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ORIGINAL PAPER

Geneticalysis of economically important apricot cultivars in gilgit baltistan based on SSR molecular markers

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Abstract

Apricot (Prunus armeniaca L.) is one of the most important fruits in Gilgit Baltistan (GB) Pakistan being used as fresh and dried as well. These local cultivars prevailing in different districts of GB were established as an orchard in the Mountain Agriculture Research Centre (MARC) Jaglot, Gilgit. In this study, molecular study was carried out using 20 different Simple Sequence Repeat (SSR) markers to assess genetic diversity in local apricot germplasms. There were 18 primers that showed clear and reproducible amplification banding pattern in 12 apricot cultivars. A high level of genetic diversity (He = 0.77, Ho = 0.64) was observed. The SSR loci PGS1.21 produced high number of alleles (14) followed by PGS1.23 (13) whereas, PGS1.252 formed (12) number of alleles. The results using genetic clustering analysis and the UPGMA dendrogram constructed from the genetic distances distinguished the apricot genotypes into three main clusters; first cluster included genotypes originating from the districts of Gilgit, Ghizer and Diamer while, the second cluster contained cultivars from Baltistan region. The third cluster comprised of cultivars mostly from the districts of Hunza and Nagar apricot germplasm. The apricots from Gilgit Baltistan revealed a high variability, and confirmed as genetic diversity is still conserved in the region. The SSR based profiles of the investigated apricot cultivars will improve the management of apricot gene banks and the information on the genetic variation in Pakistani apricot will support the international research community in the horticultural industry.

Key words: Apricot, genetic diversity, Gilgit Baltistan, SSR.

Introduction

Apricot (*Prunus armeniaca* L.) belongs to the family *Rosaceae*, genus *Prunus* that is widely cultivated in the Mediterranean region, Middle East, in Armenia, India, Pakistan and China (HORMAZA & al. 2007) [1]. The cultivated apricot belonged to Asia and Caucasus region and it has a very small genome size (2n =16). Pakistan produces 192500 tons apricot fruit annually (FAOATAT, 2012) [2]. In Gilgit Baltistan, area under apricot cultivation is 12921 hectares and its annual production is 114286 tones (Department of Agriculture Gilgit Baltistan). According to the information by the Department of Agriculture, Diamer of Gilgit-Baltistan, apricot was at the apex amongst the dry fruits transported to down country with 4,374.38 tons during 2014. The several village based surveys revealed about 180 different cultivars existed in this region. All the improved local apricot varieties have been recognized for high fruit production. Some of the apricot cultivars (Marghulam, Charmagzi, Narie, Shai Pawand and Nili Pawand) are being consumed as fresh fruit while, the cultivars (Habi, Halman and Ali Sha Kakas) as being used in dried form. The apricot fruit is being used as fresh throughout summer season whereas, dried fruit and its edible kernels are mainly used during severe winters in most parts of this region. Additionally, oil is extracted from bitter

seeds for hairs, lamps and also for firewood consumption. The practice of planting seeds from the best trees over an extended period of time has resulted in an incredible amount of variation (Thompson, 1988) [3].

Apricot was introduced into the region of Gilgit Baltistan from central Asia and Afghanistan through the silk route. In the mountainous and hilly area where the environmental conditions are harsh, the propagation of apricot from their kernels and chance seedling has been practiced for a long time. In the entire region of Gilgit-Baltistan, there were different small mini kingdoms who ruled over various races of peoples that also contributed to enrich the genetic diversity of apricot in this area.

The fruit of apricot either fresh or dried are amongst the most important agricultural commodities that share considerable capital in the economy of Gilgit Baltistan. It is a dilemma that the genetic resemblance of current apricot cultivars grown in the area of Gilgit-Baltistan is largely unknown due to lack of research studies. The current study has been aimed at the identification of mostly cultivated and native apricots cultivars, their diversity and germplasm preservation in this region. Currently, the molecular markers assisted very significantly to improve the horticultural crop plants. In this study Randomly Amplified Polymorphic DNAs (RAPD) as used by (BADENES &al. 1998 [4] and MARINIELLO & al. 2002 [5] Amplified Fragment Length polymorphisms (AFLP) as used by HAGEN & al. 2002 [6], HURTADO & al. 2002 [7] and GEUNA &al. 2003 [8] and simple sequence repeats (SSRs) used by AKPINAR & al. 2010 [9] and YILMAZ & al. 2012 [10] which show independence from the growth stage and environmental factors, provide highly discriminatory information and therefore are frequently used for genetic studies in peach and apricot. Using the molecular markers were concerned to obtain the SSR profile of apricot cultivars prevailing in this region for reliable identification of the native germplasm and to add up valuable information to the researchers of apricot in the horticultural industry.

Materials and methods

In this study the apricot germplasm established as a model experimental orchard at Mountain Agriculture Research Centre (MARC) Jaglot, Gilgit was used as experimental unit. The MARC is located at 35.42 N latitude, 74.37 E longitudes and 1527 meters altitude above the sea level. It receives approximately 120-240 mm annual precipitation with an average temperature of 25°C in summers whereas, there exists a severe winter. The soil type in the orchard is sandy loam with 6.5 soil pH.

Table 1. List of apricot cultivars used in this study

Name of cultivar	Origin District	Usage
Marghulam	Skardu/Ghanche	Fresh
Shakarfo	Skardu/Ghanche	Fresh
Shakanda	Gilgit/Hunza	Fresh
Charmagzi	Gilgit/ Diamer	Fresh
Shai Pawand	Gilgit /Diamer/Ghizer	Fresh
Nili Pawand	Gilgit /Diamer/Ghizer	Fresh
Halman	Skardu/Ghanche	Dry
Habi	Hunza/Nagar	Dry
Ali Shah Kakas	Hunza/ Nagar	Dry
Astore 1	Astore	Dry/Fresh
Narie	Gilgit /Hunza	Dry/Fresh
Skardu Local	Skardu	Dry/Fresh

DNA extraction

The DNA from young and fresh leaf samples was extracted using CTAB method (KHAN & al. 2004) [11] with minor modifications. After extraction, the DNA samples were preserved in Eppendorf tubes and properly labeled. They were shifted keeping in the ice packs to the Genome and Stem Cell Centre Erciyes University Kayseri Turkey for (microsatellite) SSR analysis. Concentration and purity of the DNA were determined with a Bio Spec-Nano spectrophotometer for life science (SHIMADZU BIOTECH).

Microsatellite Primers analysis

Twenty SSR primer pairs, Gol061,PGS1.03, PGS1.20, PGS1.21PGS1.23, PGS1.24, PGS1.252, 96P10_SP6, Gol029 (SORIANO & al. 2012 [12]), ssrPaCITA5, ssrPaCITA17, ssrPaCITA16, ssrPaCITA19, ssrPaCITA4, ssrPaCITA21, ssrPaCITA15 (LOPES & al. 2002 [13]) UDP98-412 (CIPRIANI & al. 1999 [14]), pchgms2 (SOSINSKI & al. 2000 [15]), UDAp-404 (MESSINA & al. 2004 [16]) and Aprigms18 (VILANOVA & al. 2006 [17]) were used to study the polymorphism in the apricot genotypes selected from the region of Gilgit Baltistan on the basis of published apricot and peach microsatellite framework and fingerprinting. The thermal cycler was calibrated to denaturation of DNA samples at 95ºC for 5 minutes followed by 40 cycles of 95ºC for 1 minute, the annealing temperature was adjusted at 53ºC for 1 minute and 30 sec, the at 72ºC for 1 minute 30 s, and at final stage a 7 mins extension stage at 72ºC was adjusted. The PCR mixtures were prepared by diluting with distilled water to a total volume of 15 µl containing 12 pM each of forward and reverse primers, 1x reaction buffer, 35 µM $MgCl_2$, 27 µM each of dNTPs, 3.5-25 ng of template DNA and 0.2 units of DNA polymerase (Thermo scientific USA). The PCR reactions were carried out with M13 primer fluorescently labeled with dyes FAM (Blue), NED (Black), VIC (Green) and PET (Red) and the tetraplex system was used. PCR products were separated on 2% agarose gel in 1x TBE buffer at 90 volts for 180 minutes. The fragment patterns were photographed under UV light for further analysis. A 100 bp standard DNA ladder as a molecular standard was run in order to confirm the appropriate markers for SSR analysis. Then 10µl distilled water added onto the remaining PCR product and stored at -20°C to use for further fragment analysis. Twenty primer pairs were assigned four multiplex groups (**Table 2**). When all PCR reactions with 20 different primer pairs were completed, the stored PCR products for each multiplex PCR were mixed. Thus total volume reached to about 85 µl. This concentration was further diluted 20 times and 0.75 µl of the diluted aliquot was mixed with 9 µL Hi-Di buffers and 0.25 µl LIZ 600 standards. The mixtures were kept at 95ºC for 5 minutes, and then immediately were put on ice for 2 munities and finally loaded to capillary electrophoresis on an ABI Prism 3500 DNA Analyzer (Applied Biosystems, Foster City, CA) at the core laboratory of Genome and Stem Cell Centre in Erciyes University, Kayseri, Turkey. DNA fragment sizes were determined using GeneMapper 4.1 software (Applied Biosystems).

Data analysis

A genetic distance matrix was generated on the basis of proportion of the shared alleles. Then the expected heterozygosity (He),observed heterozygosity (Ho) and polymorphism information content (PIC) were calculated using the PowerMarker V3.025 software(LIU and MUSE 2005[18]).He was calculated according to the formula $He = 1-\sum pi^2$, where pi is the frequency of the ith allele (NEI, 1973[19]). Ho was from direct counts, and the PIC value for each locus was estimated using PowerMarker program.

Table2. Forward and Reverse Primers Sequences of SSRs Markers and References

Marker No	Marker Name	Sequences (5'- 3')	References
SSR 1	Gol061_F Gol061_R	TGG CTC AAC CAC AAA GTG AC GGA GCT AGT CTT CTG TCC AAG G	Cipriani *et al*., 1999
SSR 2	PGS1.03_F PGS1.03_R	GCT CTC TCC CTG CCA TTT TT CCA TCC TCC ACT TCT CAA CC	Soriano., *et al* 2012
SSR 3	PGS1.20_F PGS1.20_R	CAC CCA ACC CTC TTC TGT CT CCA CGC CTT CTC TCT CTT TC	Soriano., *et al* 2012
SSR 4	PGS1.21_F PGS1.21_R	CCC TGG TGT TCT GCT CTC TC CAT CCA CAA ATG GGA AGC AT	Soriano., *et al* 2012
SSR 5	PGS1.23_F PGS1.23_R	TTT GTT ATT TGT TTT GGT TGG CAG GCT TTT TAT GTC CTC CT	Soriano., *et al* 2012
SSR 6	PGS1.24_F PGS1.24_R	GTA AAT GAG TGC CTG CGT GT TGC GAG AGT TGT GAT TGA TG	Soriano., *et al* 2012
SSR 7	PGS1.252_F PGS1.252_R	TCA GAT CCA GAA TGC AAG AA CTC TCC TCA AAC CCAC ACA C	Soriano., *et al* 2012
SSR 8	96P10_SP6_F 96P10_SP6_R	ACA AAA CAA GTC CCC ATT GC TGG TTT GAA AAT GGA GAA AA	Soriano., *et al* 2012
SSR 9	Gol029_F Gol029_R	GTG CAG CCC TAG ATT AAT AGC C GCA TCT CAG CAG CAT TTC TC	Soriano., *et al* 2012
SSR 10	ssrPaCITA5_F ssrPaCITA5_R	GTT GTG TTT ACT TTT TTC TTA ACG G GTA TCA CAA GTG AGA ACA TAA GAG G	Lopes., *et al* 2002
SSR 11	ssrPaCITA17_F ssrPaCITA17_R	CAC GGG GAG AAT TGG GTG GCC TTA G GGA GTC TAT AAA TAA ATG GTT GCG C	Lopes., *et al* 2002
SSR 12	Aprigms18_F Aprigms18_R	TCT GAG TTC AGT GGG TAG CA ACA GAA TGT GCG TTG CTT TA	Vilanova., *et al* 2006
SSR 13	ssrPaCITA16_F ssrPaCITA16_R	TGA CGT CTC TCT CCC TCC CCT TCC T CCC TCT CTT TTT CTC TAG CCC CAC C	Lopes., *et al* 2002
SSR 14	ssrPaCITA19_F ssrPaCITA19_R	GAC AAA TAC AAT CAA GAA GTG TCG C GAA CAG CTA GCC CCT TTG TCA TAC	Lopes., *et al* 2002
SSR 15	ssrPaCITA4_F ssrPaCITA4_R	GTG AAA ATG AAA GAA TCG CTA CC TGT CCC TTG ACG CCC AGA TTT CTC C	Lopes., *et al* 2002
SSR 16	UDAp-404_ F UDAp-404_ R	CAT GAA CAG GGT CAA AAG CA TAT ATC CTT ACG CGG CCT CA	Messina *et al*., 2004
SSR 17	ssrPaCITA21_F ssrPaCITA21_R	GAT TAT ATA AGT TGG TTT TTG TAA G GTA TTC TAT AAT GTA TAA ATG TAC G	Lopes., *et al* 2002
SSR 18	pchgms2_F pchgms2_R	GTC AAT GAG TTC AGT GTC TAC ACT C AAT CAT AAC ATC ATT CAG CCA C TG C	Sosinski*et al*., 2000
SSR 19	UDP98-412_F UDP98-412_R	AGG GAA AGT TTC TGC TGC AC GCT GAA GAC GAC GAT GAT GA	Cipriani *et al*., 1999
SSR 20	ssrPaCITA15_F ssrPaCITA15_R	GAG ATT TGC AAT GTC GGA ATA AGA C CAG ACA GCT GCT GGT TAT AGG CTC G	Lopes., *et al* 2002

Results

Total of 20 microsatellite (SSR) markers were utilized to characterize and assess genetic diversity of 12 apricot cultivars. Out of these, 2 markers (SSR 6 PGS1.24 and SSR 20ssrPaCITA15) were excluded in evaluation of accessions due to difficulty of allele coding, while the rest of 18 primers generated good and reproducible products (**Table 3**). A total number of 158 different reproducible alleles were detected across 12 cultivars with 18 SSR markers. The number of alleles generated by markers ranged from 4 to14 with an average of 8.78 alleles per locus. The highest number of allele (14) was observed in PGS1.21 and in ssrPaCITA16 respectively. While the lowest (4) in PGS1.03 and Gol029 SSR markers. The lowest and the highest He values were 0.58 and 0.91 for Gol029 and PGS1.21 with an average He value of 0.77. The lowest Ho for96P10_SP6was 0.17 while the highest one was 0.92 for Gol061, PGS1.252 and Aprigms18, with an average Ho value of 0.64 (**Table 3**). The overall size of the alleles varied from 93bp (SSR 7) to 319bp (SSR 1) for 18 loci. The PIC values varied among loci and ranged from 0.53 (SSR 9 Gol029) to 0.90 (SSR 4 PGS1.21 and SSR 13ssrPaCITA16) with an average of 0.75 per locus.

Table 3. Characterization values of SSRs and apricot population

Marker No	Marker Name	Number of alleles (n)	Expected hetrozygosity (He)	Observed heterozygosity (Ho)	PIC value
SSR 1	Gol061_F Gol061_R	8	0.78	0.92	0.75
SSR 2	PGS1.03_F PGS1.03_R	4	0.66	0.83	0.60
SSR 3	PGS1.20_F PGS1.20_R	10	0.87	0.50	0.85
SSR 4	PGS1.21_F PGS1.21_R	14	0.91	0.83	0.90
SSR 5	PGS1.23_F PGS1.23_R	13	0.90	0.67	0.89
SSR 7	PGS1.252_F PGS1.252_R	12	0.86	0.92	0.85
SSR 8	96P10_SP6_F 96P10_SP6_R	6	0.63	0.17	0.57
SSR 9	Gol029_F Gol029_R	4	0.58	0.33	0.53
SSR 10	ssrPaCITA5_F ssrPaCITA5_R	5	0.76	0.42	0.72
SSR 11	ssrPaCITA17_F ssrPaCITA17_R	11	0.87	0.83	0.85
SSR 12	Aprigms18_F Aprigms18_R	6	0.76	0.92	0.72
SSR 13	ssrPaCITA16_F ssrPaCITA16_R	14	0.91	0.75	0.90
SSR 14	ssrPaCITA19_F ssrPaCITA19_R	11	0.87	0.67	0.86
SSR 15	ssrPaCITA4_F ssrPaCITA4_R	8	0.63	0.42	0.61
SSR 16	UDAp-404_ F UDAp-404_ R	8	0.83	0.83	0.81
SSR 17	ssrPaCITA21_F ssrPaCITA21_R	8	0.59	0.50	0.57
SSR 18	pchgms2_F pchgms2_R	11	0.81	0.58	0.80
SSR 19	UDP98-412_F UDP98-412_R	5	0.71	0.50	0.67
Total		**158**	**13.93**	**11.59**	**-**
Average		**8.78**	**0.77**	**0.64**	**0.75**

Distance Matrix

The SSR-derived data were subjected to calculate the genetic distance as presented in the **Table 4**. The genetic distance of investigated apricot genotypes were ranged from 27 to 69%. Amongst the investigated cultivars, Ali Shah Kakas exhibited highest 69% genetic similarity with Narie. Likewise, Astore1 displayed 52% highest similarities with Habi. Charmagzi generated a highest genetic similarity (27%) with Marghulam. In the same way, 69% similarity was found between Halman and Shakanda. Shai Pawand and Nili Pawand also showed 69% highest similarities and 52% similarity was recorded in Skardu Local and Shakarfo Figure (1).

Discussions

In current study, eighteen SSR loci profile of 12 different apricot cultivars was analyzed, which includes some of the cultivars in the germplasm collection of the Mountain Agriculture Research Centre. AKPINAR & al. 2010 [9] obtained useful allelic profiles of the SSRs of apricots, but limited number of accessions were analyzed. Our study aimed to produce the SSR profiles of some economically important apricot collections of the country. This SSR profile data can be used to form identity charts of cultivars and accessions for facilitating the introgression of a diverse germplasm into current accessions and for forming a core collection. This was the first step to characterize the molecular diversity of commercialized apricot cultivars grown in mountainous areas of Gilgit Baltistan (Pakistan). The results of present study indicated a high level of genetic variation in the most of the investigated apricot genotypes.

Table 4. Distance Matrix for 12 Gilgit Baltistan apricot cultivars based on SSR analysis

	AliShahK	Astore1	Charmagzi	Habi	Halman	Marghulam	Narie	NiliPawand	ShaiPawand	Shakanda	Shakarfo	SkarduLocal
Ali Shah K	0.0000											
Astore 1	0.7500	0.0000										
Charmagzi	0.9444	0.7222	0.0000									
Habi	0.6944	**0.5278**	0.7778	0.0000								
Halman	0.7222	0.6944	0.8889	0.7500	0.0000							
Marghulam	0.9167	0.7500	**0.2778**	0.7222	0.8889	0.0000						
Narie	**0.6944**	0.6111	0.7500	0.5278	0.7778	0.7778	0.0000					
NiliPawand	0.8889	0.7500	0.5278	0.6944	0.8056	**0.4722**	0.7778	0.0000				
ShaiPawand	0.8889	0.7778	0.5278	0.7778	0.8611	0.5000	0.7500	**0.6944**	0.0000			
Shakanda	0.7222	0.7222	0.9167	0.8056	**0.6944**	0.8889	0.7500	0.8056	0.8333	0.0000		
Shakarfo	0.8889	0.8056	0.7500	0.8056	0.8056	0.7500	0.8333	0.8889	**0.7778**	0.9167	0.0000	
Skardu Local	0.7500	0.8333	0.8889	0.7222	0.7778	0.8611	**0.6944**	0.8611	0.8611	**0.8333**	**0.5278**	0.0000

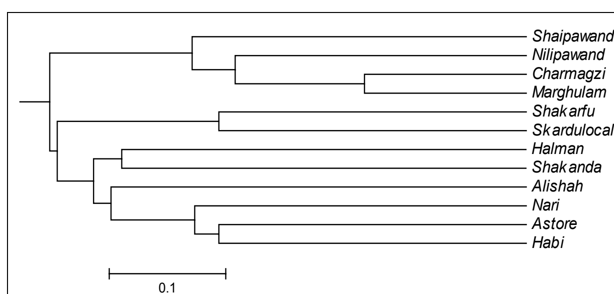

Figure 1. UPGMA dendrogram of apricot 12 genotypes from Gilgit Baltistan (Pakistan)

The analysis of the allele sizes revealed a high level of genetic distance between the cultivars. Each genotype was identified as a unique individual. The findings confirm the high genetic variation in the different districts of the region. This high genetic variation was expected because Gilgit Baltistan is a gate way and famous silk route between central Asian countries and China, which is considered an important diversification zone by the famous Russian Botanist VAVILOV, 1951[23] who reported that the Near East may be a secondary gene center because of the richness of the cultured varieties as well as the widespread seedlings. Clonal propagation through grafting has been used for commercial production in the GB. Nevertheless, most of the apricot trees in remote areas and domestic orchards are propagated by using seeds. The genetic diversity of apricots in the region is due to the rich source of cultivars and the hybridizations of clonal materials for centuries.

A total of 158 alleles were detected for 18 loci with an average number of (He) 0.77, (Ho) 0.64 and PIC value 0.75. (**Table 3**) SSR markers have already been used for variety, species identification and construction of genetic linkage maps of species belonging to family Rosacea. HORMAZA, 2002 [20] identified 48 apricot genotypes with 20 primers pairs from peach grouping the cultivars according to their geographical origin and or known pedigree information. In this experiment UDP98-412 produced 4 alleles in sweet cherry but the same SSR marker gave good result in our study that produced 5 alleles in local apricot genotype and can be use in further polymorphic study of apricot cultivars of this region.

In the present study ssrPaCITA16 and ssrPaCITA19 which gave 14 and 11 number of alleles respectively. They produced the highest number of alleles per locus is higher than previous screened same loci to characterize 25 apricot cultivars by LOPES & al. 2002 [13] likewise, pchgms-2 produced highest number of alleles (11) per locus as compared to previous studies by AKPINAR & al. 2010 [9] and YILMAZ & al.2012 [10] in which 7 numbers of alleles

were produced by same loci. The difference may be due to number and group of cultivars used in study. These microsatellites loci are the most informative one, with highest number of alleles may be used as DNA fingerprints for accession/variety identification of apricot genotypes.

The SSR loci used in this study revealed higher heterozygosity rates in apricot genotypes than those in other Prunus species, including apricots from other regions in the world, suggested that the apricot germplasm used in this study was probably more diverse (or heterozygous) than those used in other studies (AKPINAR & al. 2010 [9], SOSINSKI & al. 2000 [14]), WUNSCH and HORMAZA, 2002 [20], ROMERO & al. 2003 [21], SANCHEZ- PEREZ & al. 2005 [22]). The high heterozygosity levels and allele numbers observed in the current study were particularly useful for efficient genetic identification of Gilgit Baltistan apricot germplasm. The considerable level of genetic identity (0.52) was found between Astore1 and Habi, also correlated well with several common phenological and pomological properties of these cultivars, such as taste of seed, harvest maturity, flesh juiciness, separation of stone and shape of stone.

The Genetic distance values between apricots genotypes collected from Mountain Agriculture Research Center (MARC) Gilgit analyzed by UPGMA. A dendrogram was generated from genetic distance coefficients (**Fig. 1**). The apricot germplasm were clustered in three main groups on the basis of their place of origin in Gilgit Baltistan. The first cluster comprises of genotypes Nili Pawand, Shai Pawand, Charmagzi and Marghulam. The first three cultivars are commonly grown in Gilgit, Ghizer, and Diamer. Genotypes included in cluster II were Skardu local and Shakarfo. These genotypes had a same origin of Baltistan region. It had a low affinity level 52%. These results are consistent with their origin, showing that the members of this cluster had considerable genetic relationship to each other and genetically distant to others cultivars. The genotypes shared also some morphological characteristics (tree habit and leaf size), phenological features, (season of flowering, harvest maturity) and pomological (uniformity of ripening of fruit, firmness of fruit, taste of seed and separation of stone). Both were commercially important genotypes with respect to firmness of fruit and good fruit quality in Baltistan region. The cluster III comprised of six genotypes namely Halman, Shakanda, Ali Sha Kakas, Narie, Habi and Astore local. All the cultivars were originated from Hunza Nagar district of Gilgit Baltistan except local genotype Halman and Astore 1. Halman is belonged to Skardu and Ghanche districts and in Hunza/ Nagar some varieties known as Almas or Halmas. Astore1 is originated from Astore district. It may be assumed that the ancestor of Astore1 may be from Hunza/Nagar valley and also it had some morphological (leaf size, leaf blade shape), phenological (harvest season) and pomological feature (uniformity of ripening of fruit, percentage of fruit moisture, firmness of fruit, taste of seed, shape of stone and separation of stone) with Habi common. Overall the genotypes of this cluster were most diverse group. These results supported our hypothesis that in apricot cultivars there exists a greater genetic diversity in different districts of Gilgit-Baltistan.

In general, the genetic similarity among the cultivars was low and no synonymous cultivars were found, implying that Gilgit Baltistan is a rich source of diverse apricot germplasm. No correlation was found between the genetic resemblances and the geographical distributions of the cultivars.

Our findings reported here would be useful for better management of apricot germplasms in this region. Additionally, the data on the apricot cultivars for polymorphism reported here would be directly likened to other studies that have used or will be using the same SSR markers in other apricot genotypes or could be integrated into future studies investigating the genetic diversity of apricots from a broader geographical region.

Conclusion

The polymorphic studies carried out here, concluded that the SSR marker technique would be significantly useful in distinguishing cultivars and varieties of apricot. The present

analysis also revealed that the existence of a high level of genetic diversity within the apricot genotypes in the entire region of Gilgit Baltistan.

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