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Allelic variation of simple sequence repeats markers linked to PPV resistance in Chinese apricot

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Abstract

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Apricot is one of the oldest fruit tree crops in China and it was spread via Armenia to other areas. There are about ten species of apricot (Subg. *Armeniaca* Mill.) worldwide, among which nine species are native to China. Sharka disease caused by the *Plum pox virus* (PPV) is widely distributed in the main producing regions of apricot. In this study, linked simple sequence repeats (SSR) primers were used to detect allele variations potentially associated with PPV resistance among Chinese apricot germplasm resources, including 52 accessions belonging to *Prunus armeniaca*, 7 to *Prunus mandshurica*, 6 to *Prunus sibirica*, 4 to *Prunus mume*, 17 to other species or types. The allelic variation at loci with PPV resistance showed that these SSR markers linked to PPV resistance kept a relatively high level of diversity in Chinese apricot. The special alleles and genotypes only found in South China cultivars might reveal new PPV resistance sources. Some famous local cultivars of Chinese apricot might be considered as candidates for PPV resistance.

Keywords: *Prunus armeniaca* L.; SSR; *Plum pox virus* resistance; allele variation

Apricot (Subg. *Armeniaca* Mill.) belongs to the Rosaceae family, subfamily Prunoideae, genus *Prunus* L., together with peach, plum and cherry (Ledbetter 2008). The main producing regions include China, Turkey, Iran, southern Europe, North Africa and Australia. Sharka disease is caused by the *Plum pox virus* (PPV), which has nine strains: PPV-D, PPV-M, PPV-EA, PPV-C, PPV-Rec (Recombinant), and PPV-W, and so on. (Llácer, Cambra 2006). Both PPV strains M and D infect peach, plum, and apricot. PPV-D is the most widely distributed strain of plum pox virus worldwide and has wide experimental host range in *Prunus* species (Damsteegt et al. 2007). The disease spread from its origin in the Balkan countries to most of the European subcontinent and the areas around the Mediterranean basin. It is one of the most limiting factors in apricot production and results in deformed, unripen and unmarketable fruits (Sicard et al. 2008; Soriano et al. 2008). The PPV epidemic also appears in Russia, India, Kazakhstan and Pakistan (EPPO Bulletin 2006), its first occurrence in Japanese apricot (*P. mume* Sieb. et Zucc.) was reported in 2010 in Japan (Maejima et al. 2010). To solve this problem in the long term, the cultivation of PPV-resistant cultivars is one of the most effective solutions.

It is important in breeding that genetic base for PPV resistance has a wide extent. A few sources of PPV resistance have already been found, such as the North American 'Harlayne', 'Stark Early Orange' (SEO), 'Goldrich', 'Lito', 'Harcot', 'Veecot' and others (Soriano et al. 2008). 'SEO' is the resistant

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resource (Karayiannis et al. 2008), but 'Goldrich' and 'Harcot' are tolerant resources to PPV (Stylianidis et al. 2005). These cultivars are used as donors for resistance in conventional breeding based on the crosses between the PPV-resistant and the local cultivars susceptible to PPV virus throughout Europe (Hurtado et al. 2002; Soriano et al. 2008). Previous study indicates that this PPV resistance mechanism might have been directly or indirectly introduced from non-domesticated species found in China, for example *P. sibirica, P. mandshurica, P. mume, P. sibirica* var. *davidiana* and wild accessions of *P. armeniaca* (Zhebentyayeva et al. 2008). These few sources of resistance share a similar or genetically close progenitor, originating presumably from Northern China (Zhebentyayeva et al. 2008). This limited genetic base for resistance is expected to jeopardize the development of durable and stable resistance to PPV in fields. Therefore, identification of new virus-resistant apricot cultivars is very important for developing modern apricot industry.

To test an interesting individual, 3 years of monitoring are needed after infection to assess the level of resistance/susceptibility to PPV virus (Badenes, Glácer 2006), limiting the selection process of apricot breeding. Molecular characterization of resistance using molecular markers could be a useful new strategy for selection, independent of the factors involved in traditional evaluation methods. So, molecular-assisted selection (MAS) could significantly increase breeding efficiency of detecting new seedlings for early selection. According to previous studies, resistance to PPV is controlled by one major quantitative trait locus (QTL) and possibly one or two other minor QTLs. The major QTLs represent 60% to 70% of the total phenotypic variance and were mapped on the distal part of linkage group 1 (G1) (Lambert et al. 2007; Lalli et al. 2008; Sicard et al. 2008). However, Marandel et al. (2009) reported that four QTLs of PPV resistance were identified, three mapping on G1 and a putative fourth region on G3, explaining between 5% and 39% of the observed phenotypic variance (Marandel et al. 2009). Soriano et al. (2008) suggested that PPV resistance in apricot is controlled by at least major dominant gene located in the upper region of G1, although the involvement of other minor genes cannot be denied. Three SSR markers (ssrPaCITA05, ssrPaCITA17 and aprigms18) linked to PPV resistance were tested for MAS on 18 resistant or susceptible cultivars (Soriano et al. 2008). To search for PPV resistance-associated alleles, Zhebentyayeva et al. (2008) also scanned different geographical groups of apricot cultivars and wild species with five SSR markers linked to the targeted resistance locus. Using a linkage mapping approach, Soriano et al. (2012) found three SSR markers, PGS1.21, PGS1.23 and PGS1.24, tightly linked to PPV resistance trait in the tested progenies. These markers showed allelic variations associated with PPV resistance with no recombinants in the crosses analysed. These markers unambiguously discriminated resistant accessions from the susceptible ones in different genetic backgrounds (Soriano et al. 2012).

In China, the importation of stone fruit trees is under strict phytosanitary control. Although distribution of PPV is mentioned in the European and Mediterranean Plant Protection Organization (EPPO) Bulletin (2006), the PPV epidemic has not been reported in China (Wen et al. 2009). Chinese apricots present a high level of genetic diversity (Zhang et al. 2014), and it is hypothesized that other resistance genes potentially effective against plum pox virus might also exist. So, in this study, 6 SSR primers linked to PPV resistance region in the linkage G1 were used to scan the diverse local apricot varieties in order to examine the allele variation associated with PPV resistance and to analyse the probability of PPV infection in Chinese varieties.

MATERIAL AND METHODS

Plant material. Eighty-six apricot accessions (Table 1) from different areas were used in this study. Plant material came mainly from the germplasm collections maintained at the Chinese Germplasm Repository for Plums and Apricots, and *P. mume* accessions sampled from the Nanjing Agricultural University. The 'Stark Early Orange' and 'Harcot' characterized as resistant to PPV virus (Soriano et al. 2008), were used in the present work.

DNA extraction and primer screening. In 2014, genomic DNA was extracted from fresh young leaves using the modified cetyltrimethylammonium bromide (CTAB) procedure (Doyle 1990). DNA quality was checked with 1% agarose gel, and then diluted DNA was prepared for the 6 SSR marker (ssrPaCITA5, EPDCU5100, pchcms4, PGS1.21, PGS1.23, PGS1.24) analyses, and these SSRs linked

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Table 1. List of apricot accessions analysed using SSR markers and genotypes

Species or types	Code	Name	ssrPaCITA5	EPDCU5100	pchcms4	PGS1.21	PGS1.23	PGS1.24
P. armeniaca	1	Shanmei	**119/119**	168/**170**	223/229	**174**/200	128/128	101/101
	2	Jinmama	**119/119**	168/168	**229/231**	**174**/186	136/136	101/103
	3	Zhanggongyuan	**119/119**	168/168	229/229	186/200	126/126	101/103
	4	Tangwang dajiexing	115/115	168/168	**229/231**	**174**/190	154/137	101/103
	5	Huaxian jiexing	115/131	168/168	223/229	**174**/178	128/128	101/101
	6	Lintong caizihuang	115/131	168/168	223/229	**174**/178	128/128	101/103
	7	Zhupi shuixing	115/115	168/168	**229/231**	**174**/190	154/137	101/101
	8	Caopixing	115/115	168/168	Null	180/184	128/128	101/104
	9	Guangzongxing	**119**/131	168/168	229/230	184/198	136/146	103/103
North China	10	Badouxing	**119**/133	168/168	231/239	186/198	136/146	101/103
	11	Jixian hebao	115/131	168/168	229/229	188/198	146/146	103/103
	12	Shipianhuang	**119**/131	168/**170**	**229/231**	192/192	**142/142**	**99**/103
	13	Shajinhong	115/115	168/168	**223/231**	178/192	128/128	101/103
	14	Guanyinlian	131/133	168/174	229/229	184/188	134/134	123/129
	15	Changguohong	**119**/131	168/168	229/229	192/198	146/154	103/103
	16	Yanhuang No. 1	113/113	168/168	223/223	176/176	136/136	101/101
	17	Zhenxing	**119**/133	168/174	227/229	188/198	146/146	103/121
	18	Pingguobai	115/**119**	168/168	223/231	178/198	128/128	101/101
	19	Lingbao yesheng	131/131	168/168	231/231	194/202	138/138	103/127
	20	631	115/117	168/168	219/231	166/172	158/164	109/113
	21	Dongning No. 2	**119/119**	168/168	227/229	**174**/198	136/137	101/103
	22	Longken No. 2	**119**/133	168/168	**229/231**	**174**/198	136/146	101/103
Northeast China	23	Yitong dahongxing	**119**/131	168/168	**229/231**	184/198	146/150	103/103
	24	Zhongbai	115/**119**	168/168	227/231	**174**/194	136/**142**	101/103
	25	Lurenxing	115/131	168/168	229/229	198/198	136/146	101/103
	26	Longyuan huangxing	133/133	168/168	223/231	**174**/178	136/146	101/132
	27	Longyuan tianxing	133/133	168/168	223/231	**174**/178	136/146	101/132
	28	Zhejiangxing	null	148/148	235/235	172/172	150/150	83/83
	29	Hongqiaoxing	123/123	168/168	231/231	172/172	146/150	103/103
	30	Tongzixing	113/115	168/168	231/232	200/200	131/131	103/103
South China	31	Dahaixing	115/115	168/168	229/235	188/192	154/154	103/103
	32	Guduxing	115/115	168/168	231/231	172/180	null	129/133
	33	Huaqiuxing	**119/119**	156/**170**	229/229	**174**/188	160/160	101/101
	34	Guzanxing	113/115	168/168	229/229	172/186	**142/142**	101/101
	35	Lajiaoxing	**119/119**	**170/170**	**229/231**	176/202	140/140	103/103
	36	Jianali	131/131	168/168	229/230	204/204	131/131	131/133
	37	Kezike ximixi	113/**119**	168/**170**	**229/231**	176/202	140/140	103/103
	38	Saimaiti	115/131	168/**170**	229/229	186/204	**142/142**	101/101
Central Asia	39	Dongxing	131/131	168/168	229/229	204/204	**142/142**	101/133
	40	Tuohutikuda	113/131	168/168	229/229	172/186	140/**142**	101/103
	41	Anjiana	**119/119**	168/**170**	229/229	188/188	**142/142**	**99/99**
	42	Maolaxiao	113/**119**	168/168	229/229	172/200	140/140	101/103
	43	xiaoyexing	115/**119**	168/**170**	231/231	176/190	140/140	103/103
	44	Armenia No. 2	115/131	168/168	**229/231**	**174**/198	132/140	**99**/128

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Table 1 to be continued

Species or types	Code	Name	ssrPaCITA5	EPDCU5100	pchcms4	PGS1.21	PGS1.23	PGS1.24
Central Asia	45	Armenia No. 3	115/131	168/168	**229/231**	**174**/198	132/140	**99**/128
	46	Armenia No. 1	**119**/127	168/168	223/231	194/204	124/144	116/138
	47	Hacihaliloglu	115/115	168/168	223/231	178/200	128/128	101/103
European cultivars	48	Moorpark	131/131	168/168	225/225	**174/174**	136/136	101/101
	49	Harcot	**119**/131	**170**/176	231/231	**174**/188	140/140	101/107
	50	SEO	**119**/133	**170**/176	**229/231**	**174/174**	**142/142**	**99**/101
	51	Leala	**119**/133	**170**/176	**229/231**	180/180	**142/142**	**99**/101
	52	Watikiws	115/131	168/168	225/229	**174**/190	136/154	101/103
Kernel-using	53	Beishan dabian	115/**119**	168/168	**229/231**	**174**/190	130/154	**99**/103
	54	Longwangmao	**119**/131	168/168	227/229	**174**/196	132/140	**99/ 99**
	55	Sanganqi	**119**/131	168/168	229/229	**174**/192	132/154	101/116
	56	Yiwofeng	**119**/131	168/168	227/229	**174**/196	132/140	**99**/116
	57	Baiyubian	127/131	168/168	227/229	**174**/194	132/140	**99**/114
P. limeixing	58	Limixing	118/131	168/174	221/229	160/200	146/146	103/107
	59	Changli xingmei	118/125	168/168	**229/231**	160/198	152/160	97/97
	60	Tancheng xingmei	118/125	168/168	**229/231**	160/198	152/160	97/97
	61	Taian xingmei	118/131	168/174	221/229	160/200	134/146	103/107
	62	Hongmeixing	118/131	168/**170**	221/225	160/**174**	137/137	101/116
	63	Mu No. 3	118/131	168/**170**	221/225	160/**174**	136/121	101/116
P. mume	64	Yanxingmei	**119**/133	168/168	227/229	178/198	128/158	103/103
	65	Ruantiaohongmei	123/123	**170/170**	223/223	**174**/202	146/146	117/117
	66	Dayumei	123/123	**170/170**	223/223	**174**/184	140/146	139/143
	67	Lve	123/123	**170/170**	223/223	198/204	140/146	139/143
P. sibirica	68	Chuizhixing	115/121	168/168	227/231	**174**/196	138/160	101/125
	69	Dashanxing	**119**/131	168/168	223/227	188/200	128/128	101/101
	70	Liaomei	**119/119**	168/168	227/227	192/194	136/136	112/119
	71	Xiongyue shanxing	**119**/127	168/168	225/227	194/194	134/134	114/131
	72	Shan No. 1	**119**/127	168/168	225/225	192/212	142/154	103/112
	73	Shan No. 2	**119/119**	168/168	227/229	192/192	134/134	110/114
P. mandshurica	74	Liaoxing	**119**/131	168/168	229/233	172/192	150/154	103/103
	75	chaoxing	**119**/131	168/168	229/233	172/192	150/154	103/103
	76	Liao No. 1	117/117	168/168	225/227	184/186	144/148	110/174
	77	Liao No. 2	115/**119**	168/168	217/217	182/190	150/158	108/108
	78	Liao No. 3	117/117	168/168	217/235	null	136/136	108/108
	79	Liao No. 5	**119**/133	168/168	223/229	198/204	146/158	103/112
	80	Liao No. 6	**119/119**	168/168	**229/231**	**174/174**	136/136	101/101
P. brigantiaca	81	Fa No. 2	115/116	168/168	223/225	172/172	123/123	92/92
	82	Fa No. 3	115/116	168/168	223/225	172/172	122/122	92/92
	83	Fa No. 5	115/116	168/168	223/225	172/172	122/122	92/92
P. zhengbeensis	84	Zang No. 1	115/129	174/178	225/227	172/172	148/148	130/136
P. dasycarpa	85	Zi No. 1	113/117	168/168	229/229	186/218	156/156	101/112
P. holosericea	86	Zheng No. 1	**119/119**	168/168	225/225	190/204	164/131	130/134

resistant alleles from those SSR co-segregating with PPV resistance are in bold

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to PPV resistance region in the linkage G1 of apricot genetic map (Lambert et al. 2007; Soriano et al. 2008; 2012; Rubio et al. 2014).

PCR amplification and electrophoresis. PCR amplification was carried out in a total volume of 20 µl containing about 100 ng of template DNA, 10 µl of 2 × Taq Mix Master (Beijing Cowin Biotech Co., Ltd., Changping, Beijing, China), 0.2 µM of both the forward primer and reverse primer (the forward was labelled by fluorochrome). Amplifications were performed on a MasterCycler, with the following conditions: 5 min initial denaturation step at 94°C, then 35 cycles at 94°C for 40 s, annealing temperature at 56°C (±2°C) for 40 s, and 72°C for 45 s, and a final extension at 72°C for 5 minutes. Subsequently, the PCR products were analysed by automated sequencer capillary electrophoresis using ABI 3500XL (Applied Biosystems, Carlsbad, USA).

RESULTS AND DISCUSSION

Polymorphism of SSR

The apricot accessions were tested with 6 primers of SSR markers linked to PPV resistance in apricot (Soriano et al. 2012; Rubio et al. 2014). An extensive range of amplified fragments from 83 to 239 bp were displayed among 86 apricot accessions. The number of amplified alleles was 13 for ssrPaCITA5, 7 for EPDCU5100, 13 for pchcms4, 21 for PGS1.21, 25 for PGS1.23, and 32 for PGS1.24 (Table 1). However, the number of amplified alleles among 80 genotypes (including resistant and susceptible ones), was only 5 for PGS1.21, 6 for PGS1.23, 5 for PGS1.24, and 4 for pchcms4 (Rubio et al. 2014).

In this study, the average number of alleles per locus was 18.5 in 6 detected SSRs markers linked to PPV. The value was higher than the mean value of 11.83 alleles per locus in whole G1 linkage group by Pedryc et al. (2009), and also higher than 13.30 allele/locus (Maghuly et al. 2005) and 15.14 allele/locus (Zhang et al. 2014) among different geographical groups. These results may be attributed to the great genetic diversity of tested accessions and the PPV resistance locus remains relatively high polymorphic.

Resistant alleles of each SSR locus among different populations

Table 1 shows the accessions studied, their origin and genotypes for the polymorphic loci. The ssrPaCITA5 locus produced 13 alleles in apricot accessions. The resistant genotypes of 'SEO' displayed allele 119 and 133, and those of 'Harcot' displayed 119/131. According to the study of Soriano et al. (2008), the allele of 119-bp was probably associated with resistance. For ssrPaCITA5-119, the homozygote occurred in 5 Chinese cultivars, 2 Central Asia cultivars, 3 accessions of *P. sibirica*, and one accession of *P. mandshurica* (Table 2). Four of the five accessions in kernel-using apricot were as heterozygote. The heterozygote also occurred in nine Chinese cultivars, 4 Central Asia cultivars, 3 accessions of *P. sibirica*, 4 accessions of *P. mandshurica*, and only one cultivar of *P. mume*. It is noteworthy that the 119 allele was common in *P. sibirica* and *P. mandshurica*, but did not occur in *P. limeixing*.

Seven alleles were observed in the EDPCU1500 marker, and the resistant genotypes of cvs 'SEO'

Table 2. Number of genotypes with resistant allele of each SSR locus among different populations

Alleles/ genotypes	Chinese cultivars		Central Asia cultivars		Kernel-using apricot		*P. mume*		*P. sibirica*		*P. mandshurica*		*P. limeixing*	
	Hm	Ht	Hm	Ht	Hm	Ht	Hm	Ht	Hm	Ht	Hm	Ht	Hm	Ht
Total genotypes	34		13		5		4		6		7		6	
ssrPaCITA5-119	5	9	2	4	0	4	0	1	2	3	1	4	0	0
EDPCU1500-170	0	3	1	4	0	0	3	0	0	0	0	0	0	2
pchcms4-229/331	–	6	–	4	–	1	–	0	–	0	–	1	–	2
PGS1.21-174	0	12	0	2	0	5	0	2	0	0	1	0	0	2
PGS1.23-142	2	1	3	1	0	0	0	0	0	1	0	0	0	0
PGS1.24-99	0	1	1	2	3	1	0	0	0	0	0	0	0	0

Hm – homozygous; Ht – heterozygous

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and 'Harcot' both displayed alleles 170 and 176. According to Soriano et al. (2008), the allele of 170-bp may be associated with resistance. For EDPCU1500-170, the homozygous form only occurred in one Central Asia cultivar and three cultivars of *P. mume* (Table 2), while the heterozygous form occurred in 3 Chinese cultivars, 4 Central Asia cultivars, and 2 *P. limeixing.* The allele of EDPCU1500-170 was not detected in wild varieties of *P. sibirica* and *P. mandshurica*, which was also indicated in the study of Soriano et al. (2008).

The pchcms4 markers located in G1 were closely related to the PPV resistance locus in apricot described by Lambert et al. (2007), which produced thirteen alleles in apricot accessions in this study. The genotype of 'SEO' was 229/231, while the genotype of 'Harcot' was 231/231. The allele size of pchcms4 locus in this study was 229 instead of 234 bp, which was different from that described by Rubio et al. (2014). The highest frequency of allele in all accessions was 37.5% (229 bp), followed by 23% (231 bp). However, the genotype of 229/331 was uncommon, only found 6 in Chinese cultivars, 4 in Central Asia cultivars, 2 in *P. limeixing*, only one in kernel-using apricot and in *P. mandshurica*, and it none in *P. mume* and *P. sibirica* (Table 2). However, it is indicated that this allele must be discarded because it is present in almost 50% of susceptible cultivars (Rubio et al. 2014).

In this study, the PGS1.21, PGS1.23, and PGS1.24 locus produced 21, 25 and 33 alleles respectively. Previously, Soriano et al. (2012) and Rubio et al. (2014) tested resistant allele combination in all resistant cultivars. However, in this study it was observed that this allele was 142 bp in PGS1.23 (instead of 147 bp), 99 bp in PGS1.24 (instead of 101 bp), and 174 bp in PGS1.21 (instead of 181 bp). The genotype of resistant cultivars 'SEO' was 181/226 (Rubio et al. 2014) in PGS1.21 locus, while in this study the genotype was 174/174. The allele of PGS1.21-174 was the most frequent allele in kernel-using apricot cultivars, but it was absent in *P. sibirica;* it was a heterozygous state in this study except one accession of *P. mandshurica*. The allele of PGS1.23-142 occurred in Central Asia cultivars (3 homozygote and 1 heterozygote) and Chinese cultivars (2 homozygote and 1 heterozygote) but did not occur in kernel-using apricot, *P. limeixing*, *P. mume* and *P. mandshurica*. The allele of PGS1.24-99 most frequently occurred in kernel-using apricot cultivars, following by Central Asia cultivars, but it did not occur in *P. limeixing*, *P. mume*, *P. mandshurica* and *P. sibirica*.

The original genitor that brought resistance to PPV displayed a significant high requirement for winter chilling (Badenes et al. 1996). Zhebentyayeva et al. (2008) pointed out potential contributions of Chinese cultivars and non-domesticated species *P. mume*, *P. mandshurica*, and *P. sibirica* to PPV resistant genotypes. In fact, most cultivars of apricot in South China have similar agronomic traits with *P. mume*, such as low chilling requirements in winter. In this study, three of the four accessions in *P. mume* were as homozygote of EDPCU1500-170 allele, and only 2 accessions had the resistant alleles in two loci. There are at least three loci resistant alleles that were detected in six accessions of Chinese apricot group, in five of thirteen accessions of Central Asia group and in three-fifths accessions in kernel-using apricots. However, these resistant alleles rarely occurred in wild forms of *P. sibirica* and *P. mandshurica* except ssrPaCITA5-119 bp in this study. Therefore, it was considered that this resistance gene found in present might have been directly introduced from cultivars or wild forms of *P. armeniaca*, rather than from non-domesticated species in *P. mandshurica* or *P. sibirica.*

Noteworthy, the frequency of resistant allele in the Chinese cultivars was high in ssrPaCITA5 and PGS1.21 loci, but low in EDPCU1500, PGS1.23 and PGS1.24 loci. Some famous local cultivars, such as 'Shajinhong', 'Caopixing', 'Jixian hebao' , 'Guanyinlian', 'Yanhuang No. 1' and 'Huaxian jiexing', were more likely to infect with PPV. In six loci tested, namely 'Shipianhuang', 'Huaqiuxing', 'Jinmama', 'Shanmei', 'Longken No. 2' and 'Zhongbai' three and more loci had detected resistance alleles.

Novel allele and other alleles of SSR locus among different populations

In ssrPaCITA5 locus, the frequencies of alleles 119, 131 and 115 were 30, 21 and 19 % respectively in all apricot accessions. The allele 118 of ssrPaCITA5 locus was private allele in *P. limeixing* (frequency was 50%), and it was derived from *P. salicina* L. (Liu et al. 2010). The ssrPaCITA5-119 bp was a common allele in wild form of *P. mandshurica* and *P. sibirica* in this study, which was evidence that resistance genes might originated from *P. mandshurica* or *P. sibirica* as reported by Soriano et al.

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(2008). The allele distribution of ssrPaCITA5 locus was similar in Central Asia group and North China group. However, the 115 allele occurred at high frequency in South China group, and the 113 allele was common in *P. mume*.

For EDPCU1500 locus, all Northeast China cultivars and kernel-using apricot cultivars were homozygotes of the 168 allele, and 90% of North China group were homozygotes of the 168 allele. The 168 allele occurred in a homozygous state in most accessions studied, while the 148 bp and 156 bp were as private alleles appeared in South China group.

PGS1.24, the highest frequency of the 101 and 103 allele was both 30%. These two were common alleles in North China group, Northeast China group, South China group and Central Asia group. The allelic variation, of *P. mandshurica* (108, 110, and 112 bp), *P. mume* (117, 139, and 143 bp), and *P. sibirica* (119, 125, and 131 bp), was mainly distributed in more than 108 bp. It is noteworthy that 'Zhejiangxing' cv. of South China group was tested as a homozygous genotype of the 83 allele.

CONCLUSION

In conclusion, a high level of genetic variation was found in Chinese apricot accessions by the six SSR markers linked to PPV resistance. The observed specific alleles could be useful for future studies in apricot breeding. The South cultivar group and wild species of *P. mandshurica* or *P. sibirica* had a novel allelic variation and might be a unique genetic source for selection of PPV resistance in breeding programs. The results of the present study indicated that Sharka disease was not currently prevalent in Chinese apricots, but many local varieties might be proven susceptible to PPV virus. Therefore, it is important to broaden the genetic base of PPV resistance in future apricot cultivars by pyramiding multiple PPV resistance genes. Marker-assisted selection could greatly facilitate the transfer of needed PPV-resistant genes, markers and their frequencies described in this study, which provide a basis for developing of MAS protocols.

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