96.25	TAACCCACAACCCACTTC	CTCCCACTCGTCAATGCT	55	327	(TCACCA) ₃	<ef×eg>	(ee,ef,eg,fg)
PS365*#	LG2	104.089	AACCAAACTAACCCCTAAATG	GTTGGAGTTGGAGAGGTTG	49	350	(CAA) ₇	<nn×np>	(nn,np)
PS101*#	LG2	120.065	AAACCCCTTACTTCCACTT	CCCTACATAACAGACGAAAAG	51	153	(CTA) ₈	<nn×np>	(nn,np)
PS162*#	LG2	124.166	CAGTCTTTCATGGCTTCAC	AAGCAACACCGACAGAGG	51	357	(AG) ₆	<nn×np>	(nn,np)
PS112*#	LG2	128.334	TCCAAATACACGCTCGTT	ATCTCCTGCGACCTTATC	54	320	(ACC) ₅	<lm×ll>	(lm,ll)
PS047	LG2	129.706	AGACGACGAGCAAAGATAT	CGATGCGTAAATGTCAAAT	54	126	(TC) ₈	<nn×np>	(nn,np)
PS004*	LG2	179.158	GTGCTTAGCCTCTAATCTG	CTTTGCTCCAAGTCTGTC	50.5	274	(GA) ₈	<ef×eg>	(ee,ef,eg,fg)
PS029*#	LG2	185.679	CAACTTGTTCTCCGTCCTT	GCAGGCGATGCTACAAAC	54	304	(GA) ₇	<ef×eg>	(ee,ef,eg,fg)
PS265*#	LG2	187.771	TTTTATGGGTCCTGTTGC	GACAACCTTGCCTAGAAT	54	290	(ACAGCC) ₄	<hk×hk>	(hh,hk,kk)
PS356*#	LG2	215.101	TCAAGCCCAAGGTCATTC	TGCTATGGTAAGCGGAAA	53	354	(GAT) ₇	<ef×eg>	(ee,ef,eg,fg)
PS139	LG2	215.883	CAACAATTTAACACGCAGAG	ATCTCGGCTCAAATCGTC	56.5	482	(CCG) ₆	<nn×np>	(nn,np)
PS309*#	LG2	223.047	AAGCAAAGCCGTGGAGAT	ACCATCTCCACCATTTCTG	55	257	(CT) ₆	<nn×np>	(nn,np)
PS149*#	LG3	1.563	AGTCGCCTCCTACACCTC	CTCAACAACCTATCACAT	55.5	173	(AGG) ₅	<nn×np>	(nn,np)
PS335	LG3	18.683	TAATCACCCAATGAGCCA	CCTCATCAGGGTTCTCAC	50	395	(TTCATT) ₃	<nn×np>	(nn,np)
PS061*#	LG3	26.013	CTCCTCCAACATTGACCC	ATTCTGGTCAATGTGGC	57	154	(TG) ₈	<nn×np>	(nn,np)
PS158*	LG3	36.732	TTTCCTGCTTCTTCTGAC	TGTTAGTGATGAAATGGGAT	55	423	(CT) ₇	<nn×np>	(nn,np)
PS199*	LG3	41.905	ACAAAAGGAAATGAGAAGCG	CTGTTGATCGTTGGGTTT	55	351	(GA) ₆	<nn×np>	(nn,np)
PS323	LG3	70.221	CTCACCCGTTCTAAAGTCA	CGTCGTCGCCGAATACTT	53	466	(CGATT) ₃	<nn×np>	(nn,np)
PS260*#	LG3	70.221	ATTACGCCAGTATCAAAG	CCCTTACTCGCCATAGCAC	53	349	(CCTGGA) ₃	<nn×np>	(nn,np)

PS045	LG3	78.434	CGGAGTGGTGGATAGTGT	TAACATCCAAAGCAACTC	52	110	(GA) ₆	<nn×np>	(nn,np)
PS066	LG3	81.664	AAGAACATCAAGGGGAGA	CGTCCCTTTCTGTATCCTT	51.5	183	(TG) ₇	<nn×np>	(nn,np)
PS367*#	LG4	0	AGACGGACGGAAATAGGG	AAATACTCCGTCTTAGTGTGAA	53.5	265	(TCC) ₇	<nn×np>	(nn,np)
PS146	LG4	15.294	GACCACCTCCTCCCAATC	CACCTCCTCCTTCTTACT	57	117	(TCT) ₅	<nn×np>	(nn,np)
PS329	LG4	18.299	ATCTTTCGTTGGCTTCCT	GATGCCGTTTCATGCTCCC	56	408	(GCCTTC) ₃	<lm×ll>	(lm,ll)
PS249*#	LG4	46.854	GGTTCGTCTAGGGTCG	TTTCATCGGAAAGGACAAC	57.5	303	(GGTGGA) ₃	<hk×hk>	(hh,hk,kk)
PS333*#	LG4	50.019	AAGCACGGTGTTCCAGAT	CAACAGGCAGAAGAAAGG	52.5	415	(TCACCA) ₃	<lm×ll>	(lm,ll)
PS157	LG4	68.574	CTCCCTGAACCTCCCTACC	AAAGGGAAGAAGAGTGAG	56	322	(AG) ₆	<nn×np>	(nn,np)
PS290*#	LG4	82.911	TTCTTTCACCTCCACTTCA	GATGTCCCGTCGCTTG TG	53	245	(AGTAGG) ₄	<lm×ll>	(lm,ll)
PS033	LG4	99.188	AAGGAATAGAGTTGTTGGGATG	CTTTCGCTTACTGGTTGA	54.5	323	(CT) ₇	<nn×np>	(nn,np)
PS006*	LG5	0	TTGTTCTGTTCAAGGGTT	TTCTTATCCAGCCGAAAG	54.5	217	(AT) ₆	<nn×np>	(nn,np)
PS311*#	LG5	8.353	AACGCCACCATCACCTTT	CCTCCTCCCTGTTCTTCT	60	277	(TTC) ₆	<nn×np>	(nn,np)
PS076*#	LG5	9.915	ATGCCACCTTTTCCTAAT	AGACGGTGATAGTGAGGA	48.5	258	(TC) ₈	<nn×np>	(nn,np)
PS183*#	LG5	18.878	CACGTAGGTGCCTTGTAAC	CTTCTTCCTGGGCTGTGAG	52	144	(CT) ₆	<nn×np>	(nn,np)
PS369	LG5	39.562	CACAAGTTGGGTAGAAAAGA	TATACTCAGCCTCGAAAAGAA G	55.5	251	(CCA) ₅	<nn×np>	(nn,np)
PS187*#	LG5	52.348	AAGCGGCGTCCATCATAC	TGAACCATCGTGGGAAGC	57	233	(GA) ₇	<nn×np>	(nn,np)
PS014	LG5	86.034	ATGGAAAGTATTGTGGGC	AAAAGGAAGGGGAAGAAAAC	51	358	(GT) ₆	<nn×np>	(nn,np)
PS166*	LG5	116.803	TTCAGTGGGCAAGACCTAC	GGGCGAGAAGAAGGAGAAG	55	337	(AT) ₇	<nn×np>	(nn,np)
PS030	LG5	162.386	ACCCTCCACCACCATCTT	CGCGAAACAAGGATGGAG	57	237	(CT) ₇	<nn×np>	(nn,np)
PS069	LG5	194.037	GAGAAAGGAGGAGGGAGG	ATGATTCCGAGGAGGGTG	54.5	128	(GA) ₆	<nn×np>	(nn,np)
PS144*#	LG5	275.638	CAACCTACAATCCGACAATG	TGTGGGTAGTGGTTTGT TAG	54.5	317	(TGC) ₅	<ef×eg>	(ee,ef,eg,fg)

Table S2. Twenty pairs of EST-SSR markers associated with phenotypic traits in tree peony populations.

Primer name		Primer sequence (5'-3')	Repeat motif	Annealing	Expected size (bp)	Function annotation	Gene ID
				temperature (°C)			
PS2	F	GCTCGTAGCTCTCACTGTCTGA	(GA) ₆	60.4	194	MADS-box protein 5	PB.55834.2
	R	CTTCTCTTGGCGAAGGTCAC				[Paeonia suffruticosa]	
PS12	F	CACTCTCTCCTCCTGCCAAG	(CT) ₁₁	59.6	200	PREDICTED: transcription factor MYB114	PB.59960.1
	R	TATCTTCCTCGGCTGTCCAT				[Ricinus communis]	
PS21	F	TGGACCGGAAGATATGAAGC	(TC) ₁₀	57.8	282	AP2-like ethylene-responsive transcription factor AIL6	PB.16895.1
	R	GGCGGCACATCTGATTAAGT				[Theobroma cacao]	
PS24	F	TTGAGCAATCAGGTTCAATTAGG	(CAA) ₅	56.4	155	PREDICTED: ethylene-responsive transcription factor RAP2-4-like isoform X1	PB.48645.2
	R	TAGCCTCCGGTTCTGAATTG				[Vitis vinifera]	
PS33	F	CAGGACGACTACCTGCGTTA	(GT) ₆ (AT) ₁₀	56.7	207	bHLH transcription factor	PB.12882.2
	R	TCTTCCTGGCAATCTGAGGT				[Paeonia suffruticosa]	
PS36	F	TCCAAGCTACTCCATGCCTTA	(TCT) ₅	58.8	277	PREDICTED: transcription factor bHLH147 isoform X1	PB.53994.4
	R	GAATACTCACTCGCGGCTTC				[Vitis vinifera]	
PS46	F	TCCAGGTATCTCCTGTCATTAACAT	(GA) ₇	57.8	210	PREDICTED: transcription factor bHLH93	PB.51785.1
	R	GGATCTGGTAGAAGAGTTGCTG				[Vitis vinifera]	
PS47	F	TCTCAGCTTCTAATCTTCTCCTCA	(AG) ₆	57.5	246	PREDICTED: transcription factor bHLH96-like	PB.36910.10
	R	ATGTCATGCCTCCAATCTCC				[Nelumbo nucifera]	
PS50	F	TTACAGCAGGCCACGACTG	(AGC) ₆	55.9	262	PREDICTED: transcription factor TCP11	PB.61740.1
	R	CATGACATCATGTGGTCCAA				[Vitis vinifera]	
PS57	F	GCGACAGTACATTCCATCAA	(TC) ₇	57.7	128	PREDICTED: transcription factor CYCLOIDEA	PB.42060.4
	R	GTCAACCACACGTCTGCAAG				[Vitis vinifera]	
PS59	F	CTTGATACCTGTCCGCCATT	(GAA) ₅	56.6	205	PREDICTED: scarecrow-like protein 4	PB.47737.1
	R	CATAACCATGAGCCATTCAAGA				[Vitis vinifera]	

PS64	F	GATTCTGTCTGGCATTGACG	(GA) ₅	58.1	293	heat stress transcription factor C-1	PB.52165.4
	R	CCATCTGTCTGGATCGACCT				[Ziziphus jujuba]	
PS94	F	TCGATCTATATCCATGGCTCAC	(TC) ₈	57.4	255	PREDICTED: axial regulator YABBY 5 isoform X1	PB.57368.1
	R	AGTCTCTCTCCTTGCTTGGA				[Vitis vinifera]	
PS96	F	AAGAGTAACATGCGCCAACA	(CT) ₁₈	58.8	242	PREDICTED: protein YABBY 4	PB.49311.9
	R	AACACTACAAGACCTCCACTGC				[Vitis vinifera]	
PS98	F	CAGCAACAACCGATAATGGA	(CAA) ₅	51.7	289	PREDICTED: B3 domain-containing protein At2g36080-like	PB.54752.2
	R	CATCCACTTCCTCGTCGTCT				[Vitis vinifera]	
PS105	F	TTCATATCGGACACGCAGAG	(GTA) ₅	59	279	putative basic leucine-zipper transcription factor fragment, partial	PB.40196.1
	R	AGTTCTGCACTCGAGCTTCC				[Diospyros kaki]	
PS118	F	GGATTACATGTGAAGCGGATG	(TC) ₆	58.2	290	PREDICTED: GATA transcription factor 8-like	PB.45875.1
	R	GCGCCACAGACTTCAATACC				[Vitis vinifera]	
PS123	F	TTCAGCAGCAACAACAACA	(ACA) ₅	55.9	245	PREDICTED: probable WRKY transcription factor 21	PB.32099.6
	R	CTGAGCGAGAACCACCAGTT				[Prunus mume]	
PS131	F	CAACCTTGGTCTTGCTCTCC	(GAA) ₆	57.7	210	WRKY transcription factor 22	PB.52783.1
	R	GCTCTAATCCTCGAATATTACCTGA				[Manihot esculenta]	
PS163	F	CTCGAGCAAGAGTTGGTGGT	(TC) ₆ CT(CA) ₇	61	276	PREDICTED: transcription initiation factor TFIID subunit 15b	PB.45295.1
	R	ACAGGAGTCTCGCCTAGCAA				[Vitis vinifera]	

Table S3. Summary of private alleles in each population.

Population	Locus	Allele	Frequency
Japan	PS074	244	0.050
Japan	PS118	389	0.333
Japan	PS311	283	0.333
Japan	PS371	166	0.083
Jiangnan	PS50	262	0.091
Jiangnan	PS64	373	0.056
Northwest	PS074	248	0.009
Northwest	PS24	143	0.010
Northwest	PS24	155	0.177
Northwest	PS24	164	0.042
Northwest	PS47	275	0.097
Northwest	PS119	291	0.031
Northwest	PS068	144	0.029
Northwest	PS068	168	0.010
Northwest	PS64	381	0.058
Northwest	PS311	238	0.026
Northwest	PS311	259	0.053
Northwest	PS311	265	0.013
Northwest	PS144	259	0.019
Southwest	PS308	201	0.063
Southwest	PS144	274	0.143
Zhongyuan	PS57	118	0.013
Zhongyuan	PS57	120	0.007
Zhongyuan	PS57	122	0.026
Zhongyuan	PS57	134	0.002
Zhongyuan	PS57	136	0.011
Zhongyuan	PS57	138	0.004
Zhongyuan	PS57	140	0.013
Zhongyuan	PS57	147	0.002
Zhongyuan	PS57	154	0.002
Zhongyuan	PS57	156	0.035
Zhongyuan	PS57	164	0.002
Zhongyuan	PS57	166	0.053
Zhongyuan	PS57	172	0.002
Zhongyuan	PS57	180	0.002
Zhongyuan	PS074	216	0.226
Zhongyuan	PS074	242	0.015
Zhongyuan	PS074	252	0.007
Zhongyuan	PS074	268	0.002
Zhongyuan	PS074	274	0.002
Zhongyuan	PS074	276	0.017
Zhongyuan	PS36	288	0.006

Zhongyuan	PS36	298	0.003
Zhongyuan	PS36	303	0.023
Zhongyuan	PS36	306	0.003
Zhongyuan	PS36	312	0.003
Zhongyuan	PS24	149	0.005
Zhongyuan	PS24	167	0.041
Zhongyuan	PS24	171	0.018
Zhongyuan	PS24	174	0.005
Zhongyuan	PS24	176	0.025
Zhongyuan	PS24	179	0.124
Zhongyuan	PS24	180	0.002
Zhongyuan	PS47	267	0.012
Zhongyuan	PS47	269	0.035
Zhongyuan	PS47	271	0.023
Zhongyuan	PS119	301	0.003
Zhongyuan	PS119	304	0.003
Zhongyuan	PS119	307	0.005
Zhongyuan	PS119	309	0.005
Zhongyuan	PS068	140	0.007
Zhongyuan	PS068	146	0.013
Zhongyuan	PS068	157	0.007
Zhongyuan	PS068	158	0.010
Zhongyuan	PS068	162	0.044
Zhongyuan	PS068	174	0.010
Zhongyuan	PS068	176	0.013
Zhongyuan	PS068	178	0.017
Zhongyuan	PS118	313	0.003
Zhongyuan	PS308	184	0.003
Zhongyuan	PS308	185	0.003
Zhongyuan	PS308	197	0.003
Zhongyuan	PS308	203	0.003
Zhongyuan	PS308	207	0.014
Zhongyuan	PS308	209	0.006
Zhongyuan	PS308	212	0.003
Zhongyuan	PS308	217	0.003
Zhongyuan	PS308	219	0.003
Zhongyuan	PS308	220	0.023
Zhongyuan	PS308	222	0.014
Zhongyuan	PS308	227	0.003
Zhongyuan	PS308	230	0.003
Zhongyuan	PS50	268	0.018
Zhongyuan	PS50	271	0.002
Zhongyuan	PS50	274	0.125
Zhongyuan	PS50	278	0.002

Table S4. Analysis of the genetic diversity of tree peony populations in China.

Population	<i>Ss</i>	<i>Na</i>	<i>Ne</i>	<i>PA</i>	<i>I</i>	<i>Ho</i>	<i>He</i>	<i>PPL (%)</i>	<i>H</i>	<i>PIC</i>	<i>F_{ST}</i>	<i>P_{HWE}</i>
Japan	12	2.813	1.988	4	0.705	0.372	0.405	81.250	0.508	0.479	0.124	0.306
Jiangnan	11	2.875	1.947	2	0.684	0.444	0.373	68.750	0.420	0.369	0.225	0.405
Northwest	54	5.813	2.220	13	0.944	0.422	0.454	100.000	0.454	0.423	0.171	0.178
Southwest	8	2.938	2.030	2	0.739	0.427	0.420	87.500	0.498	0.456	0.030	0.416
Zhongyuan	237	11.125	2.590	91	1.135	0.410	0.508	93.750	0.405	0.358	0.218	0.006
Mean	-	5.113	2.155	22.4	0.842	0.415	0.432	86.250	0.457	0.417	0.154	0.262

Ss: Sample size; *Na*: Number of different alleles; *Ne*: Effective number of alleles; *PA*: Number of Private Alleles; *I*: Shannon's Information index; *Ho*: Observed heterozygosity; *He*: Expected heterozygosity; *PPL*: Percentage of Polymorphic Loci; *H*: Gene Diversity; *PIC*: Polymorphism information content; *F_{ST}*: Fixation index; *P_{HWE}*: P Value for Hardy Weinberg equilibrium.