

Supplementary material

Table S1 Microsatellite pair sequences, expected and observed product size, and chromosomal location in the present study

Microsatellite loci Name	Primer sequences	Product size in references (bp)	Observed product size (bp)	Chromal location *	Annealing temperature (°C)	References
EMPA026	ATTGAAAAAGCCAAAGAGCG TTCACGGTTTGAAGCAAGTG	219	190-219	8	55	
EMPA027	GCCAACACCCAAATGGTTAG CTCTCCACGGTCTTGCTTTC	210	198-225	7	55	Clarke, 2009
EMPA029	GCTGCTGATTGTCTGTGGTC CAAACCCCTCTTCTTCCAC	137	126-137	6	55	
EMPaS02	CTACTTCCATGATTGCCTCAC AACATCCAGAACATCAACACAC	133-145	136-160	3	55	
EMPaS06	AAGCGGAAAGCACAGGTAG TTGCTAGCATAGAAAAGAATTGTAG	200-218	222-237	4	55	Vaughan & Ussell, 2004
EMPaS10	GCTAATATCAAATCCCAGCTCTC TGAAGAAGTATGGCTTCTGTGG	151-183	153-183	4	55	
UDP96-005	GTAACGCTCGCTACCACAAA CCTGCATATCACCAACCCAG	155	98-126	1	55	Cipriani, 1999
pchgms1	GGGTAAATATGCCCATTTGTGCAATC GGATCATTGAACTACGTCAATCCTC	194	183-202	2	55	Sosinski, 2000
UCD-CH18	GATGGAAGGCCAAGGCAAC AATGTTCCCGTTATATGC	178/184 186/188	160-188	4	55	
UCD-CH31	TCCGCTTCTCTGTGAGTGTG CGATAGTTTCCCTTCCAGACC	111/123 125/148	80-118	1	55	Struss, 2003
UCD-CH12	AGACAAAGGGATTGTGGGC TTTCTGCCACAAACCTAATGG	173/175/177/ 180/120	175-198	2	55	
UCD-CH39	CACTGTCTCCAGTTAAACTC CCTGAGCTTTTGACACATGC	122/142/ 144/146	133-164	7	55	
BPPCT040	ATGAGGACGTGTCTGAATGG AGCCAAACCCCTCTTATACG	135	124-149	4	55	Dirlewanger, 2002
BPPCT013	ACCCACAAATCAAGCATATCC AGCTTCAGCCACCAAGC	183	154-166	2/4	55	
CPSCT012	ACGGGAGACTTTCCAGAAAG CTTCTCGTTTCCCTCCCTCT	156	150-172	5	55	Mnejja, 2004
M01a	CACGAGGCGCCATTTCTACG GTACGACGGGTTTTGGCTCA	80	75-90	2	55	
M12a	AGGTGCCTCATCTTCTTCTTTG GTGTGGTGAGGGGTGAGAGC	197/177	177-200	4	55	Yamanoto, 2002
MA006	ACAACCTACCATTGAGGCT CAATCATTCAAGCTCTCTCC	295/301	129-156	5	55	
MA027a	GGCAGTGAAGAATCTATGA GATAGCATAAACCCCGTGAA	147/151	130-159	6	55	
PMS2	CACTCTCTCCAGTTAAACT CCTGAGCTTTTGACACATGC	132-152	143-164	7	55	Cantini, 2001

* Chromosomal location was determined by referring a linkage map of sweet cherry (Clarke, 2009)

Table S2 Characteristic statistics of 20 microsatellite loci used in the study

Loci Name	<i>Na</i>	<i>RA</i>	<i>MAF</i>	<i>Ne</i>	<i>Ho</i>	<i>He</i>	<i>I</i>	<i>PIC</i>	<i>f</i>	<i>BI</i>
EMPA026	5	2	0.423	3.074	0.482	0.678	1.251	0.616	0.278*	0.111
EMPA027	6	2	0.348	3.594	0.648	0.725	1.379	0.670	0.094	0.038
EMPA029	4	1	0.485	2.805	0.812	0.646	1.146	0.579	- 0.260	- 0.103
EMPaS02	10	7	0.381	3.346	0.633	0.704	1.486	0.651	0.102	0.040
EMPaS06	6	3	0.736	1.767	0.286	0.436	0.899	0.407	0.345*	0.103
EMPaS10	10	6	0.418	3.720	0.508	0.734	1.586	0.694	0.309*	0.129
UDP96-005	5	2	0.443	2.608	0.829	0.619	1.096	0.539	0.444*	0.176
pchgms1	8	5	0.407	3.481	0.449	0.716	1.445	0.662	- 0.341	- 0.132
UCD-CH18	6	3	0.597	2.412	0.310	0.588	1.168	0.549	0.624*	0.242
UCD-CH31	8	4	0.525	2.936	0.372	0.662	1.397	0.631	0.360*	0.148
UCD-CH12	8	5	0.507	2.760	0.241	0.640	1.260	0.581	- 0.060	- 0.025
UCD-CH39	5	2	0.450	2.717	0.672	0.635	1.153	0.561	0.490*	0.181
BPPCT040	6	3	0.687	1.934	0.374	0.485	0.941	0.440	0.229*	0.073
BPPCT013	4	1	0.688	1.905	0.496	0.477	0.841	0.425	- 0.038	- 0.014
CPSCT012	6	4	0.526	2.221	0.555	0.552	0.949	0.453	- 0.005	- 0.003
M01a	6	2	0.604	2.421	0.468	0.589	1.176	0.551	0.207*	0.075
M12a	5	2	0.408	3.016	0.691	0.671	1.176	0.601	- 0.030	- 0.014
PMS2	5	1	0.469	3.298	0.372	0.700	1.362	0.652	0.478*	0.195
MA006	5	1	0.580	2.180	0.730	0.543	0.921	0.455	- 0.336	- 0.119
MA027a	8	0	0.227	6.610	0.500	0.854	1.977	0.831	0.416*	0.189
Mean	6	3	0.495	2.940	0.521	0.633	1.230	0.577	0.177	0.065

Na Observed number of alleles, *RA* rare alleles, *He* expected heterozygosity, *MAF* Major allele frequency, *Ne* Effective number of alleles, *Ho* Observed heterozygosity, *He* Nei's expected heterozygosity, *I* Shannon's Information index, *PIC* Polymorphism information content, *f* inbreeding coefficient (loci deviated from Hardy-Weinberg equilibrium at $P < 0.05$), *BI* null allele frequency averaged over all populations (Brookfield method). * $P < 0.05$.

Table S3 Pairwise F_{st} values (below diagonal) and significant test P value (above diagonal) among 17 *Prunus pseudocerasusu* landraces populations

	YA	MS	PJ	JY	XC	SM	BC	CQ	SN	FP	HZ	XX	GY	BJ	TH	TS	WF
YA		0.027	0.018	0.009	0.000	0.000	0.027	0.405	0.000	0.009	0.000	0.009	0.000	0.000	0.000	0.009	0.000
MS	0.056*		0.577	0.739	0.027	0.198	0.009	0.036	0.054	0.099	0.018	0.090	0.000	0.009	0.000	0.009	0.000
PJ	0.060*	0.026		0.486	0.000	0.153	0.000	0.081	0.072	0.739	0.000	0.216	0.000	0.018	0.018	0.018	0.018
JY	0.144**	0.056	0.025		0.018	0.009	0.000	0.009	0.018	0.045	0.099	0.126	0.009	0.000	0.000	0.009	0.000
XC	0.208**	0.108*	0.167**	0.132*		0.000	0.000	0.000	0.000	0.009	0.000	0.000	0.000	0.000	0.000	0.009	0.000
SM	0.095**	0.022	0.044	0.097**	0.180**		0.018	0.000	0.045	0.072	0.036	0.054	0.000	0.000	0.000	0.000	0.000
BC	0.089*	0.106**	0.174**	0.291**	0.276**	0.060*		0.081	0.000	0.000	0.081	0.036	0.000	0.000	0.000	0.018	0.000
CQ	0.029	0.060*	0.027	0.153**	0.211**	0.070**	0.014		0.000	0.063	0.027	0.054	0.000	0.000	0.000	0.000	0.000
SN	0.317**	0.154	0.194	0.245*	0.249**	0.087*	0.229**	0.222**		0.027	0.820	0.054	0.000	0.009	0.018	0.135	0.000
FP	0.084**	0.060	0.047	0.133*	0.206**	0.067	0.107**	0.020	0.149*		0.009	0.126	0.000	0.036	0.009	0.027	0.009
HZ	0.410**	0.229*	0.268**	0.316	0.277**	0.167*	0.369	0.308*	0.081	0.230**		0.009	0.000	0.009	0.000	0.000	0.000
XX	0.190**	0.062	0.042	0.128	0.205**	0.072	0.180*	0.106	0.107	0.095	0.181**		0.000	0.045	0.153	0.144	0.216
GY	0.408**	0.274**	0.245**	0.341**	0.347**	0.233**	0.376**	0.325**	0.162**	0.228**	0.191**	0.117**		0.090	0.144	0.000	0.000
BJ	0.240**	0.178**	0.099*	0.213**	0.271**	0.156**	0.248**	0.181**	0.117**	0.087*	0.128**	0.075*	0.045		0.018	0.000	0.000
TH	0.317**	0.161**	0.130*	0.201**	0.268**	0.154**	0.299**	0.235**	0.064*	0.153**	0.124**	0.035	0.037	0.052*		0.036	0.216
TS	0.334**	0.164**	0.224*	0.227**	0.226**	0.141**	0.319*	0.272**	0.097	0.250*	0.184**	0.108	0.189**	0.163**	0.094*		0.081
WF	0.206**	0.098**	0.085*	0.139**	0.181**	0.106**	0.194**	0.157**	0.092**	0.119**	0.163**	0.015	0.084**	0.091**	0.001	0.028	

Statistical significance test (*significant difference $P<0.05$, ** Significant differences $P<0.01$)

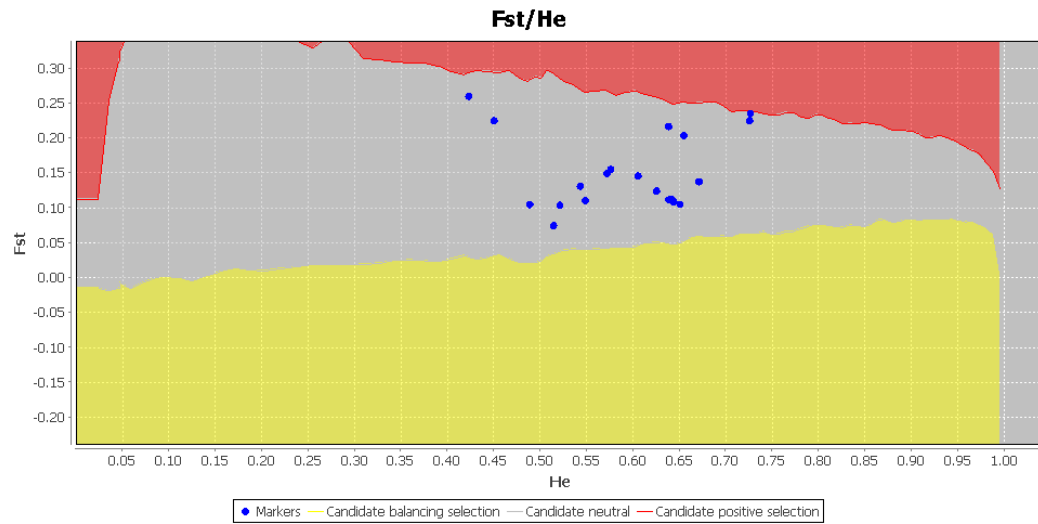


Fig. S1 The neutral evolution test of the whole 20 microsatellite loci detected by java workbench Lositan.

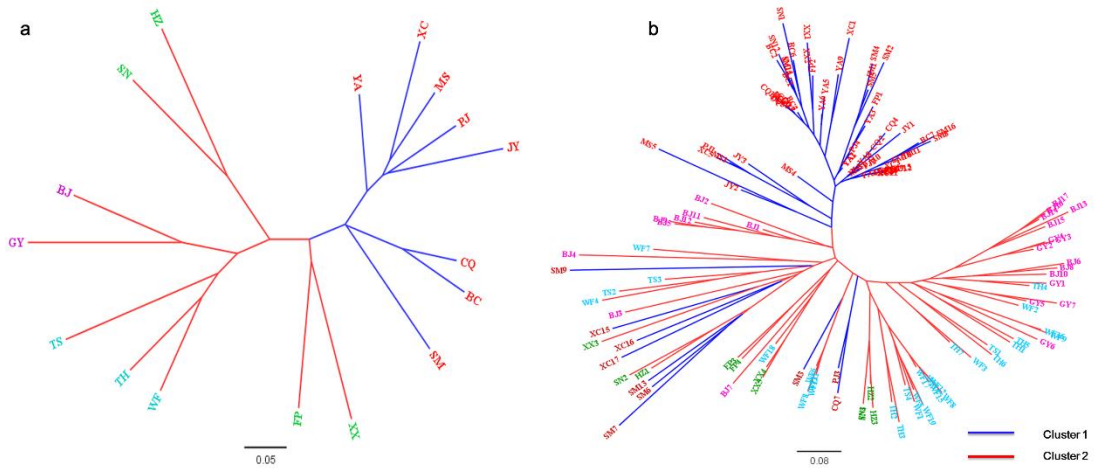


Fig. S2 Unrooted neighbor joining tree of 17 populations **(a)** and 140 individuals **(b)** of *Prunus pseudocerasus* landrace. Branch with red and blue lines represent the two clusters based on STRUCTURE analysis and population cluster. The individuals were sorted according to population code with red, green, purple and blue colors represent the SC, QL, YG and NC regions respectively as shown in Table 1

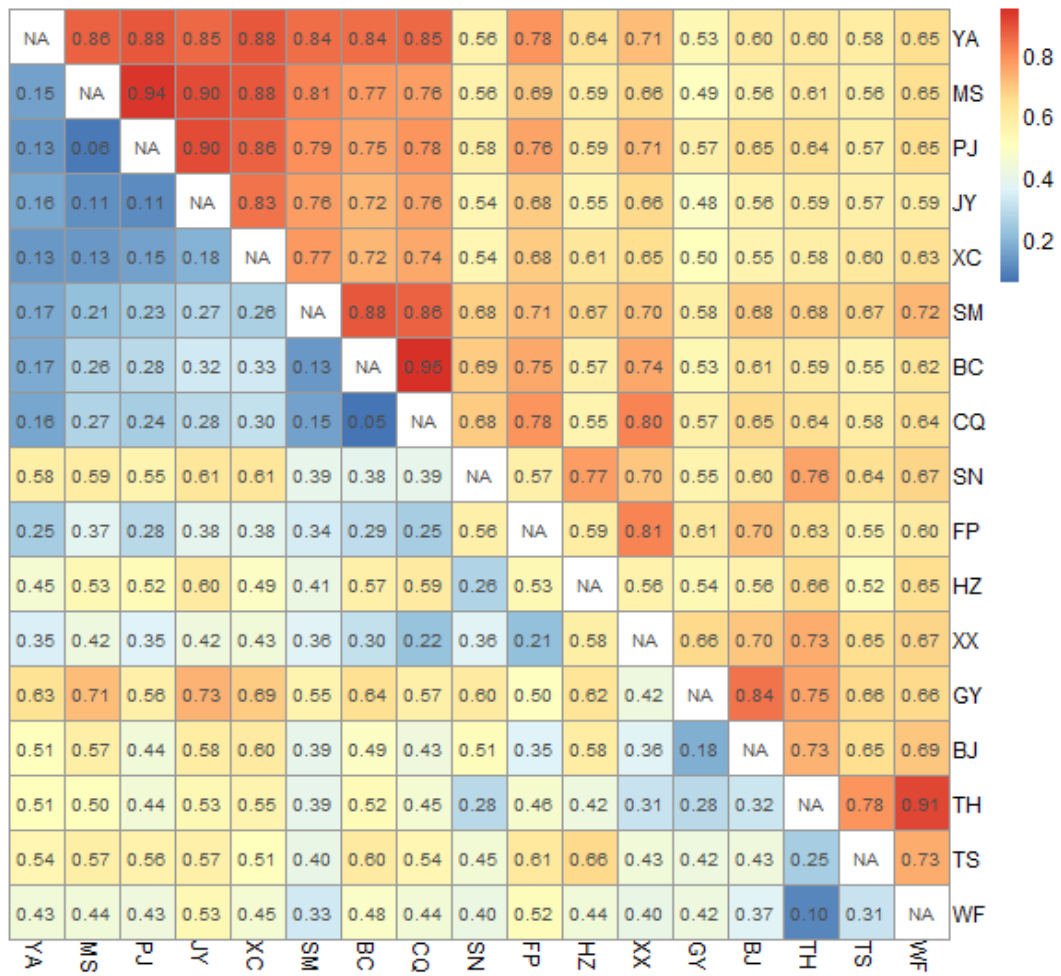


Fig. S3 Heat map of genetics identify (above diagonal) and genetics distance (below diagonal) among 17 *Prunus pseudocerasus* populations