Amplified Fragment Length Polymorphism Analysis of Genetic Diversity and Relationships of Wild and Cultivated Peach (*Prunus persica* L.)

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Abstract. To date, a narrow genetic base is a serious obstacle in peach (*Prunus persica* L.) production. Wild peach resources are useful germplasms for breeding new cultivars. In this study, amplified fragment length polymorphisms (AFLPs) were used to analyze the genetic diversity and relationships of wild and cultivated peach germplasms. These results showed that AFLP is an efficient technique for identifying the genetic relationships of wild and cultivated peach. Thirteen AFLP primer combinations generated a total of 377 scorable and clear fragments, all of which (100%) were polymorphic. Moreover, the polymorphism information content (PIC) values ranged from 0.91 to 0.96 with a mean of 0.95. The results of the principal component analysis (PCoA) largely corresponded to those obtained using cluster analysis. The three principal axes accounted for 2.6%, 5.79%, and 25.26% of the total variation, respectively. In conclusion, wild peach germplasms should receive special attention to ensure their conservation.

Peach (*Prunus persica* L.) is native to China and has been cultivated in China for the past 4000 to 5000 years (Ahmad et al., 2011; Maynard, 2008; Thacker, 1985). The homogeneity of peach recently resulted in the erosion of genetic diversity. In fact, the main commercial varieties represent a narrow genetic diversity, and there is concern that the narrow genetic base of the commercial varieties is a serious obstacle to improving peach production. Wild peach germplasms are useful in the control of disease and fruit quality and yield (Staudt et al., 2010; Wang, 1984). In addition, wild peach germplasms have been found to contain traits associated with tolerance to cold, drought, and high temperature and resistance to root-knot nematode (*Meloidogyne incognita*), aphids (*Myzus persicae*), and crown gall (*Agrobacterium tumefaciens*) (Tsipouridis and Thomidis, 2005; Wang et al., 2002). Thus, these diverse resources provide useful alleles to the cultivated peach gene pool, which is indispensable

in peach breeding. Despite their importance, there is limited information on the genetic relationships of wild peach.

To explore the genetic diversity and relationships of these wild peach germplasms, traditional methods based on morphological characteristics have been used. However, these methods have a disadvantage because most morphological traits are highly affected by environmental factors (Quinsavi and Sokpon, 2010). Consequently, many molecular marker techniques have been used for genetic linkage map construction and analysis of the genetic diversity of peach germplasms (Bouhadida et al., 2011; Cheng and Huang, 2009; Yamamoto et al., 2005).

The AFLP technique has been widely used to identify cultivars and germplasms in many fruit crops such as apple (Kenis and Keulemans, 2005), citrus (Pang et al., 2007), and kiwifruit (Prado et al., 2005). AFLP markers have some advantages over other molecular markers such as a high level of polymorphism, high reproducibility, a wide distribution of markers in the genome, and a lack of prerequisite sequences (Mueller and Wolfenbarger, 1999).

The objectives of the present study were to 1) assess the informativeness of AFLP for identifying wild peach germplasms; and 2) analyze the genetic diversity and relationships of wild and cultivated peach germplasms.

This study provides beneficial information for cultivated peach breeding.

Materials and Methods

Plant materials. A total of 77 peach germplasms, including 54 *P. mira* Koehne ex Sargent from the Tibetan Plateau and 23 peach materials from Zhengzhou Fruit Research Institute (Zhengzhou, China), were examined (Table 1; Fig. 1).

DNA extraction. The total genomic DNA was extracted using the modified CTAB method as described by Bouhadida et al. (2011). The DNA concentration and quality were estimated using a ultraviolet-VIS spectrophotometer (ultraviolet-1800; Shimadzu Corporation) and 0.8% agarose gel electrophoresis. The extracted DNA was then stored at –80 °C for polymerase chain reaction (PCR) amplification.

PCR amplification. The AFLP reactions were performed according to the method described by Vos et al. (1995) with some modifications. All of the primers and adapters are listed in Table 2. The DNA (150 ng) was digested with 5 U of EcoRI and 5 U of MseI (Promega, Madison, WI) in a total volume of 40 µL at 37 °C for 3 h and then incubated at 75 °C for 15 min. The digested DNA products were then ligated with 1 µL of EcoRI adapter (50 µM) and 1 µL of MseI adapter (5 µM) at 16 °C for 16 h. After ligation, the mixture was diluted 10-fold with ddH₂O. The pre-amplified reaction was performed using pre-selective primers. The pre-amplified mixture consisted of 5 µL diluted solution, 10 × PCR buffer, 2 mM dNTPs, 20 mM MgCl₂, 20 mM pre-amplification primer, and 1 U of Taq DNA polymerase in a 20-µL volume. The pre-amplified reaction was performed under the following conditions: denaturation at 94 °C for 3 min, 30 cycles of 94 °C for 30 s, 56 °C for 30 s, and 72 °C for 1 min and a final extension at 72 °C for 5 min. The amplified products were diluted 30-fold with ddH₂O and used as the template for selective amplification. The selective amplification reactions were performed in a 20-µL volume containing 5 µL of template, 10 × PCR buffer, 2 mM dNTPs, 25 mM MgCl₂, 20 mM selective amplification primer, and 1 U of Taq DNA polymerase. The PCR selective amplification was performed as follows: initial denaturation at 94 °C for 3 min, 13 cycles of 94 °C for 30 s, 65 °C for 30 s (–0.7 °C at each cycle) and 72 °C for 1 min, 23 cycles of 94 °C for 30 s, 56 °C for 30 s, and 72 °C for 1 min, and a final step at 72 °C for 5 min. The PCR products were separated on a 6% polyacrylamide gel for 2.5 h at 80 W and detected using silver staining as previously described by Bassam et al. (1991).

Data analysis. Only reproducible, clear, and well-resolved AFLP fragments were scored as the presence (1) or absence (0) for each primer pair. The genetic parameters, including the total number of fragments, number of polymorphic fragments, and percentage of polymorphic fragments (%), were

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Table 1. List and description of 77 individuals used in this study.

Accession no.	Species	Original place	Collection	Flesh color	Flesh type
Bujiu	<i>Prunus mira</i> Koehne ²	The Tibetan Plateau; Sichun Province; Yunan Province	Bujiu City in the Tibetan Plateau	Yellow–white	Soft
Jiaohuichu5			Joining of two rivers in the Tibetan Plateau		
Bujiu1			Bujiu City in the Tibetan Plateau		
Maiba1			Maiba Village in the Tibetan Plateau		
Farm			Linzhi City in the Tibetan Plateau		
Jiaohui2			Joining of two rivers in the Tibetan Plateau		
Bujiu0			Bujiu City in the Tibetan Plateau		
Bujiu2			Bujiu City in the Tibetan Plateau		
Maiba2			Maiba Village in the Tibetan Plateau		
Jiaohui4			Joining of two rivers in the Tibetan Plateau		
Erqiaoxia4			Zire Village of Kaze Region in the Tibetan Plateau		
Erqiaoxia8			Zire Village of Kaze Region in the Tibetan Plateau		
Bujiu13			Bujiu City in the Tibetan Plateau		
Zire			Zire Village of Kaze Region in the Tibetan Plateau		
Bomi			Bomi City in the Tibetan Plateau		
TongmaiBomi			Tangmai City of Cangdu in the Tibetan Plateau		
Zire-erqiao			Zire Village of Kaze Region in the Tibetan Plateau		
Yangzhichang			Linzhi City in the Tibetan Plateau		
Bomi2			Bomi City in the Tibetan Plateau		
Bomi3			Bomi City in the Tibetan Plateau		
Erqiaoxiao2			Zire Village in the Tibetan Plateau		
Yongjiubianba			Linzhi City in the Tibetan Plateau		
L6-120			Linzhi City in the Tibetan Plateau		
Bayi2			Bayi Town in the Tibetan Plateau		
Baiba3			Linzhi City in the Tibetan Plateau		
L1120			Buda City in the Tibetan Plateau		
L4-82			Buda City in the Tibetan Plateau		
Buda7			Buda City in the Tibetan Plateau		
Zhangbai2			Zhangmai Village in the Tibetan Plateau		
Z510			Zhangmai Village in the Tibetan Plateau		
Shangzhangmai			Zhangmai Village in the Tibetan Plateau		
Zhangmai2			Zhangmai Village in the Tibetan Plateau		
School1			Linzhi City in the Tibetan Plateau		
Dianzhan2			Linzhi City in the Tibetan Plateau		
Zhangmai1			Zhangmai Village in the Tibetan Plateau		
Shangzhangmai1			Zhangmai Village in the Tibetan Plateau		
Dianzhan4			Linzhi City in the Tibetan Plateau		
School3			Linzhi City in the Tibetan Plateau		
Shangzhangmai4			Zhangmai Village in the Tibetan Plateau		
Dianzhan1			Linzhi City in the Tibetan Plateau		
Dianzhan3			Linzhi City in the Tibetan Plateau		
School2			Linzhi City in the Tibetan Plateau		
Dejichun			Dingji Town in the Tibetan Plateau		
Erqiaoxia1			Zhangmai Village in the Tibetan Plateau		
Caikangchun			Zhangkang City in the Tibetan Plateau		
Bomijianyu			Bomi City in the Tibetan Plateau		
Bomijianyu2			Bomi City in the Tibetan Plateau		
Bomiyi3			Bomi City in the Tibetan Plateau		
Bomi4			Bomi City in the Tibetan Plateau		
Bomiyi2			Bomi City in the Tibetan Plateau		
Geni			Song Zong Town in the Tibetan Plateau		
Bomiyi1			Bomi City in the Tibetan Plateau		
Chanchangyigong2			Yigong National Geopark in the Tibetan Plateau		
Niangsuochun	<i>Prunus persica</i> L. var. pendula	Landrace	Gongga County in the Tibetan Plateau	No food value	
Hongfenchuizhi			Zhengzhou Fruit Research Institute		
Fenchuizhi					
Gansutao					
Zhubo					
Fenshouxing21					
Fenshouxing					
Hongshouxing					
	<i>Prunus kansuensis</i> Rehd	Gansu Province, Shanxi Province		Blue–white	Soft
	<i>Prunus persica</i> L. var. vulgaris	Japan		White	Hard
	<i>Prunus persica</i> L. var. densa	Landrace		Yellow–white	Soft
	<i>Prunus persica</i> L. var. densa	Landrace		Yellow–white	Soft

(Continued on next page)

Table 1. (Continued) List and description of 77 individuals used in this study.

Accession no.	Species	Original place	Collection	Flesh color	Flesh type
Chunmitao	<i>Prunus persica</i> L. Batsch	Zhengzhou Fruit Research Institute		White	Hard
Huangyoupantao	<i>Prunus persica</i> L. var. <i>platycarpa</i>	South China		White	Hard
Youpantao36-3	<i>Prunus persica</i> L. var. <i>platycarpa</i>	South China		Ivory	Hard
Maotao	<i>Prunus persica</i> L. var. <i>aganopersica</i> Reich	Gansu Province, Shanxi Province		White	Soft
Baihuashantao	<i>Prunus davidiana</i> Franchet	North and Northwest in China		No food value	
Juhuatao	<i>Prunus persica</i> L. Juhuatao	Japan		No food value	
Youpantao36-3	<i>Prunus persica</i> L. var. <i>compressa</i>	Xinjiang Province, Gansu Province		Ivory	Hard
Chunhong	<i>Prunus persica</i> L.	Jiangsu Province		White	Hard
Zhongyou3	<i>Prunus persica</i> L. var. <i>necturina</i>	Zhengzhou Fruit Research Institute		Yellow	Hard
Zhongyou4	<i>Prunus persica</i> L. var. <i>necturina</i>	Xinjiang Province, Gansu Province		Yellow	Hard
Zhongyou6	<i>Prunus persica</i> L. var. <i>necturina</i>	Xinjiang Province, Gansu Province		Yellow	Hard
Zhongyou7	<i>Prunus persica</i> L. var. <i>necturina</i>	Xinjiang Province, Gansu Province		Yellow	Hard
Zhongyou8	<i>Prunus persica</i> L. var. <i>necturina</i>	Xinjiang Province, Gansu Province		Yellow	Hard
Zhongyou9	<i>Prunus persica</i> L. var. <i>necturina</i>	Xinjiang Province, Gansu Province		White	Soft
Zhongyou10	<i>Prunus persica</i> L. var. <i>necturina</i>	Xinjiang Province, Gansu Province		Ivory	Moderate hardness

^aAccessions are wild.

Fig. 1. Geographic sampling sites. (A) Tibetan Plateau; (B) Henan Province (Zhengzhou Fruit Research Institute).

estimated. A dendrogram corresponding to the similarity coefficient and PCoA results was constructed using NTSYS-pc software (Version 2.10) (Rohlf, 2000). The resolving power (Rp) was used to assess the power of the primers to discriminate all individuals (Prevost and Wilkinson, 1999). The assessment of Rp was performed using the Gilbert formula: $R_p = \sum I_b$, where $I_b = 1 - [2 \times |0.5 - P|]$ and P is the frequency of the individuals containing the I band (Gilbert et al., 1999). In addition, the PIC was used to discriminate the ability of the primers. The formula was as follows:

$$PIC = 1 - \sum_{i=1}^k P_i^2$$

where k is the total number of alleles detected by a primer and P_i is the frequency of the allele in all individuals (Lynch and Ritland, 1999).

Results

AFLP polymorphism. Thirteen AFLP primer combinations generated a total of 377 scorable and clear fragments for 77 individuals, and all of these fragments (100%) were

polymorphic (Table 1; Fig. 2). The total number of fragments of each primer pair varied from 15 for *EcoRI*-AC/*MseI*-AG to 42 for *EcoRI*-AG/*MseI*-AG with an average of 28.40. Moreover, the PIC values ranged from 0.91 to 0.96 with a mean of 0.95 (Table 2; Fig. 3). The mean of the Rp was 15.00 and ranged from 8.60 to 18.68 (Table 2).

Genetic diversity analysis. All 377 AFLP fragments scored were used for genetic diversity studies. A high level of similarity coefficients was observed. The average of the similarity coefficients values was 0.56. The lowest similarity (0.23) occurred between Dejichun and Dianzhan2 and the combination of Youpantao 36-3 and Zhongyou 10 showed the highest similarity (0.76) (data not shown).

Based on Nei's genetic distance, an unweighted pair group method with arithmetic average (UPGMA) dendrogram was constructed (Fig. 4). In the dendrogram, all of the materials were divided into three main groups at the similarity level of 0.31 (Fig. 3). Group I consisted of most of the materials from the Tibetan Plateau. Group II included some of the materials from the Tibetan Plateau and all of the individuals from the center of the peach resource. Only the Dejichun individual belonged to Group III. In addition, Group II contained two groups (Subgroups I and II). There were 10 individuals from the Tibetan Plateau in Subgroup I, and all of the materials from the Zhengzhou Fruit Research Institute were in Subgroup II.

PCoA analysis. The relationship among all of the individuals was also estimated using PCoA. The results of the PCoA analysis largely corresponded to those obtained using

Table 2. Characteristics of the amplification products obtained using 13 amplified fragment length polymorphism primers.

Primer pairs	Sequences (5'-3')	TNF	NPF	PP (%)	Rp	PIC
<i>EcoRI</i> -AA/ <i>MseI</i> -AA	GAC TGC GTA CCA ATT C-AA/GAT GAG TCC TGA GTA A-AA	32	32	100	16.36	0.96
<i>EcoRI</i> -AA/ <i>MseI</i> -AG	GAC TGC GTA CCA ATT C-AA/GAT GAG TCC TGA GTA A-AG	20	20	100	12.18	0.94
<i>EcoRI</i> -AA/ <i>MseI</i> -GT	GAC TGC GTA CCA ATT C-AA/GAT GAG TCC TGA GTA A-GT	24	24	100	15.53	0.95
<i>EcoRI</i> -AC/ <i>MseI</i> -AC	GAC TGC GTA CCA ATT C-AC/GAT GAG TCC TGA GTA A-AC	34	34	100	12.16	0.95
<i>EcoRI</i> -AC/ <i>MseI</i> -GC	GAC TGC GTA CCA ATT C-AC/GAT GAG TCC TGA GTA A-GC	15	15	100	8.60	0.91
<i>EcoRI</i> -AC/ <i>MseI</i> -GT	GAC TGC GTA CCA ATT C-AC/GAT GAG TCC TGA GTA A-GT	33	33	100	18.68	0.96
<i>EcoRI</i> -AG/ <i>MseI</i> -AG	GAC TGC GTA CCA ATT C-AG/GAT GAG TCC TGA GTA A-AG	42	42	100	16.91	0.96
<i>EcoRI</i> -AT/ <i>MseI</i> -AT	GAC TGC GTA CCA ATT C-AT/GAT GAG TCC TGA GTA A-AT	37	37	100	15.35	0.96
<i>EcoRI</i> -AT/ <i>MseI</i> -GC	GAC TGC GTA CCA ATT C-AT/GAT GAG TCC TGA GTA A-GC	23	23	100	12.29	0.94
<i>EcoRI</i> -AT/ <i>MseI</i> -GG	GAC TGC GTA CCA ATT C-AT/GAT GAG TCC TGA GTA A-GG	26	26	100	11.97	0.94
<i>EcoRI</i> -AT/ <i>MseI</i> -GT	GAC TGC GTA CCA ATT C-AT/GAT GAG TCC TGA GTA A-GT	25	25	100	13.82	0.94
<i>EcoRI</i> -CA/ <i>MseI</i> -CA	GAC TGC GTA CCA ATT C-CA/GAT GAG TCC TGA GTA A-CA	32	32	100	18.03	0.96
<i>EcoRI</i> -TA/ <i>MseI</i> -AA	GAC TGC GTA CCA ATT C-TA/GAT GAG TCC TGA GTA A-AA	26	26	100	23.12	0.96
Total		369	369	—	195	—
Average		28.40	28.40	100	15.00	0.95

TNF = total number of fragments; NPF = number of polymorphic fragments; PP (%) = percentage of polymorphic fragments; Rp = resolving power; PIC = polymorphic information content.

Fig. 2. Amplified fragment length polymorphism image of parts of individuals amplified using the primer combination E11–M41. M indicates the DNA marker ladder.

Fig. 3. Distribution of the polymorphism information content obtained using amplified fragment length polymorphism.

cluster analysis. The three principal axes accounted for 2.6%, 5.79%, and 25.26% of the total variation, respectively. The first two axes separated all of the individuals into two

groups. One group included all of the individuals from the center of the peach resource. The remaining individuals (from the Zhengzhou Fruit Research Institute) with the

exception of Dejichun were clustered together to form one group (Fig. 5).

Discussion

AFLP polymorphism. AFLP has been extensively used in previous studies as a technique to detect molecular polymorphisms in cultivars and wild peach germplasms (Aranzana et al., 2003; Hu et al., 2005; Wang et al., 2008). Using AFLP, Wang et al. (2006) found a polymorphic percentage of 29.5% for nine primer combination pairs among 94 wild peach germplasms. Sixteen AFLP primer combinations produced a total of 837 fragments and 146 polymorphic bands with a polymorphism percentage of 17.5%, as reported by Xu et al. (2006). These results suggested that a low level of genetic diversity is present among peach germplasms based on the AFLP technique. Compared with previous studies, high levels of polymorphism (100%) were found in this study through the evaluation of the genetic diversity in *Prunus mira* (*P. mira* Koehne ex Sargent) germplasms based on AFLP. This result suggested that *P. mira* and other peach species have a broad relationship. However, some potential reasons for these different levels of polymorphism may be correlated with the material size and the level of polymorphism of the primer combinations.

Although the AFLP technique may be useful for detecting genetic diversity in different peach germplasms, none of the results can be simply compared with those of other studies as a result of different genotypes and primer pairs. Thus, different marker techniques should be used to estimate DNA polymorphisms in peach germplasms (Testolin et al., 2000). For instance, Bouhadida et al. (2011) analyzed 94 peach cultivars using six simple sequence repeat (SSR) markers and found that SSR is very useful for future peach identification studies. Cao et al. (2012) detected highly polymorphic SSR markers among 104 peach landrace accessions using 53 SSR markers. Despite having a high variability for the identification of all peach cultivars, SSR was found to be relatively less variable compared with other species

Fig. 4. Dendrogram of 77 individuals based on the data of amplified fragment length polymorphism using the unweighted pair group method with arithmetic average method. The genotype names are shown in Table 1.

(Aranzana et al., 2012). Thus, considering the limitation of different marker techniques, the combination of two or more molecular marker systems is most likely efficient for the conservation and management of peach germplasms. Furthermore, the effects of factors on morphological traits and fruit development should be taken into account when elucidating the genetic structure in peach germplasm resources (Cao et al., 2012).

Genetic diversity analysis. In China, peach, as a cultivated plant, has existed for thousands of years (Everett, 1982). As a self-pollinating plant, peach has very low genetic variation (Scorza et al., 1985). To enrich the genetic diversity of peach, we need to identify more wild peach resources. The rich genetic basis of wild peach germplasms is well known and has been demonstrated;

however, the relationships among these germplasms remain unclear (Wang et al., 2008).

To date, peach is widely cultivated in China as an important fruit crop. In particular, many wild peach germplasms have attracted much attention as a result of their specific characteristics (Aradhya et al., 2004; Guan et al., 2014; Wang et al., 2006). This may be helpful for breeding peach cultivars with potentially new biotic and abiotic stresses (Cao et al., 2012). However, their genetic relationships are controversial and unclear. For example, Gansutao (*P. kansuensis* Rehd) and *Prunus mira* (*P. mira* Koehne ex Sargent) have a relatively close relationship, as reported by Zong and Duan (1987). However, this result was inconsistent with our findings. In the present study, Gansutao was clustered with Zhongyou6 (*P. persica* var.

necturina), which is consistent with the results obtained by Yu et al. (2004). In addition, Youpantao36-3 (*P. persica* var. *platycarpa*) was closely clustered with Zhongyou10 (*P. persica* var. *necturina*), which is consistent with the findings reported by Cheng et al. (2001). In addition, Chunmitao (*P. persica* L. Batsch) and Huangpantao (*P. persica* var. *platycarpa*) were clustered together in Sub-group I, most likely as a result of their evolutionary relationship (Cheng et al., 2001, 2002; Yang et al., 2001). It is common that Shouxingtao (*P. persica* var. *densa*) is derived from Maotao (*P. persica* var. *agano-persica* Reich.) (Yang et al., 2001). However, Maotao was clustered not with Shouxingtao but with Fenchuzhi (*P. persica* var. *pendula*). We hypothesized that Maotao may be closely related to Chuizhitao (*P. persica* var. *pendula*). Guo et al. (1986) reported that

Fig. 5. Principal coordinate analysis of 77 individuals based on amplified fragment length polymorphism marker data.

a close relationship existed among Gansutao, Shantao (*P. davidiana* Franchet), and cultivated *P. persica* L., which is consistent with our findings.

The dendrogram showed that all of the individuals from the Zhengzhou Fruit Research Institute were localized in Group II, possibly as a result of the existence of a common genetic basis within this group. Moreover, the high genetic distances (data not shown) detected between these materials confirmed the higher diversity of individuals from the Zhengzhou Fruit Research Institute in this study. Importantly, the Zhengzhou Fruit Research Institute of the Chinese Academy of Agricultural Sciences, which was founded in 1960, is a national professional research organization of deciduous fruit that studies peach germplasms and develops new cultivars. Thus, we should enrich the peach gene pool to conserve them for the breeding of new varieties and to avoid genetic erosion.

In the present study, the relationship between *P. mira* and other peach germplasms was remote (Fig. 4). This finding indicated that *P. mira* demonstrates a genetic difference with other *P. persica* germplasms. Wang and Zhou (1990) confirmed that *P. mira* is the ancestor of cultivated peach. In addition, at the level of 0.31, Dejichun formed a distinct group (Group III), indicating its clear differentiation from the other materials. This result is most likely because of the adaptation to a socioeconomic factor or geographical isolation. Indeed, the Tibetan Plateau is a unique geographic area with many geographic barriers such as the Tanggula Mountains, Lanchang River, Kunlun Mountains, and Nujiang River (Zhang and Jiang, 2006). Thus, many specific germplasms may be formed in the Tibetan Plateau.

Based on the genetic similarity matrices, the UPGMA dendrogram indicated that most of the individuals from Bomi City in the Tibetan Plateau were clustered to form one group (Subgroup I). This result indicated that most of the individuals belonging to the Bomi group had close genetic relationships. This low diversity may be the result of a self-mating system, environmental similarities, and a small population size, which would not facilitate genetic drift and cause a low level of genetic variation.

Conservation of wild peach germplasms. China is the native homeland of the peach tree and has abundant peach germplasms. However, the genetic narrowness of modern peach cultivars is a bottleneck to the breeding of new peach varieties. Wild peach germplasms have a high level of genetic diversity and are known to have many valuable genes that have not been used, e.g., resistance to disease and environmental stress (Cho et al., 2012; Sauge et al., 1998). However, there is an extremely dispersed distribution of wild peach germplasms. Moreover, some wild peach germplasms have been in danger of extinction as a result of human activities such as agriculture and pasture needs (Li et al., 2013; Wang et al., 2010; Wu et al., 2003). Thus, these germplasms should receive special attention to ensure their conservation, which would necessitate a variety of conservation approaches depending on the specific biological factors. These approaches should include the conservation of ecosystems/agro-ecosystems, naturally occurring gene pools, and specific genetic stocks such as the tubers and roots used by communities (Altieri et al., 1987; Brush, 1991). Furthermore, more national research institutes have been founded as priority conservation sites, and areas where the wild peach

germplasms are found within the protected areas should be demarcated to not allow any activity.

Overall, our results indicated that AFLP is a powerful and effective tool for the analysis of the genetic diversity of wild and cultivated peach germplasms. Furthermore, further analyses using several molecular markers are required to confirm our conclusions, and more potential peach germplasms should be collected for the breeding of new varieties.

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