

Development and Cross-species Transferability of Novel Genomic-SSR Markers and Their Utility in Hybrid Identification and Trait Association Analysis in Chinese Cherry

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Table S1. F₁ populations and their parents' phenotype characters.

Mating design (♀×♂)	Code range	F ₁ populations (n)	Parents phenotype characters
NZH × HF	NH528~NH710, NH931~NH1020	211	NZH: Early-matured, medium fruit size (3.8~4.5 g), light flavor (11.5~13.5% TSS, 0.75 g·100mL ⁻¹ titratable acid), kidney shape, orange red peel color; susceptible to gummosis disease.
HF × NZH	HN711~HN920	145	HF: Large fruit size (4.5~5.5 g), full-flavored (14.5~16.2% TSS, 17.74 mg·100mL ⁻¹ vitamin C, 0.51 g·100mL ⁻¹ titratable acid), heart shape, purple red peel color; susceptible to shot hole disease.
HF × PJHH	HP1~HP526, HP1041~HP1860	766	PJHH: Semi-wild, intensive adaptability and disease/pest resistance, very small fruit size (1.5~2.5 g), flat round shape, red peel color, sour-sweet flavor (11.5~13.2% TSS, 0.79 g·100mL ⁻¹ titratable acid)
Total		1122	

Note: NZH: Nanzaohong; HF: Hongfei; PJHH: Pujianghonghua.

Table S2. List of information for each accession in this study.

Taxon	Accession no.	Name	Locality (latitude N/Longitude E/Altitude (m))	Sequencing results		FLD (cm)	FTD (cm)	TSS (%)
				Clean Bases (bp)	Mean depth			
<i>Cerasus</i>								
Subg. <i>Cerasus</i> (CER)								
<i>C. pseudocerasus</i> (landrace)	1	CAN2	Anning, Yunnan					
	2	CES1	Eshan, Yunnan			1.33	1.48	23.00
	3	CFM2	Fumin, Yunnan			1.33	1.48	NA
	4	CJN1	Jinning, Yunnan			1.43	1.52	20.00
	5	CMZ3	Mengzi, Yunnan			1.46	1.77	20.73
	6	CYiL1	Yiliang, Yunnan					
	7	CYiL2						
	8	CYX3	Yuxi, Yunnan					
	9	CYX4	(24°15.545'/102°28.895'/1644-1769)	1722435300	5.74	1.49	1.51	27.70
	10	CYX6				1.50	1.57	24.00
	11	CZT1	Zhaotong, Yunnan					
	12	CZT2				1.48	1.76	19.70
	13	CZT3						
	14	CHC	Miyi, Sichuan					
	15	CHF	Xinjin, Sichuan					
	16	CHY1	Hanyuan, Sichuan			1.29	1.50	10.40
	17	CHY2				1.26	1.43	7.60
	18	CHY3				1.43	1.59	16.87
	19	CHY4				1.38	1.53	13.10
	20	CHY5				1.49	1.67	16.90
	21	CHY6				1.41	1.58	NA0
	22	CHZZ	Xinjin, Sichuan			1.33	1.52	NA
	23	CJY1	Jianyang, Sichuan			1.56	1.83	17.50
	24	CJY4						
	25	CLD3	Luding, Sichuan			1.22	1.37	20.50
	26	CLoQ	Longquan, Sichuan					
	27	CMY2	Miyi, Sichuan			1.46	1.55	18.70
	28	CMY3				1.34	1.63	33.23
	29	CMY4				1.51	1.73	29.70
	30	CMY5				1.60	1.97	29.00
	31	CNZH	Xinjin, Sichuan					
	32	CPJB1	Pujiang, Sichuan			1.37	1.44	NA
	33	CPJHH				1.38	1.44	NA
	34	CPZB	Pengzhou, Sichuan			1.48	1.74	15.33
	35	CPZH				1.40	1.69	17.50
	36	CPZH2						
	37	CXC1	Xichang, Sichuan	2053758870	6.01	1.44	1.72	24.33
	38	CXC2				1.36	1.52	19.50
	39	CXC3				1.43	1.71	26.50
	40	CXC4				1.02	1.34	31.00
	41	CAQ2	Anqiu, Shandong			1.49	1.44	13.93
	42	CAQ3				1.41	1.47	13.80
	43	CAQ4				1.40	1.40	15.90
	44	CAQ5				1.48	1.39	15.73
	45	CCL1	Changle, Shandong			1.29	1.17	15.50
	46	CCY2	Changyi, Shandong					
	47	CHaY1	Haiyang, Shandong					
	48	CHaY3						

	49	CLaY2	Laiyang, Shandong			1.42	1.33	20.00
	50	CLiY3	Linyin, Shandong					
	51	CLiY5				1.52	1.60	13.80
	52	CLiY6				1.38	1.44	16.67
	53	CWL1	Wulian, Shandong			1.29	1.18	15.97
	54	CWL2				1.56	1.55	16.37
	55	CZaZ1	Zaozhuang, Shandong			1.65	1.40	20.83
	56	CZaZ2				1.51	1.60	15.70
	57	CZaZ3				1.57	1.64	27.73
	58	CZaZ6				1.89	1.58	11.50
	59	CZaZ8				1.43	1.47	18.70
	60	CZaZ9				1.37	1.25	21.00
	61	CZC1	Zhucheng, Shandong			1.57	1.52	15.33
	62	CZC2				1.48	1.35	15.33
	63	CLuY1	Luoyang, Henan					
	64	CLuY16	(34°43.331'/112°18.155'/251-263)					
	65	CLuY3						
	66	CLuY4				1.61	1.48	18.00
	67	CLuY41						
	68	CLuYg						
	69	CZeZ1	Zhengzhou, Henan			1.41	1.51	NA
	70	CZeZ9				1.37	1.25	21.00
	71	CAS1	Anshun, Guizhou			1.58	1.54	13.80
	72	CBJ2	Bijie, Guizhou			1.58	1.81	20.90
	73	CBJ3	(27°18.761'/105°19.492'/1453-1500)			1.81	1.88	13.57
	74	CBJ4		965582820	3.22	1.62	1.54	31.80
	75	CBJ5				1.51	1.74	23.03
	76	CBJ6				1.61	1.71	28.33
	77	CBJ7 ^b		1987875450	6.63			
	78	CGuY1	Guiyang, Guizhou			1.47	1.54	23.00
	79	CGuY2				1.82	1.74	17.00
	80	CHeZ1	Hezhang, Guizhou					
	81	CNY1	Nayong, Guizhou					
	82	CPD3	Puding, Guizhou			1.79	1.82	14.70
	83	CWN1	Weining, Guizhou			1.39	1.32	23.00
	84	CWN2				1.30	1.50	24.00
	85	CZN1	Zhenning, Guizhou			1.42	1.38	17.00
	86	CZN2				1.33	1.34	18.50
	87	CZY1	Zunyi, Guizhou					
	88	CZY2				1.47	1.58	12.50
	89	CZY3						
	90	CXJ4	Xianju, Zhejiang					
	91	CBLHZZ	Banan, Chongqing			1.16	1.17	18.50
	92	CTH2	Taihe, Anhui			1.33	1.24	NA
	-	CQhzz	Chongqing	1219313880	4.06			
			(29°56.301'/106°55.156'/240-284)					
	-	CPZB2	Pengzhou, Sichuan	2053758870	6.85			
			(31°11.988'/103°50.010'/1011-1028)					
<i>C. pseudocerasus</i> (wild)	93	WBZ	Bazhong, Sichuan					
	94	WBN	Ba'nan, Chongqing					
	-	WQX13	Qingxi, Sichuan	1862509950	6.21			
			(32°24.086'/104°24.076'/1285-1467)					
<i>C. avium</i>	95	Van	Zhengzhou Fruit Research Institute,					
	96	Zaodaguo	Chinese Academy of Agricultural					
	97	Mazzard	Sciences (ZFRI, CAAS)					

	98	Stella	
<i>C. avium</i> × <i>C. pseudocerasus</i>	99	Landing 2	
<i>C. vulgaris</i> × <i>P./C. canescens</i>	100	Gisela 6	
<i>C. vulgaris</i>	101	-	
	102	ZY-1	
<i>C. campanulata</i>	103	-	Chengdu Botanical Garden, Sichuan
<i>C. yedoensis</i>	104	Yoshino cherry	
<i>C. serrulata</i>	105	-	
<i>C. cerasoides</i>	106	-	
<i>C. mahaleb</i>	107	-	ZFRI, CAAS
Subg. <i>Microcerasus</i> (MIC)			
<i>C. humilis</i>	108	-	ZFRI, CAAS
<i>C. glandulosa</i>	109	-	
<i>C. japonica</i>	110	-	
<i>C. tomentosa</i>	111	-	
<i>Armeniaca</i> (ARM)			
<i>Armeniaca mume</i>	112	-	Chengdu Botanical Garden, Sichuan
<i>Amygdalus</i> (AMY)			
<i>Amygdalus persica</i>	113	-	Chengdu Botanical Garden, Sichuan
<i>Amygdalus triloba</i>	114	-	

Note: Name in bold and green: whole genome sequencing accession; Name in bold and red: whole-genome resequencing accessions; NA, data missing; -, represents the name is unknown; FLD: fruit longitudinal diameter; FTD: fruit transverse diameter; TSS: total solid content. Accession no.112-114 were only used to test the transferability of SAUCps203, the species-specific marker.

Table S3. Information of five SSR markers for hybrids identification

Marker	Primer sequence (5'-3')	Repeat motif
SAUCps303	F: TCTTTCCAAACTCCCTTCATCTCC; R: TCCCAGCATCATCATTCAACTCT	CT
SAUCps102	F: TCAGTGAGGCAGTAAGGAAC; R: ATGGCGTCTACACGGTAAT	AT
SAUCps706	F: GCCATTTCGTTTATTCCCTTT; R: TTTCTCCGTGCTCTCTCTGTTT	CTCTA
SAUCps202	F: CCACTTGCTCTTCTATCTTCTT; R: GCCCACCATCCACATCAA	GAA
SAUCps304	F: AGATGTCCTCGTGTTGTAAGC; R: CGTAGTTGGTCAGTTGGTCA	TTA

Table S4. Characteristics of 39 microsatellite loci across 94 Chinese cherry accessions.

Marker	MAF	Genotype No.	<i>Na</i>	<i>Ne</i>	<i>Ho</i>	<i>He</i>	<i>PIC</i>
SAUCps101	0.935	4	3	1.140	0.090	0.123	0.117
SAUCps305	0.690	5	4	1.885	0.100	0.472	0.417
SAUCps503	0.645	5	3	2.075	0.090	0.521	0.462
SAUCps602	0.450	6	3	2.807	0.610	0.647	0.570
SAUCps704	0.640	5	3	1.891	0.140	0.474	0.373
SAUCps705	0.895	3	2	1.232	0.110	0.189	0.170
SAUCps801	0.780	6	4	1.545	0.010	0.354	0.333
SAUCps807	0.680	4	4	1.790	0.530	0.444	0.353
SAUCps601	0.815	7	5	1.468	0.210	0.320	0.296
SAUCps202	0.445	9	5	2.783	0.180	0.644	0.574
SAUCps703	0.575	3	2	1.956	0.030	0.491	0.369
SAUCps502	0.535	7	4	2.549	0.120	0.611	0.541
SAUCps204	0.835	3	2	1.380	0.250	0.277	0.238
SAUCps605	0.815	4	3	1.439	0.010	0.307	0.264
SAUCps402	0.765	10	5	1.610	0.101	0.381	0.364
SAUCps504	0.625	4	2	1.871	0.374	0.468	0.372
SAUCps301	0.550	7	4	2.452	0.560	0.595	0.524
SAUCps205	0.870	5	4	1.308	0.020	0.237	0.224
SAUCps203	0.980	5	5	1.041	0.040	0.040	0.039
SAUCps302	0.875	5	3	1.288	0.030	0.225	0.207
SAUCps401	0.600	5	3	1.981	0.250	0.498	0.391
SAUCps701	0.385	11	6	4.081	0.130	0.759	0.720
SAUCps806	0.385	6	3	2.934	0.061	0.663	0.594
SAUCps803	0.420	7	4	2.843	0.440	0.652	0.575
SAUCps802	0.445	9	4	2.611	0.475	0.620	0.551
SAUCps604	0.955	4	2	1.031	0.010	0.031	0.085
SAUCps607	0.475	8	5	2.234	0.818	0.555	0.464
SAUCps501	0.480	9	4	2.768	0.313	0.642	0.581
SAUCps606	0.670	7	4	1.921	0.133	0.482	0.453
SAUCps804	0.520	5	3	2.014	0.323	0.506	0.396
SAUCps702	0.770	8	4	1.595	0.263	0.375	0.360
SAUCps808	0.445	14	6	3.124	0.152	0.683	0.637
SAUCps206	0.465	10	4	3.010	0.133	0.671	0.630
SAUCps104	0.530	10	5	2.387	0.153	0.584	0.527
SAUCps805	0.805	6	3	1.448	0.327	0.311	0.316
SAUCps103	0.830	3	2	1.238	0.215	0.193	0.276
SAUCps603	0.735	8	5	1.441	0.079	0.308	0.415
SAUCps304	0.325	7	4	3.289	0.139	0.700	0.728
SAUCps201	0.315	8	4	2.863	0.211	0.655	0.692
mean	0.640	6.462	3.718	2.060	0.211	0.454	0.415

Note: *MAF*: major allele frequency, *Genotype No*: number of genotype, *Na*: number of alleles observed, *Ne*: effective number of alleles, *Ho*: observed heterozygosity, *He*: expected heterozygosity, *PIC*: polymorphism information content.

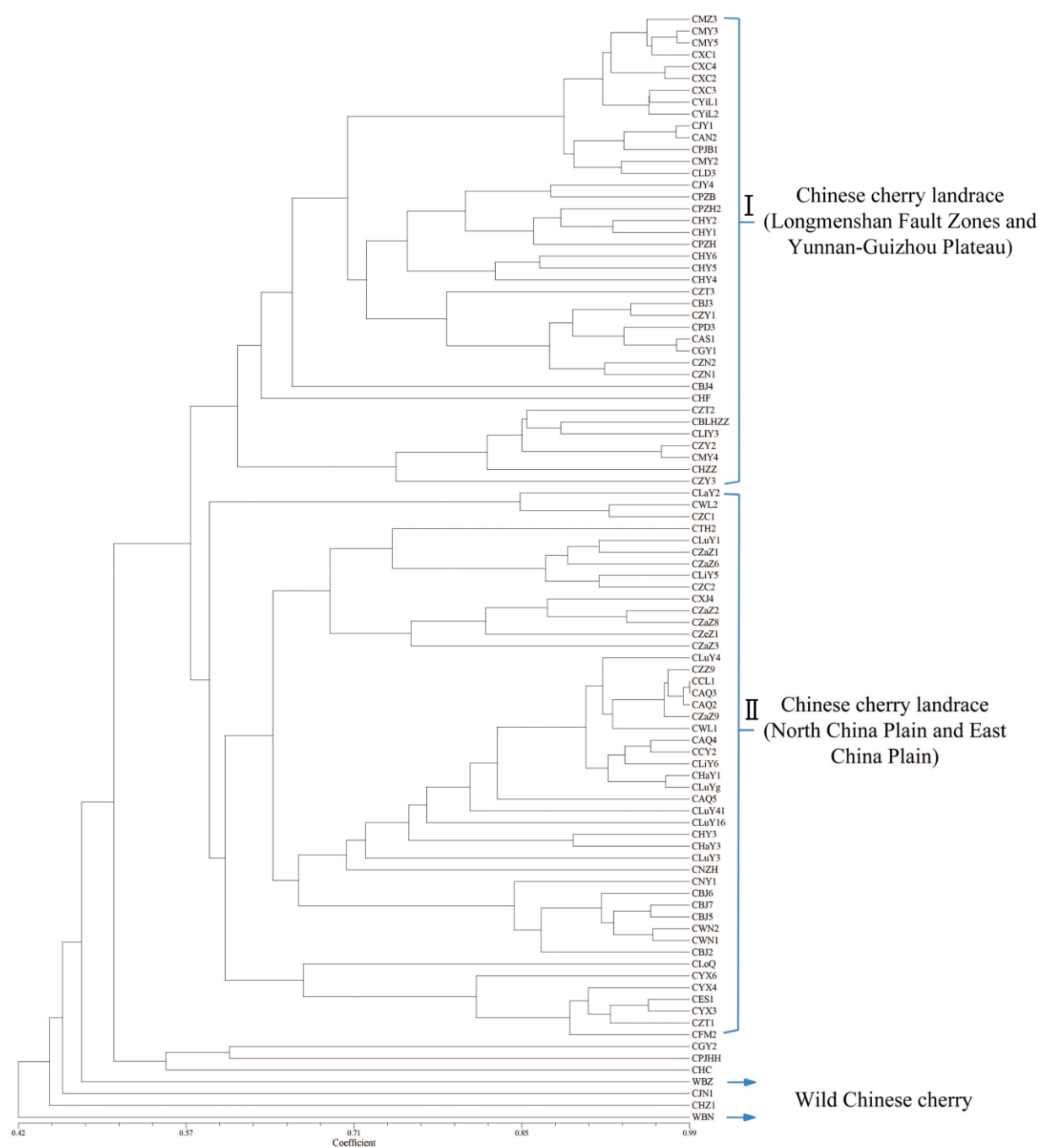


Figure S1. Phenograms by UPGMA cluster analysis of 94 Chinese cherry accessions.

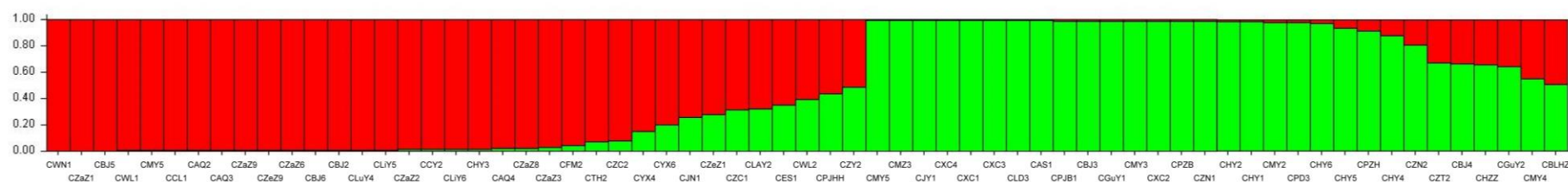


Figure S2. Population structure distribution of 65 Chinese cherry accessions.

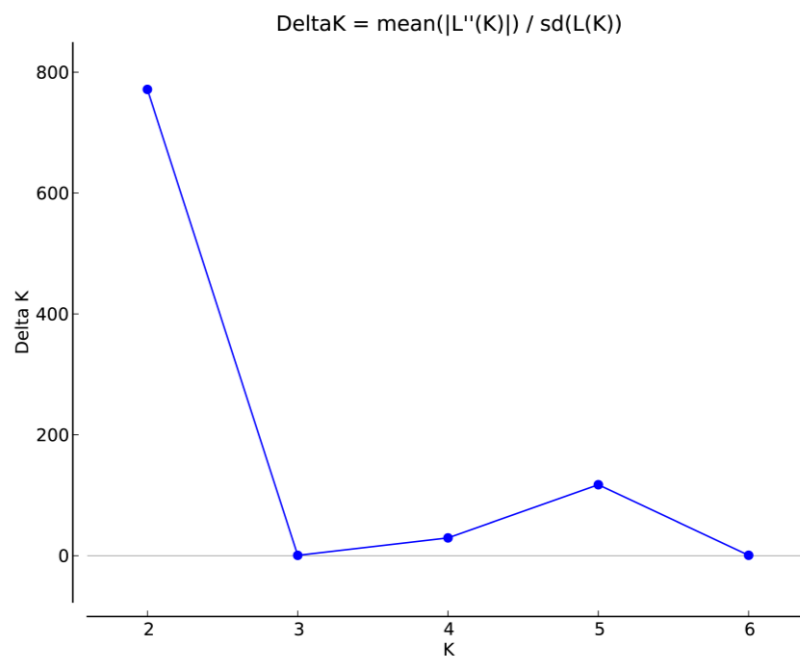


Figure S3. Curve diagram of K value.