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POPULATION GENETIC DIVERSITY AND STRUCTURE ANALYSIS OF WILD APRICOT (PRUNUS ARMENIACA L.) REVEALED BY SSR MARKERS IN THE TIEN-SHAN MOUNTAINS OF CHINA

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Abstract

The simple sequence repeat markers were used to investigate the population genetic diversity and structure of 212 germplasm samples from 14 apricot (*Prunus armeniaca*) populations in the western of Tien-Shan Mountains, Sinkiang, China. The relatively high expected heterozygosity and Shannon's diversity index indicated the apricot populations maintained a high level of genetic diversity (He = 0.6109, I = 1.2208), with the population in Tuergen ditch of Xinyuan County having the highest genetic diversity index. A high level of intra-population genetic differentiation (91.51%) and a lower level of inter-population genetic differentiation were occurred, as well as a moderate but steady inter-population gene flow (Nm = 2.3735). The self-incompatible pattern, wide distribution, and long-distance pollen transmission via insects and gale are the main factors underlying the genetic variation structure. The UPGMA cluster analysis and genetic structure analysis showed that apricot germplasm could be divided into two or four groups, which was basically consistent with the geographic distribution pattern. The inter-population genetic distance and geographic distance showed a significant correlation ($r = 0.2658$, $p<0.05$).

Key words: Apricot, Genetic diversity, Population structure, *Prunus armeniaca*.

Introduction

Genetic diversity is the core of biological diversity, and the presence of genetic diversity is essential to ensure thelong-term adaptation of plants to the constantly changing ecological environment (Sreekanth *et al*., 2012; Pauls *et al*., 2013). Collecting wild germplasm resources and investigating their genetic diversity information are very important for the protection of endangered plant resources and genetic breeding implement (Dawson *et al*., 2013; Li *et al*., 2014; Nasir *et al*., 2017). Apricot belongs to Rosaceae family, *Prunus* genus and section *Armeniaca*, which is a diploid temperate deciduous fruit tree with widely distributed in the world (Zhang *et al*., 2014). Apricot was cultivated for more than 2,000 years in China, China and Central Asia (from the Tien-Shan Mountains to Kashmir) and were considered as the two-original cultivation center in the word (Hormaza *et al*., 2007). The Tien-Shan Mountains was mainly occurs in Xinjiang, China, and the Ili river flows through the bottom of the mountains. The valleys located in the western of Tien-Shan Mountains has a very unique geographic location, with three sides surrounded by mountains and one open side having the warm air from the ocean to the west (Wang *et al*., 2015). This location has led to the formation of an oceanic deciduous broadleaf forest community that is present in the Central Asian desert (Xu *et al*., 2010). The wild fruit forest in the valley is a relict community from warm temperate broadleaf forests in the 3rd century and is an important source of origin for many cultivated temperate fruit trees (Xu *et al*., 2011; Yan *et al*., 2008). The wild apricot, which belongs to the common apricot (*Prunus armeniaca* L.) species is the main tree species distributed up to 11,355 hm^2 on the two sides of valleys (Hou & Xu, 2004).

The wild apricot populations are currently only growing in Central Asia, and the domesticated apricot are thought to originate in Asia about five thousand years ago (Decroocq *et al*., 2016). Thus, the western Tien-Shan apricot populations are considered to be the oldest genotypes and play an important role on apricot spread and domestication from Central Asia to more westerly regions (Zhebentyayeva *et al*., 2012). (He *et al.*, 2007) reported that the wild apricots in Ili valley were the direct ancestors of cultivated apricots in South Sinkiang and provided an ancestral gene pool for central Asian apricot domestication. Based on morphological and molecular data, (Zhebentyayeva *et al.*, 2003) also recommended the apricot in the Tien-Shan Mountains was one of the two primary centers of origin for the common apricot. The apricot germplasm disseminated from here eastward to the germplasm gene pool of the North China apricot ecological group and westward to the majority of the Tien-Shan area and arrived in Europe and other western regions along the Silk Road, leading to the formation of ecological groups in Iran-Transcaucasia, Europe and other areas (Zhebentyayeva *et al.*, 2012, Yuan *et al.*, 2007).

In view of the vital and historical genetic germplasm resources, the wild apricot was selected as a national key protected plant since 1984. However, overgrazing, tourism development and spreading of apricot bacterial spot disease have posed serious threats to the growth and natural regeneration of apricot in recent years, causing in gradual shrinking areas of apricot distribution, the gradual disappearance of some germplasms, and a huge loss of genetic diversity of resources (Feng *et al.*, 2015, Li *et al.*, 2013). Strengthening the study of population genetic diversity and structure is of great significance for the protection and breeding utilization of this rare resource (Liu *et al.*, 2015, Peng *et al.*, 2014). In this study, we used

simple sequence repeats (SSR) markers to characterize the apricot germplasm in the valleys of the Tien-Shan Mountains. The results will help to (1) assess the genetic diversity, (2) analyze the genetic structure and genetic differentiation of apricot populations, and (3) provide a reference for the protection of apricot germplasm in the Tien-Shan Mountains of China.

Materials and Methods

Totally 212 apricot germplasm accessions were collected from 14 populations in four counties in the Tien-Shan Mountains (Fig. 1, Table 1). Each population was collected over 3 km apart from each other, and each accession was 50 meters apart from each other. Mature seeds of each sample were collected, and the testa, a maternal inherited tissue, was used for DNA extraction.

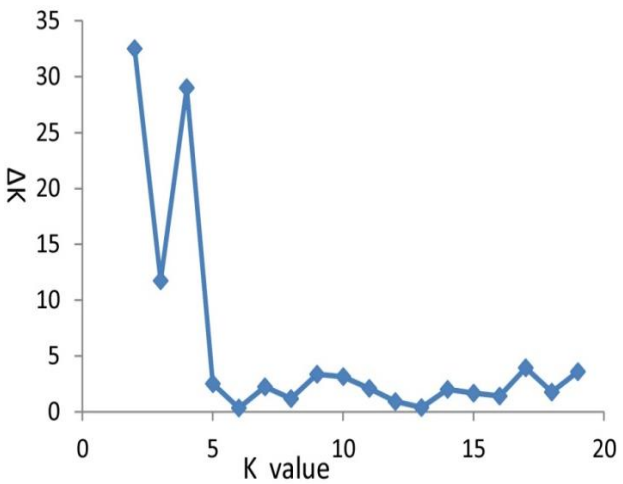

Fig. 1. Delta K values for different numbers of populations assumed (K) in the Structure analysis.

Standard protocols for extracting genomic DNA from testa was performed according to (Martin *et al.*, 2011), and the DNA purity and concentration was checked using the Nano Photometer® spectrophotometer (IMPLEN, CA, USA). Ten SSR primers were used to amplify the genomic DNA by polymerase chain reaction (Table 2). The ABI-Veriti 96-well gradient PCR instrument (Applied Biosystems, Foster, CA, USA) was used for the DNA amplification reactions. The 15-μL PCR reaction mixture contained 30 ng genomic DNA, 20 mM Tris-HCl pH 8.4, 50 mMKCl, 3.0 mM $MgCl_2$, 0.25 mM forward and reverse primers, 0.4 mM of each dNTP and 1.0 U Taq DNA polymerase (Invitrogen, CA, USA). The PCR amplification program was subjected to an initial 3 minutes denaturation at 95°C; and followed by 35 cycles for 94°C (30 sec) and 51-57°C (30 sec) and 72°C (60 sec); and a final extension step 72°C 5 min. The 6% degeneration PAGE gel electrophoresis was used to separate the PCR products. After silver staining, the gels were transferred on the fluorescent plate to assessed and recorded the genotypes.

Statistics were performed on the SSR profiles, all clearly detectable polymorphic and monomorphic bands were scored to analysis the allelic composition. The genetic diversity parameters of the number of alleles (n_a), effective number of alleles (n_e), Shannon-Weaver index (I) (Nei 1973, Shannon 2001), observed heterozygosity (Ho) and expected heterozygosity (He) were estimated using POPGENE 1.32 (Yeh *et al.*, 1999). The population genetic differentiation coefficient (F_{st}) and gene flow (N_m) were calculated, and the inter-population UPGMA phylogenetic tree was constructed by POPGENE 1.32. The molecular variance analysis of population genetic differentiation was performed by GenAlEx 6.5 (Peakall & Smouse 2012). The correlation analysis between genetic divergence and geographic distance among populations was calculated by the Mantel test function in GenAlEx 6.5.

The structure 2.3.4 software based on Bayesian clustering was used to infer genetic population structure (Falush *et al*., 2007). The K values (the number of sub-groups) was assumed by 7 independent runs for each K (from 2 to 20) by using the admixture model with 100,000 Markov chain Monte Carlo (MCMC) repetitions and a 100,000 burn-in period. To identify the most probable sub-groups (K) that would best fit with the model, a ΔK index was calculated using the formula of Ä ΔK=|L″(K)|/s[Pr(x|k)], which was described by (Evanno *et al*., 2005).

Table 1. Geographic locations of the 14 apricot populations.

Population	Sample size	Altitude (m)	Latitude	Longitude	Sampling locations
Xia	10	1153	44.4367°N	80.7844°E	Downstream of the great west ditch, Huocheng County
Shang	15	1169	44.4106°N	80.7853°E	Upstream of the great west ditch, Huocheng County
Ma	15	1307	44.4231°N	80.7561°E	Mazi ditch, Huocheng County
Guo	15	1193	44.3572°N	80.9828°E	Guozhi ditch, Huocheng County
Pi	17	1124	44.1553°N	81.5175°E	Piliqin ditch, Yining County
Ji	15	961	44.0497°N	81.5369°E	Jiligelang ditch, Yining County
Qiong	18	972	43.8117°N	81.9497°E	Qiongbulake ditch, Yining County
Xiao	20	1321	43.2133°N	82.7256°E	South Mohuer farm, Gongliu County
Da	20	1277	43.2417°N	82.7422°E	North Mohuer farm, Gongliu County
Ba	10	1233	43.2533°N	82.8431°E	Ba village, Gongliu County
Jin	10	935	43.4358°N	83.2417°E	Jinshanxiao township, Xinyuan County
Tu	25	1008	43.5433°N	83.4822°E	Tuergen ditch, Xinyuan County
Ze	12	1024	43.5542°N	83.3272°E	Zeketai township, Xinyuan County
Ye	10	1304	43.3806°N	83.5758°E	Wild fruit forest, Xinyuan County

Table 2. List of SSR primers and genetic diversity parameters in this study.

Primer	Reference	SSR motive	Annealing temp (°C)	n_a	n_e	Ho	He	*I*	*Fst*	*Nm*
AMPA101	(Hagen *et al*., 2004)	$(TC)_{11}(AC)_{12}$	56	5	4.0764	0.6604	0.7565	1.5027	0.0741	3.1260
AMPA119	(Hagen *et al*., 2004)	$(TA)_9$	57	7	4.9216	0.5943	0.7987	1.7150	0.1677	1.2408
BPPCT039	(Dirlewanger *et al*., 2002)	$(GA)_{20}$	55	5	3.8544	0.7358	0.7423	1.4642	0.0731	3.1686
pchgms3	(Sosinski *et al*., 2000)	$(CT)_{19}$	57	5	4.6829	0.5896	0.7883	1.5728	0.0732	3.1665
pchgms5	(Sosinski *et al*., 2000)	$(CA)_9(TA)_8$	51	2	1.0834	0.0519	0.0772	0.1682	0.1405	1.5297
ssrPaCITA23	(Lopes *et al*., 2002)	$(AC)_2(AG)_{18}$	51	7	4.3888	0.8443	0.774	1.6593	0.0565	4.1759
UDAp-414	(Messina *et al*., 2004)	$(AG)_{21}$	56	4	3.3175	0.6226	0.7002	1.2900	0.0736	3.1482
UDAp-415	(Messina *et al*., 2004)	$(GA)_{21}$	56	4	3.5895	0.5047	0.7231	1.3273	0.0493	4.8159
UDAp-420	(Messina *et al*., 2004)	$(CT)_{20}$	56	5	3.4489	0.9151	0.7117	1.4149	0.0550	4.2928
UDP96-001	(Cipriani *et al*., 1999)	$(CA)_{17}$	57	2	1.0384	0.0094	0.0371	0.0936	0.1503	1.4135
Mean	-	-	-	4.6	3.4402	0.5528	0.6109	1.2208	0.0953	2.3735

Table 3. Genetic diversity parameters of the 14 apricot populations.

Population	n_a	n_e	Ho	He	*I*
Xia	3.1	2.2606	0.4700	0.5068	0.8489
Shang	3.7	2.5326	0.5200	0.5310	0.9525
Ma	3.8	2.7336	0.5667	0.5577	1.0012
Guo	4.1	2.9494	0.6200	0.5793	1.0720
Pi	3.7	3.0427	0.5529	0.5909	1.0741
Ji	4.0	3.0399	0.6400	0.5738	1.0704
Qiong	4.0	3.1747	0.5611	0.5940	1.1163
Xiao	4.1	3.2513	0.5050	0.6055	1.1448
Da	4.1	3.1029	0.5600	0.5940	1.1077
Ba	3.9	2.9781	0.6300	0.5926	1.0806
Jin	3.6	2.4632	0.4200	0.5163	0.9166
Tu	4.5	3.1526	0.5800	0.6423	1.2105
Ze	3.9	3.0123	0.5167	0.5866	1.0785
Ye	4.1	2.8814	0.5300	0.6037	1.1052
Mean	4.6	3.4402	0.5528	0.6109	1.2208

Table 4. Genetic differentiation and molecular variance analysis of apricot populations.

Source of variance	Degree of freedom (df)	Sum of squared differences (SSD)	Mean squared deviation (MSD)	Variance component	Variance ratio	P-value
Inter-population	13	191.987	14.768	0.572	8.49%	< 0.001
Intra-population	198	1220.159	6.162	6.162	91.51%	

Results

Genetic diversity analysis: The 10 SSR primers amplified 46 alleles, and each primer pair amplified 3.4402 effective alleles (Table 3). The AMPA119 primer amplified the largest number of alleles and effective alleles (7 and 4.9216, respectively), and also performed the highest genetic diversity parameters (He= 0.7987, *I* =1.7150). The pchgms5 and UDP96-001 primers amplified the lowest numbers of alleles and the lowest numbers of effective alleles, 1.0834 and 1.0384, respectively. Similarly, the pchgms5 and UDP96-001 primers revealed relatively low He and *I* value, whereas the other primers all showed high genetic diversity index levels. Table 3 shows the genetic diversity of 14 apricot populations in the Tien-Shan Mountains, in which the population Tu had the highest genetic diversity (He = 0.6423, *I* = 1.2105) and the population Xia had the lowest diversity parameters (He = 0.5068, *I* = 0.8489). At the species level, the genetic diversity parameters showed great increases, wherein the average Ho was 0.5528, He was 0.6109 and *I* was 1.2208. The fairly high genetic diversity indices support that the apricot population in the Tien-Shan Mountains still maintain a high level of genetic diversity.

Genetic differentiation analysis: The population genetic differentiation index was calculated by POPGENE 1.32 software revealed the differentiation coefficient (F_{ST}) was 0.0953 and gene flow (N_m) was 2.3735 (Table 4). The AMOVA based on GenAlEx 6.5 software revealed the inter-population genetic differentiation accounted for 8.49% of all genetic differentiation, whereas the intra-population genetic differentiation accounted for 91.51% of all genetic differentiation. The genetic differentiation analysis revealed there were high levels of intra-population differentiation and low levels of inter-population differentiation in wild apricot populations, which was consistent with the moderate but steady gene flow among the populations (Table 5).

Table 5. Nei'sunbiased genetic identity (above diagonal) and genetic distance (below diagonal) among apricot populations.

Population	Xia	Shang	Ma	Guo	Pi	Ji	Qiong	Xiao	Da	Ba	Jin	Tu	Ze	Ye
Xia	-	0.9623	0.947	0.9854	0.8198	0.7997	0.8607	0.8658	0.8937	0.8833	0.8335	0.8615	0.9136	0.8636
Shang	0.0384	-	0.9892	0.9849	0.8575	0.8369	0.8707	0.907	0.9267	0.906	0.8768	0.8911	0.9195	0.893
Ma	0.0545	0.0108	-	0.9871	0.8554	0.8353	0.8791	0.9226	0.9339	0.9331	0.9111	0.9229	0.9449	0.9027
Guo	0.0147	0.0152	0.0129	-	0.8744	0.8567	0.9001	0.9345	0.9417	0.9464	0.8987	0.9171	0.9517	0.9187
Pi	0.1987	0.1538	0.1562	0.1342	-	0.987	0.9736	0.9741	0.9779	0.9253	0.7755	0.8334	0.8903	0.8331
Ji	0.2235	0.1781	0.18	0.1547	0.0131	-	0.9882	0.9605	0.9727	0.9153	0.8043	0.8118	0.8623	0.8245
Qiong	0.1501	0.1385	0.1288	0.1052	0.0268	0.0119	-	0.9715	0.9728	0.937	0.8377	0.8569	0.9042	0.854
Xiao	0.1441	0.0976	0.0805	0.0677	0.0262	0.0403	0.0289	-	0.9913	0.9661	0.85	0.8998	0.9232	0.8846
Da	0.1124	0.0761	0.0684	0.0601	0.0223	0.0277	0.0276	0.0088	-	0.9862	0.8565	0.8873	0.9328	0.8772
Ba	0.1241	0.0987	0.0693	0.0551	0.0777	0.0885	0.0651	0.0345	0.0139	-	0.8555	0.8935	0.9449	0.8786
Jin	0.1822	0.1314	0.0931	0.1068	0.2543	0.2178	0.1771	0.1625	0.155	0.1561	-	0.9189	0.9315	0.9279
Tu	0.149	0.1153	0.0803	0.0866	0.1823	0.2085	0.1545	0.1056	0.1196	0.1127	0.0846	-	0.9545	0.9626
Ze	0.0904	0.0839	0.0567	0.0495	0.1162	0.1482	0.1007	0.0799	0.0696	0.0567	0.0709	0.0466	-	0.9487
Ye	0.1467	0.1132	0.1024	0.0848	0.1826	0.193	0.1578	0.1226	0.131	0.1294	0.0748	0.0381	0.0527	-

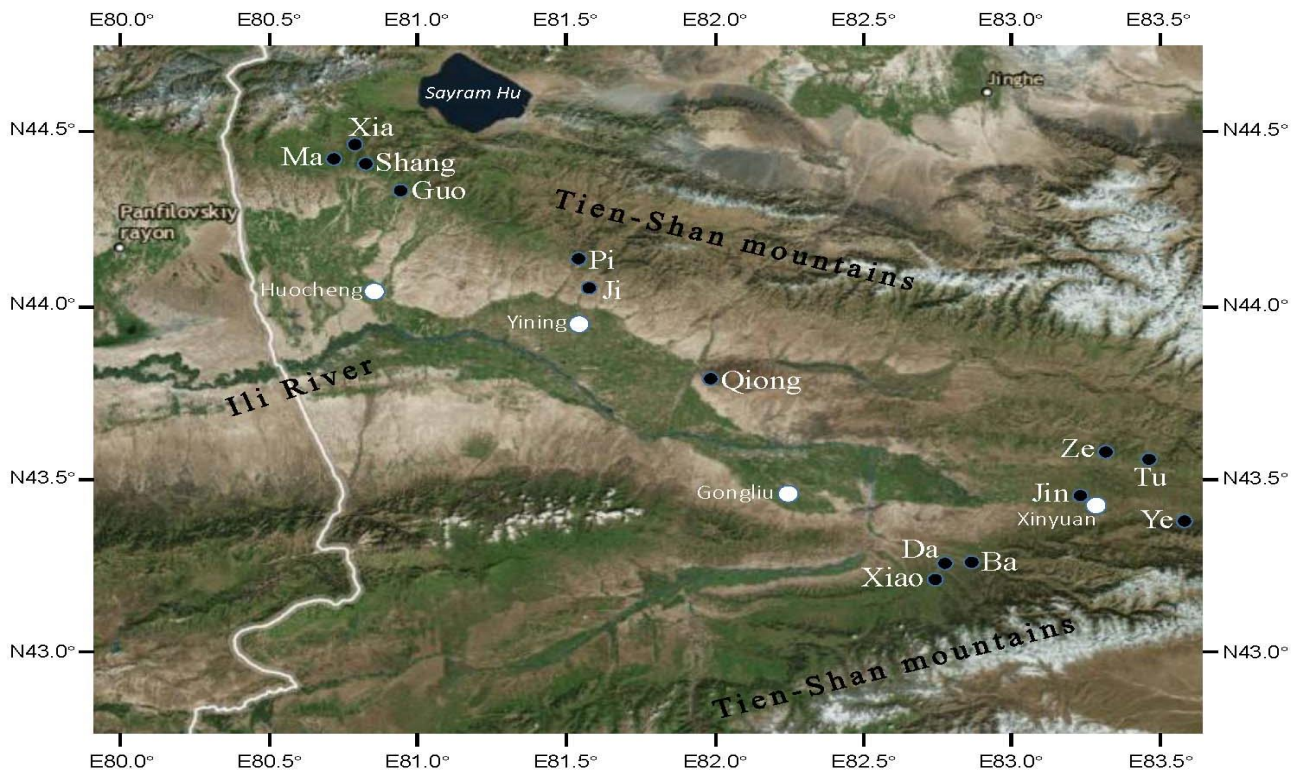

Fig. 2. Area of distribution of 14 wild apricot populations.

Population structure and cluster analysis: The ΔK value corresponding to each K value was calculated and established the corresponding scatter plot (Fig. 2). The results show that the maximum ΔK value occurs when K = 2 and that the ΔK value is also large when K = 4, indicating the entire apricot population can be divided into two or four sub-groups according to the genetic structure analysis (Fig. 3). When K = 2, the genetic structure of eight populations in Huocheng County and Xinyuan County were more closely related to one another, whereas the genetic structure of the six populations in Yining County and Gongliu County were more closely related to one another. When K = 4, the four sub-groups could be divided as follows with group I includes four populations in Huocheng County (Xia, Shang, Ma, and Guo), group II includes four populations in Xinyuan County (Jin, Tu, Ze and Ye), group III includes three populations in Yining County (Pi, Ji and Qiong), and group IV includes three populations in Gongliu County (Xiao, Da and Ba). The UPGMA cluster analysis also revealed the existence of four sub-groups in the wild apricot populations, and the grouping results were similar to those of the population genetic structure analysis. Overall, the grouping results of the four groups are basically consistent with the geographic distribution patterns of the counties where the populations are located. The populations in the same group belong to the same county, suggesting that the genetic differences and geographical distribution of apricot populations are likely to be relevant. The Mantel test performed by GenAlEx 6.5 showed a significant positive correlation ($r = 0.2658$, $p<0.05$) among the populations genetic divergence and geographic distance matrices.

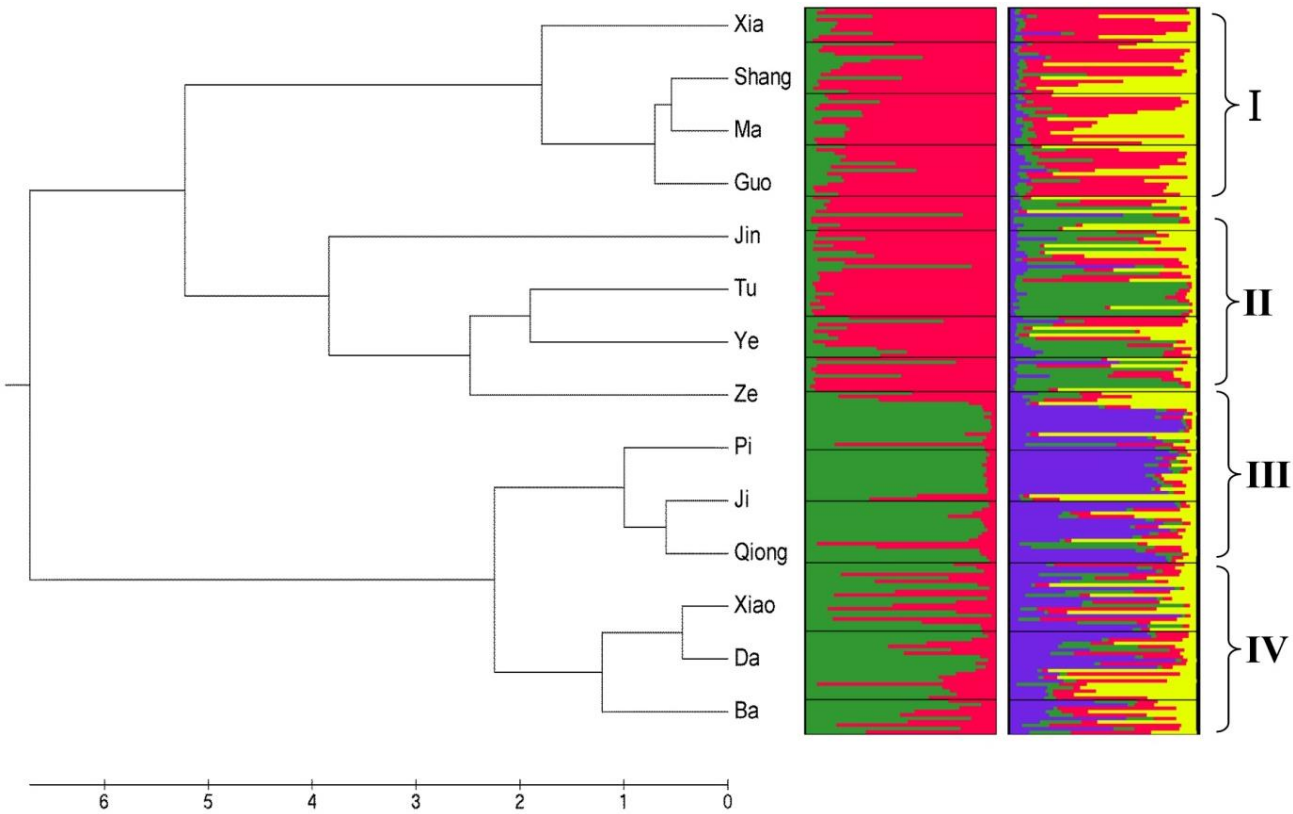

Fig. 3. Clustering of 14 apricot populations based on the UPGMA and Structure analysis.

Discussion

Genetic diversity analysis: In contrast to previous studies of apricot, the population genetic diversity of wild apricot in the Tien-Shan Mountains maintained at a fairly high level (He = 0.6109, I = 1.2208), which was higher than that of apricot germplasms in the Mediterranean Maghreb region (He = 0.593) and similar to the European apricot (He = 0.645) (Bourguiba *et al.*, 2012, Zhebentyayeva *et al.*, 2003). Compared to the wild Siberian apricot (He = 0.713, I = 1.3278), the genetic diversity of apricot in the Tien-Shan Mountains is relatively low, which may be the result of years of deforestation, overgrazing, and reduced areas of apricot resources, leading to reduced population genetic diversity (Li *et al.*, 2014). (He *et al.*, 2007) used SSR markers to investigate the genetic diversity of 81 germplasm samples from three apricot populations in Xinyuan, Gongliu and Daxigou. The result showed that the entire population of expected heterozygosity was 0.287 andShannon-Weaver index was 0.428, which were significantly lower than the results of this study, and may be explained by the relatively low number of regions and samples. In the field survey, we found that the vast majority of apricot germplasms had the characteristics of self-incompatibility and for a long time relied on seedlings from seeds for propagation, which increased the genetic diversity to a large extent (Peng *et al.*, 2014). Relatively high genetic diversity also confirms the status of wild apricot in Tien-shanmountains as the center of origin for cultivated apricot.

Genetic differentiation analysis: There is a high level of intra-population genetic differentiation (91.51%) performed of wild apricot in the Tien-Shan Mountains, whereas the inter-population genetic variation has a relatively small contribution, which is similar to the results of (He *et al.*, 2007) (83.6%). There are a lot of studies which support that genetic differentiation primarily occurs within natural populations or ecological geographic groups, whereas inter-population genetic variation only has small contributions (Wang *et al.*, 2014, Yuan *et al.*, 2007). The cross-pollination characteristics and self-incompatible pattern of apricot population in the Tien-Shan Mountains also determines that the inter-population coefficient of gene differentiation is small (F_{st} = 0.0953). There was a moderate but steady gene flow (N_m = 2.3735) among apricot populations in the Tien-Shan Mountains, which was higher than the result reported by (Li *et al.*, 2014) for Chinese Siberian apricot (N_m = 1.37) and slightly lower than the result reported by (He *et al.*, 2007) (N_m = 2.684). According to previous studies of plants, an N_m> 1 usually indicates that the level of gene flow among populations is high and the genetic differentiation among populations is small (Crandall *et al.*, 2000). Therefore, the existing level of genetic diversity of the apricot in the Tien-Shan Mountains should not be sensitive to genetic drift (Slatkin & Barton, 1989).

The gene flow among apricot populations primarily relies on the spread of foreign genes through pollen and seed dispersal, which partially leads to the moderate level of genetic differentiation. Based on our field investigation, the fruit of apricot in the Tien-Shan Mountains is small (6-8 g), the stone is light (approximately 1.2 g), and the

fruit is sweet, which makes it suitable for animals to devour, carry and propagate. Additionally, there are many steep cliffs along the Tien-Shan Mountains create conditions that facilitate seed spread based on gravity. The rich resource of insect pollinators and widely distribution of apricot populations in the Tien-Shan Mountains also contributes to the gene flow (Hou & Xu, 2004). Because pollination by insects and seed spread by animals are easily limited by the propagation distance, the resulting gene flow level is also limited, which leads to an existing moderate level of gene flow (He *et al.,* 2007). Because of the wind activity and strong wind speed and power in the spring, long-distance propagation of pollen during the pollination season becomes possible, thereby facilitating the steady gene flow among apricot populations (Xu *et al.,* 2010). Thus, the self-incompatible patterns, wild distribution of populations, and long-distance pollen transmission via insects and gale are the main factors underlying the genetic differentiation of apricot in the Tien-Shan Mountains.

Population structure and cluster analysis: Understanding the genetic structure of germplasm resources is a prerequisite for the efficient genetic breeding utilization and conservation of the diversification resources (Laidò *et al.,* 2013). The UPGMA cluster analysis and Structure analysis both indicated two groups or four groups of the apricot may be recognized in the Tien-Shan Mountains, and there is a significant correlation between the genetic divergence and geographical distance. (He *et al.,* 2007) analyzed the genetic structure of three apricot populations in Xinyuan, Gongliu and Daxigou, and also revealed a significant correlation between the distance matrix of genetics and geographical distribution ($r = 0.9766$, $p = 0.0452$). (Liu *et al.,* 2012) conducted the Mantel test of 17 Siberian apricot populations in the Yanshan Mountains and found a significant correlation between the two distance matrix factors ($r = 0.5894$, $p<0.0001$). Most self-incompatible apricot populations have moderate or high levels of inter-population gene flow. However, the level of gene flow is easily limited due to the geographic distance, and most apricot populations present higher levels of genetic differences with expanding geographic distances.

Conservation

To maintain the existing level of genetic variation of natural resources is the primary objective for genetic diversity conservation considerations. Since 1984, the Chinese government has listed wild apricots in the list of endangered plants in the Tien-Shan Mountains, and established a nature reserve for wildlife in Xinyuan County, people still lack awareness of apricot resource protection, development and utilization. Human activities in recent years, such as fruit harvesting, overgrazing, tourism, and bacterial spot disease have posed serious threats to apricot resources and reduced the distribution area (Liu *et al.,* 2007). The genetic diversity of wild apricot in the Tien-Shan Mountains seems a little weak with other wild apricot types such as Siberia apricot (Li *et al.,* 2014).

According to the existing genetic diversity and genetic structure of the apricot populations, this study presents a conservation strategy mainly based on *in situ* protection supplemented by *ex situ* protection. Firstly, a core protected area need to be established based on existing natural reserves to conduct *in situ* protection of wild apricot resources. The population Tu has the highest genetic diversity, and this area contains many pure wild apricot forests, with trees older than 50 years. It is a priority to establish a core protection area in the Tuergen ditch. The population structure consisted of two groups and the good growth conditions in their natural habitat, population Xiao should also be given priority to the strategy of *in situ* conservation. Secondly, the *ex situ* strategy should be implement as to establish resource nurseries and seed banks for expanding apricot germplasm exchange among populations, and focus on the protection of some rare and endangered germplasms and to achieve their perpetual existence. Additionally, a nature reserve has been established for wildlife in the population Ye, that should strengthen the protection of wild apricot resources and limit the human interference activities.

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