A Morphometric Study of Autochthonous Plum Genotypes Based on Multivariate Analysis

Abdollah Khadivi-Khub · Maryam Barazandeh

Abstract Iran is one of the most important plum producers in the world. The present study was conducted to compare agro-morphological characteristics of 100 traditional plum genotypes in Iran. The results showed statistically significant differences between the studied genotypes and leaf dimensions, fruit shape, fruit density, fruit color and fruit flesh firmness showed the highest relative range of variation. Flowering time was extended from 25 March to 5 April and fruit ripening from late July to early August. There were high positive correlations between fruit weight and fruit dimensions and between fruit weight and leaf dimensions. Principal component analysis showed high discrimination capabilities of variables measured. Most of these variables were characters linked to fruit and leaf size. Cluster analysis grouped the studied genotypes into two main clusters with several sub-clusters. In can be concluded that fruit weight, fruit color and fruit flesh firmness are very important characteristics and probably are the first characters to be considered in a farmers selection process. The results of the current study provided information which may be useful for determining the biodiversity of autochthonous genotypes, for the purposes of obtaining guidelines in determining *in situ* and *ex situ* germplasm characterization.

Keywords Plum · Phenotypic diversity · Morpho-pomological variables · Multivariate analyses

Eine morphometrische Untersuchung von autochtonen Pflaumen-Genotypen mit Hilfe der multivariaten Analyse

Zusammenfassung Der Iran ist einer der wichtigsten Pflaumenproduzenten der Welt. Diese Untersuchung wurde durchgeführt, um die agrar-morphologischen Eigenschaften von 100 Pflaumen-Genotypen im Iran zu vergleichen. Die Ergebnisse zeigten statistisch signifikante Unterschiede zwischen diesen Genotypen. Die Blattgröße, die Fruchtform, das spezifische Gewicht der Frucht, die Fruchtfarbe und die Fruchtfleischfestigkeit zeigten die größte relative Variationsbreite. Die Blütezeit erstreckte sich vom 25. März bis zum 5. April und die Reifezeit von Ende Juli bis Anfang August. Es gab eine enge positive Korrelation zwischen dem Fruchtgewicht und der Fruchtgröße und zwischen dem Fruchtgewicht und der Blattgröße. Die Hauptkomponentenanalyse zeigte eine hohe Erkennungssicherheit bei den gemessenen Variablen. Die meisten dieser Variablen bildeten Eigenschaften ab, die sich auf Frucht- und Blattgröße bezogen. Die Clusteranalyse gruppierte die untersuchten Genotypen in zwei Haupt-Cluster und mehrere Sub-Cluster. Es kann daraus gefolgert werden, dass das Fruchtgewicht, die Fruchtfarbe und die Fruchtfleischfestigkeit sehr wichtige Eigenschaften sind und vom Anbauer als erste Parameter beim Auswahlprozess angesehen werden. Die Ergebnisse dieser Untersuchung können hilfreich sein, die biologische Vielfalt autochthoner Genotypen zu erfassen, um die Genressourcen *in situ* und *ex situ* nach einem Leitfaden genau zu beschreiben.

Schlüsselwörter Pflaume · Phänotypisches Erscheinungsbild · Agrar-morphologische Variablen · Multivariable Analyse · Genressource

A. Khadivi-Khub (✉) · M. Barazandeh
Faculty of Agriculture and Natural Resources,
Department of Horticultural Sciences, Arak University,
38156-8-8349, Arak, Iran
e-mail: a-khadivi@araku.ac.ir

Introduction

The genus *Prunus* (*Rosaceae*, sub-family *Prunoideae*) comprises five subgenera with a basic number x=8 (Badenes and Parfitt 1995). The *Prunus* L. genus includes about 400 species of trees and shrubs originating mainly in the northern hemisphere and widely represented in Europe (Bouhadida et al. 2007). In fact, many important fruit trees species are classified into *Prunus* genus, like peach, almond, apricot, Japanese plum, Japanese apricot, European plum, sweet cherry and sour cherry. These species are economically important as sources of fruits, nuts, oil, timber and ornamentals (Aradhya et al. 2004). Plums (hexaploid *Prunus domestica* L. and diploid *P. salicina* L.) are classified systematically into the subgenus *Prunophora* of the genus *Prunus*.

Watkins (1976) postulated a center of origin for *Prunus* in central Asia and concluded that plum species in the *Prunophora* are the central species for *Prunus* evolution, due to their ability to hybridize with species from the other subgenera (Badenes and Parfitt 1995). Plums have been cultivated in three different continents, European plums belong to *P. domestica* L., *P. cerasifera* Ehrh., *P. spinosa* L. and *P. insititia* species, while Japanese type plums are commonly included in *P. salicina* Lindl species. American plums arose from numerous species such as *P. americana* Marsh., *P. munsoniana* Wight and *P. angustifolia* Marsh. A number of hypotheses have been extended with supportive cytogenetic data in efforts to elucidate the origin of plums. Many authors proposed that *P. domestica* consists of three genomes implicating diploid and polyploidy forms of *P. cerasifera* as the sole ancestor (Bajashvili 1990; Zohary 1992). However, the European plum has been reported as a product of natural crossing between *P. spinosa* and *P. cerasifera* (Crane and Lawrence 1952). It is commonly known that many plums are self-incompatible and in many cases, it is difficult to determine whether cultivars are pure species. Thus, many cultivars are hybrids resulting from natural crossing among plum species, or with mume (*P. mume* Sieb. and Zucc.), apricot (*P. armeniaca* L.), or even peach (*P. persica* Batsch) (Howard 1945). It is difficult to classify plum cultivars for these reasons; many of the currently cultivated diploid plums are hybrids whose parents are unknown.

One of the major concerns of conservation biology is the knowledge on biodiversity. In the other hand, knowledge of the genetic diversity of existing germplasm can informatively guide parental selection in breeding improvement programs. Cultivated species of *Prunus* have been examined for intraspecific diversity and differentiation. Plum species have been classified primarily based on morphological characteristics (Hegi 1923; Roder 1940) and former studies were conducted to establish the genetic diversity of plum cultivars involving physiological and pomological parameters (Ertekin et al. 2006). Local germplasm is men-

aced by genetic erosion caused by biotic and abiotic stresses and many local cultivars have disappeared or cultivated in private orchards. In this critical situation, knowledge of the phenotypic diversity and relationships among plum genotypes and species is important to recognize gene pools, identify local germplasm and develop effective conservation and management strategies.

Traditional methods for cultivar and genotype characterization and identification of plums are based on phenotypic observations. Morphological traits are useful for preliminary evaluation because they facilitate fast and simple evaluation and can be used as a general approach for assessing genetic diversity among morphologically distinguishable accessions. Morphological characterization combined with multivariate statistical methods, such as principal component analysis (PCA), the most commonly applied, and cluster analysis, are useful tools for screening plum accessions (Crisosto et al. 2007; Hend et al. 2009; Aazami and Jalili 2011; Milošević and Milošević 2012).

In Iran, numerous plum genotypes and cultivars exist including very old ones of unknown origin and not derived from breeding programs, but reports their phenotypic and genotypic diversity are rare. Thus, the objective of the current study was to describe the variability in 100 local plum genotypes, determine the correlation among traits, identify the most useful variables for discrimination among genotypes, and detect relationships among genotypes. Furthermore, an evaluation of economically valuable traits was performed to identify useful genotypes for plum producers and breeding programs.

Materials and Methods

Plant Materials

We have used a set of 100 local plum genotypes, selected from central parts of Iran. Genotypes were selected after evaluation based on regular fruit production and observed phenotypic diversity. Selection of genotypes was mainly conducted according to relevant morphological traits of the tree, fruit and phenology. The examined genotypes were 8-year-old.

Phenotypic Characterization

Morphological and pomological characterization of each genotype was performed according to the guidelines provided by the International Plant Genetic Resources Institute (IBPGR 1984), in the descriptor list for plum and allied species. This manual includes agronomic and biological characters to be recorded for the plum trees. In this work, 32 phenotypic characteristics, comprising 17 quantitative

and 15 qualitative traits, were used to assess the range of morphological variation among the genotypes. Characters related to the fruit were measured, calculated and visually estimated at harvest stage (full maturity). The samples of 50 fruits per genotype were harvested randomly. Quantitative traits were measured by using laboratory equipment such as digital caliper, precision weighing balance and digital measuring tape. In addition, qualitative characteristics were considered based on rating and coding according to plum descriptor (IBPGR 1984).

Statistical Analysis

The data resulting from the 2 year study (2012 and 2013) were grouped, and the average values were used for statistical analysis. The following parameters were evaluated for the measured variables: mean, minimum value, maximum value, and coefficient of variation (CV %). Analysis of variance was performed for all morphological traits by SAS software (SAS Inst. 1990). Relationships among genotypes were investigated by multivariate analysis of variance (principal component analysis, PCA) using SPSS statistics software. The correlation between all variables was also evaluated using Pearson correlation coefficient using SPSS® version 16 (Munich, Germany). Scatter plot of the first two PCs was created by PAST statistics software (Hammer et al. 2001). To avoid the effects due to scaling differences, mean of each character was normalized prior to cluster analysis using Z scores. Thereafter, Euclidean distance coefficient for pairs of entries (*i.e.* genotypes) was computed using NTSYSY-pc (Numerical Taxonomy and Multivariate Analysis for personal computer) software program version 2.00 (Rohlf 2000). To better understand the patterns of variation among genotypes, distance matrix generated from morphological data was used as input data for cluster analysis based on unweighted pair-group method of arithmetic average to better understand (UPGMA).

Results and Discussion

Descriptive Statistic and Phenotypic Variation Among Genotypes

The studied genotypes showed significant variability in many of the characters analyzed. The descriptive statistical analysis values for each of the traits are reported in Table 1. Differences were observed in the maximum and minimum values for all traits. Some traits, such as canopy diameter, leaf dimensions, fruit shape, fruit density, fruit color and fruit flesh firmness showed the highest relative range of variation. The coefficient of variation varied from 7.43 % (total soluble solid, TSS) to 81.65 % (fruit density).

Most of characters reached CV values of higher than 20 %, while some traits of fruit and flowers reached values lower than 20 %, *e.g.* flower color and fruit dimensions. The coefficient of variation is a parameter that is not related to a unit of measured traits, and is to be effective in comparing the traits examined. The CV value may be an indicator of the ability of a morphological trait to distinguish between genotypes. Morphological characteristics with a low CV % are more homogeneous and repeatable among genotypes, while descriptors with high CV % values are more discriminating than the other ones, and can be reliable markers for the characterization of genotypes. Among quantitative traits, the highest maximum/minimum value ratio variation was observed in leaf dimensions. In contrast, the lowest maximum/minimum ratio was displayed by TSS, tree height and fruit dimensions.

The plum collection was characterized by genotypes with medium-strong or strong tree vigor, and most of the genotypes had an upright habit and some spreading, while a drooping habit was not observed. In addition, most of the genotypes showed a medium-strong branching with no or low suckering. In our agro-ecological zone, most of the genotypes concentrated their flowering between 25 March to 5 April, while fruits of most genotypes were harvested in late July and/or early August, depending on genotype (Garcia-Marino et al. 2008), and a genetically programmed process (de Dios et al. 2006), and considered as a quantitative trait in *Prunus* species (Vargas and Romero 2001; Dirlewanger et al. 2004). Although blooming and harvesting times may change every year, depending on the environmental conditions, they remained quite stable during the 2 years in which we observed most genotypes. In addition, both traits depend on environmental conditions (temperature, altitude, etc.) and may change every year (Liverani et al. 2010). Due to the interaction between environment and genotype, it is very important to evaluate preliminarily blooming and harvesting time performance of all genotypes in the areas in which they will be cultivated (Koskela et al. 2010).

The highest values for spur leaf length and spur leaf width were 4.51 and 2.63 cm, respectively, the lowest mean for spur leaf length was 1.00 cm and for spur leaf width was 0.58 cm. Shoot leaf length and width had a mean value of 3.90 and 1.94 cm, respectively, and with a variation between genotypes ranging from 2.13 to 5.32 cm for shoot leaf length and 1.06 to 4.77 cm for shoot leaf width. The basal and apical leaf angles were quite similar for all genotypes, with no marked differences. Among leaf traits, wide variability was observed in the shoot and spur petiole length traits. The values of shoot petiole length was ranging from 0.62 to 2.00 cm, while spur petiole length varied from 0.47 to 1.54 cm. Aazami and Jalili (2011) reported that leaf related criteria had significant morphological diversity in Iranian plums.

Table 1 Descriptive statistics for the measured morphological variables among the studied 100 plum genotypes

Trait	Abbreviation	Unit	Min	Max	Max/Min	Mean	CV (%)
Flowering time	FlTi	Date	25 March	5 April	–	–	–
Harvesting time	HaTi	Date	Late-July	Early-August	–	–	–
Flower color	FlCo	Code	1	2	–	1.02	13.82
Suckering	Su	Code	1	2	–	1.06	22.55
Tree height	TrHe	cm	178.00	320.00	1.80	244.73	13.09
Growth habit	GrHa	Code	1	5	–	4.44	24.03
Shoot flexibility	ShFl	Code	1	7	–	4.50	40.13
Trunk color	TrCo	Code	1	9	–	4.90	33.51
Fruit shape	FrSh	Code	1	3	–	1.10	39.82
Trunk diameter	TrDi	Code	3	8	–	5.89	18.64
Leaf shape	LSh	Code	1	5	–	4	36.58
Leaf color	LCo	Code	1	5	–	4.18	30.48
Shoot leaf length	ShLLe	cm	2.13	5.22	2.46	3.90	16.99
Shoot leaf width	ShLWi	cm	1.06	4.77	4.50	1.94	28.25
Shoot leaf length/width	ShLLe/Wi	Ratio	0.45	2.91	6.47	2.09	15.58
Shoot petiole length	ShPeLe	cm	0.62	2.00	3.22	1.25	24.80
Spur leaf length	SpLLe	cm	1.00	4.51	4.51	3.02	25.96
Spur leaf width	SpLLe	cm	0.58	2.63	4.53	1.51	23.37
Spur leaf length/width	SpLLe/Wi	Ratio	0.45	2.57	5.71	2.02	17.33
Spur petiole length	SpPeLe	cm	0.47	1.54	3.28	0.91	25.31
Shoot density	ShDe	Code	1	5	–	4.56	27.59
Leaf density	LDe	Code	3	5	–	4.78	13.16
Canopy diameter	CaDi	Code	1	5	–	2.80	56.07
Fruit density	FrDe	Code	1	9	–	2.72	81.65
Fruit color	FrCo	Code	1	5	–	3.76	39.84
Fruit length	FeLe	cm	2.00	3.78	1.89	2.71	14.04
Fruit diameter	FrDi	cm	2.30	4.35	1.89	3.44	10.11
Fruit stalk length	FrStLe	cm	1.00	2.00	2.00	1.47	15.33
Fruit weight	FrWe	g	16.30	31.00	1.90	17.76	25.16
Fruit stone weight	FrStWe	g	0.73	1.64	2.25	1.18	16.70
Total soluble solid	TSS	%	18	24	1.33	19.44	7.43
Fruit flesh firmness	FrFlFi	Code	1	3	–	2.28	42.32

Fruit length showed a range of 2.00 to 3.87 cm, while fruit diameter varied from 2.30 to 4.35 cm. In addition, fruit weight ranged from 16.30 to 31.00 g. Milošević and Milošević (2012) reported fruit weight of Serbian plum cultivars within a range of 6.20–28.00 g. Furthermore, in the present study, the predominant shape of the fruits in the studied genotypes was round, followed by elliptic and broad elliptic. In plums, round shapes without protruding tips are prefered by consumers (Crisosto et al. 2007). For most of the genotypes, fruit skin was not cracked. In the present study, TSS varied from 18 to 24% and most of genotypes showed TSS values higher than 20%. Milošević and Milošević (2012) reported range of 10.30 to 19.50% for TSS in Serbian plums. A considerable phenotypic diversity regarding this trait was reported previously by other authors (Jovancevic 1977; Mratinic 2000). The TSS content is a very important quality attribute, influencing notably the sweet taste (Crisosto et al. 2007).

The average of fruit stone weight was 1.18 g, with a range of 0.73 and 1.64 g. Most of the genotypes had medium stones. Properties of the stones of *Prunus* taxa are the most stable ones (Woldring 2000), and their dimensions are very useful for the identification of *P. domestica, P. insititia* and *P. spinosa* (Behre 1978). The fruit skin color of the sampled fruits ranged from pink to blackish-red. A considerable phenotypic diversity regarding plum sensorial traits was reported previously by Milošević et al. (2010). Fruit skin color has been found to be controlled by a single gene, with a dark color being dominant over a light color: indeed, the genotypes were prevalently characterized by fruits having a blackish-red color. Most of the genotypes had intermediate and taut fruit flesh firmness.

Fruit density showed high differences among genotypes, which is in agreement with previous studies of local plum cultivars (Paunovic and Paunovic 1994; Milošević and Milošević 2012). The observed variability supports the quantitative genetic control of yield previously reported in *Rosaceae* fruit crops (Dirlewanger et al. 2004).

The fruit characteristics provide important groups of traits relative to the characterization of plum, and certain traits

such as fruit size, fruit diameter and skin color have been used to distinguish between plum cultivars and genotypes (Paunovic and Paunovic 1994). In the present study, the largest variability among the traits of fruits corresponded to fruit shape, fruit density, fruit color and fruit flesh firmness. Our results are in accordance with the results of other authors (Paunovic and Paunovic 1994; Milošević and Milošević 2012), who have reported that fruit color and fruit shape may be the most important characteristics for differentiating plum cultivars. The fruit weight is a very important characteristic because of its economic importance: some genotypes, *e.g.* genotypes P4, P19, P28, P33, P42, P65 and P98, have shown large fruits with high weights. This could be explained by the fact that the size of the fruit was probably one of the first characters to be considered in a traditional farmer's selection process (Paunovic and Paunovic 1994). Although the most important variables in distinguishing genotypes have been fruit size, certain dimensional traits of fruit can be also important.

Besides, the skin color of fruit is a very important quality attribute, and serves in estimating the stage of maturity of the fruit. Several studies have evaluated the changes in color of plum and have used color to monitor pigment evolution (Behre 1978; Paunovic and Paunovic 1994; Milošević and Milošević 2012). The fruit skin color also has a significant impact on consumer perception of fruit quality, especially as regards the attractiveness of fruit, and consumers generally seem to prefer blakish-red plum (Ruiz and Egea 2008). Fruit flesh firmness is relevant to an assessment of the quality of fruit, to affecting fruit shelf life, and to consumer acceptance. Fruit flesh firmness is a combination of skin and flesh strength, and in general, cultivars with the firmest fruit are preferred (Hend et al. 2009).

Correlations Among Characters

Simple correlation coefficient analysis showed the existence of significant positive and negative correlations among characteristics (Table 2). Growth habit exhibited a correlation to shoot density and leaf density and a positive strong correlation was observed between shoot density and leaf density, in agreement with others (Sedaghathoor et al. 2009). Significantly, positive correlations were found between shoot leaf length and shoot leaf width and spur leaf length and spur leaf width, and between these four traits with each other. Leaf dimensions were also positively correlated to petiole length. A positive correlation between leaf descriptors was determined in plum (Sedaghathoor et al. 2009) and other *Prunus* species (Rakonjac et al. 2010; Khadivi-Khub et al. 2012).

Leaf dimensions were correlated with fruit weight and dimensions. Our results are in accordance with the results of studies in plum (Sedaghathoor et al. 2009) and other *Prunus*

species (Rakonjac et al. 2010; Khadivi-Khub et al. 2012), who found that the fruit and leaf traits were highly correlated with each other. Increasing leaf area, that is the main place to trap sunlight for photosynthesis, consequently provides the condition to produce larger fruits (Taiz and Zeiger 2002). Some correlations were also observed between the fruit variables. Fruit length and diameter were related positively to fruit weight; therefore, these characters can be used to predict each other (Okut and Akca 1995). This relationship was also detected in plum (Milošević and Milošević 2012) and other *Prunus* spp. (Demirsoy and Demirsoy 2004; Ruiz and Egea 2008; Khadivi-Khub et al. 2013). In addition, fruit length, diameter and weight were negatively correlated to fruit density. It indicated that higher yield induced lower fruit size, which is in agreement with previous works (Sestraş et al. 2007 ; Milošević and Milošević 2012). The fruit weight positively correlated to fruit stone weight, as previously described by others (Hend et al. 2009; Milošević and Milošević 2012). This can be explained by the existence of different genetic mechanisms among organs, which control the developmental pathways.

The correlation coefficient can provide information on the traits that are most important in assessing genotypes (Milošević et al. 2010; Norman et al. 2011). Nevertheless, some authors recommend analyzing correlation coefficients close to 0.70: in these conditions, the variance of one trait is strongly dependent on the others (Skinner et al. 1999). These variables can be used to predict other ones, and could be considered of importance for the characterization of genotypes. In addition, a close relationship between traits could facilitate or hinder gene introgression since strong selection for a desirable trait, could favour the presence of another desirable trait from germplasm (Dicenta and Garcia 1992).

Principal Component Analysis

Principal component analysis (PCA), one of the multivariate statistical procedures, was used to identify the most significant traits in the data set. The aim of principal component analysis is determining the number of main factors for reducing the number of effective parameters to discriminate genotypes. In addition, associations between traits emphasized by this method may correspond to genetic linkage between loci controlling traits or a pleiotropic effect (Iezzoni and Pritts 1991). Previously, PCA had been used to establish genetic relationships among cultivars and genotypes, to study correlations among tree traits and to evaluate germplasm of plum (Crisosto et al. 2007; Hend et al. 2009; Aazami and Jalili 2011; Milošević and Milošević 2012) and different *Prunus* species such as apricot (Ruiz and Egea 2008), sour cherry (Rakonjac et al. 2010; Khadivi-Khub et al. 2013) and several wild *Cerasus* species (Khadivi-Khub et al. 2012).

Table 2 Bivariate correlations among measured variables in the studied plum genotypes

Trait	FlCo	Su	TrHe	GrHa	ShFl	TrCo	FrSh	TrDi	LSh	LCo	ShLLe	ShLWi	ShLLe/Wi	ShPeLe	SpLLe	SpLLe/Wi
FlCo	1.00															
Su	0.27[b]	1.00														
TrHe	−0.20[a]	0.06	1.00													
GrHa	0.08	−0.03	0.07	1.00												
ShFl	−0.04	0.07	−0.12	0.17	1.00											
TrCo	−0.17	−0.04	0.12	0.08	0.07	1.00										
FrSh	−0.03	−0.06	−0.35[b]	0.04	0.01	0.13	1.00									
TrDi	−0.14	−0.03	0.52[b]	0.09	0.04	0.20[a]	−0.13	1.00								
LSh	0.10	0.00	0.09	0.03	0.21[a]	−0.13	−0.03	0.08	1.00							
LCo	−0.02	0.16	0.14	−0.07	0.00	0.00	0.08	−0.05	0.01	1.00						
ShLLe	−0.06	−0.08	−0.08	−0.03	−0.02	0.16	0.13	0.05	−0.31[b]	0.20	1.00					
ShLWi	−0.05	−0.07	0.01	0.05	−0.10	0.25[a]	0.04	−0.08	−0.25[a]	−0.19	0.26[a]	1.00				
ShLLe/Wi	−0.01	0.01	−0.04	−0.06	0.13	−0.17	0.05	0.16	0.06	0.20	0.20[a]	−0.82[b]	1.00			
ShPeLe	−0.08	−0.05	0.05	−0.05	−0.17	0.17	0.06	−0.01	−0.30[b]	0.13	0.60[b]	0.47[b]	−0.17	1.00		
SpLLe	0.05	0.01	0.17	0.12	0.15	0.24[a]	0.06	0.38[b]	−0.06	0.00	0.34[b]	0.08	0.09	0.11	1.00	
SpLLe/Wi	0.04	0.01	0.22[a]	0.14	0.07	0.20[a]	−0.02	0.17	−0.24[a]	−0.01	0.14	0.28[b]	−0.19	0.00	0.56[b]	1.00
SpPeLe	0.01	−0.03	−0.07	0.02	0.10	0.08	0.10	0.22[a]	0.16	−0.04	0.28[b]	−0.13	0.24[a]	0.16	0.55[b]	0.35[b]
ShDe	−0.08	−0.04	0.27[b]	0.01	0.10	0.17	0.01	0.42[b]	−0.13	−0.06	0.25[a]	0.17	0.00	0.13	0.78[b]	0.56[b]
LDe	−0.18	−0.18	−0.01	0.30[b]	0.08	0.33[b]	0.08	0.05	−0.20[a]	−0.18	0.34[b]	0.28[b]	−0.12	0.22[a]	0.28[b]	0.24[a]
CaDi	−0.18	−0.18	−0.01	0.30[b]	0.08	0.33[b]	0.08	0.05	−0.20[a]	−0.18	0.34[b]	0.28[b]	−0.12	0.22[a]	0.28[b]	0.24[a]
FrDe	−0.17	−0.13	0.13	0.03	0.09	0.10	−0.03	0.07	−0.09	0.08	0.12	−0.01	0.03	0.06	0.22[a]	0.14
FrCo	−0.05	−0.01	0.07	0.02	−0.13	0.05	−0.18	−0.10	−0.16	0.00	0.13	0.08	−0.08	0.10	0.25[a]	0.28[b]
FeLe	0.02	0.10	−0.04	−0.06	−0.14	0.05	−0.12	−0.02	−0.11	0.01	0.06	0.15	−0.08	0.18	−0.25[a]	−0.30[b]
FrDi	−0.13	−0.01	−0.06	0.03	0.22[a]	0.06	−0.06	0.15	0.09	−0.08	0.34[b]	0.31[b]	0.06	−0.10	0.23[a]	0.20[a]
FrStLe	0.05	−0.05	−0.20[a]	−0.08	−0.13	0.02	0.15	0.07	0.04	0.03	0.34[b]	0.35[b]	−0.05	0.00	0.39[b]	0.38[b]
FrWe	0.01	0.05	0.03	−0.04	−0.01	−0.10	0.04	0.01	−0.03	0.01	−0.22[a]	−0.06	−0.08	0.02	0.01	−0.04
FrStWe	−0.04	−0.13	−0.01	0.10	0.04	−0.09	0.15	0.12	0.02	0.06	0.34[b]	0.24[a]	0.24[a]	−0.06	0.35[b]	0.34[b]
TSS	−0.06	−0.13	0.14	0.00	0.02	0.03	−0.15	0.15	0.01	−0.01	0.00	0.04	0.01	0.19	0.05	0.07
FrFlFi	0.11	−0.07	−0.17	0.00	−0.05	−0.05	−0.02	0.03	0.14	−0.06	0.02	−0.05	0.06	0.03	−0.12	−0.17

Table 2 (Continued)

Trait	FlCo	Su	TrHe	GrHa	ShFl	TrCo	FrSh	TrDi	LSh	LCo	ShLLe	ShLWi	ShLLe/Wi	ShPeLe	SpLLe
Trait	SpLLe/Wi	SpPeLe	ShDe	LDe	CaDi	FrDe	FrCo	FeLe	FrDi	FrStLe	FrWe	FrStWe	TSS	FrFlFi	SpLLe
SpLLe/Wi	1.00														
SpPeLe	0.30[b]	1.00													
ShDe	0.17	0.18	1.00												
LDe	0.17	0.18	1.00[b]	1.00											
CaDi	0.08	0.16	0.12	0.12	1.00										
FrDe	0.03	−0.23[a]	0.16	0.16	0.02	1.00									
FrCo	0.02	−0.20	−0.12[a]	−0.12	0.00	0.25	1.00[a]								
FeLe	0.04	0.19	−0.02	−0.02	0.01	−0.34[b]	−0.27[b]	1.00							
FrDi	0.14	−0.07	−0.04	−0.04	−0.11	−0.14	−0.10	0.30[b]	1.00						
FrStLe	0.03	−0.06	−0.11	−0.11	−0.16	0.13	0.04	0.09	0.12	1.00					
FrWe	0.14	0.01	−0.08	−0.08	−0.13	−0.19	−0.39[b]	0.33[b]	0.52[b]	0.02	1.00				
FrStWe	−0.01	0.16	0.17	0.17	0.03	0.13	0.10	0.01	0.07	−0.10	0.25[a]	1.00			
TSS	0.14	−0.03	−0.14	−0.14	0.200[a]	−0.02	−0.01	−0.01	−0.04	0.03	0.03	0.03	1.00		
FrFlFi	0.01	−0.10	−0.06	−0.06	−0.203[a]	−0.04	−0.18	0.01	0.15	−0.02	0.16	0.16	0.00	1.00	

**Table 3** Eigenvectors of the first three principal component axes from PCA analysis of the studied plum genotypes

Trait	Component 1	2	3
Growth habit	−0.06	**0.56**	0.01
Shoot leaf width	0.11	0.16	**0.88**
Shoot leaf length/width	0.05	−0.06	**−0.90**
Spur leaf length	**0.87**	0.18	−0.05
Spur leaf width	**0.69**	0.15	0.21
Spur petiole length	**0.87**	0.06	0.04
Shoot density	0.14	**0.90**	0.12
Leaf density	0.14	**0.90**	0.12
Fruit length	0.31	−0.08	**57.00**
Fruit diameter	−0.06	−0.08	**0.77**
Fruit weight	0.00	0.03	**−0.80**
Total	2.87	2.56	2.22
% of Variance	12.01	10.95	9.83
Cumulative %	9.57	18.09	32.79

For each factor, a principal component loading of more than 0.56 was considered as being significant that indicated 12 components with explaining 76.45 % of the total variance (Table 3). Result of PCA analysis showed that 32.79 % of the total variation was explained by the first three principal components, which accounted for 12.01, 10.95 and 9.83 %, respectively of the observed variation (Table 3), indicated that these attributes have the highest variation between the genotypes and had the greatest impact on separation of the genotypes (Iezzoni and Pritts 1991). The most important traits found to explain the variation including spur leaf length, spur leaf width and spur petiole length had high loadings on and were associated with PC1. On the other hand, growth habit, shoot density and leaf density had high loadings on and were associated with PC2. Also, shoot leaf width, shoot leaf length/width, fruit length, fruit diameter and fruit weight had high loadings on and were associated with PC3. These results in some cases were in agreement with the results reported by other plum studies (Crisosto et al. 2007; Hend et al. 2009; Aazami and Jalili 2011; Milošević and Milošević 2012). They have suggested that fruit and leaf traits are important factors in differentiating and analyzing breeding materials dealing with the morphological characterization of plum. Factor analysis had great potential to differentiate the highlighted distinctions between the studied genotypes and agreed with finding of others in study of plum (Kaufmane et al. 2002; Ogasanovic et al. 2007; Aazami and Jalili 2011). Correlations between characteristics revealed by PCA method may correspond to a genetic linkage between loci of controlling traits or a pleiotropic effect (Iezzoni and Pritts 1991).

UPGMA Cluster Analysis and Scatter Plot

UPGMA cluster analysis was used in order to divide the available data up into groups of increasing dissimilarity.

Fig. 1 UPGMA dendrogram of the studied plum genotypes using Euclidean distance coefficient matrix, based on morphopomological data
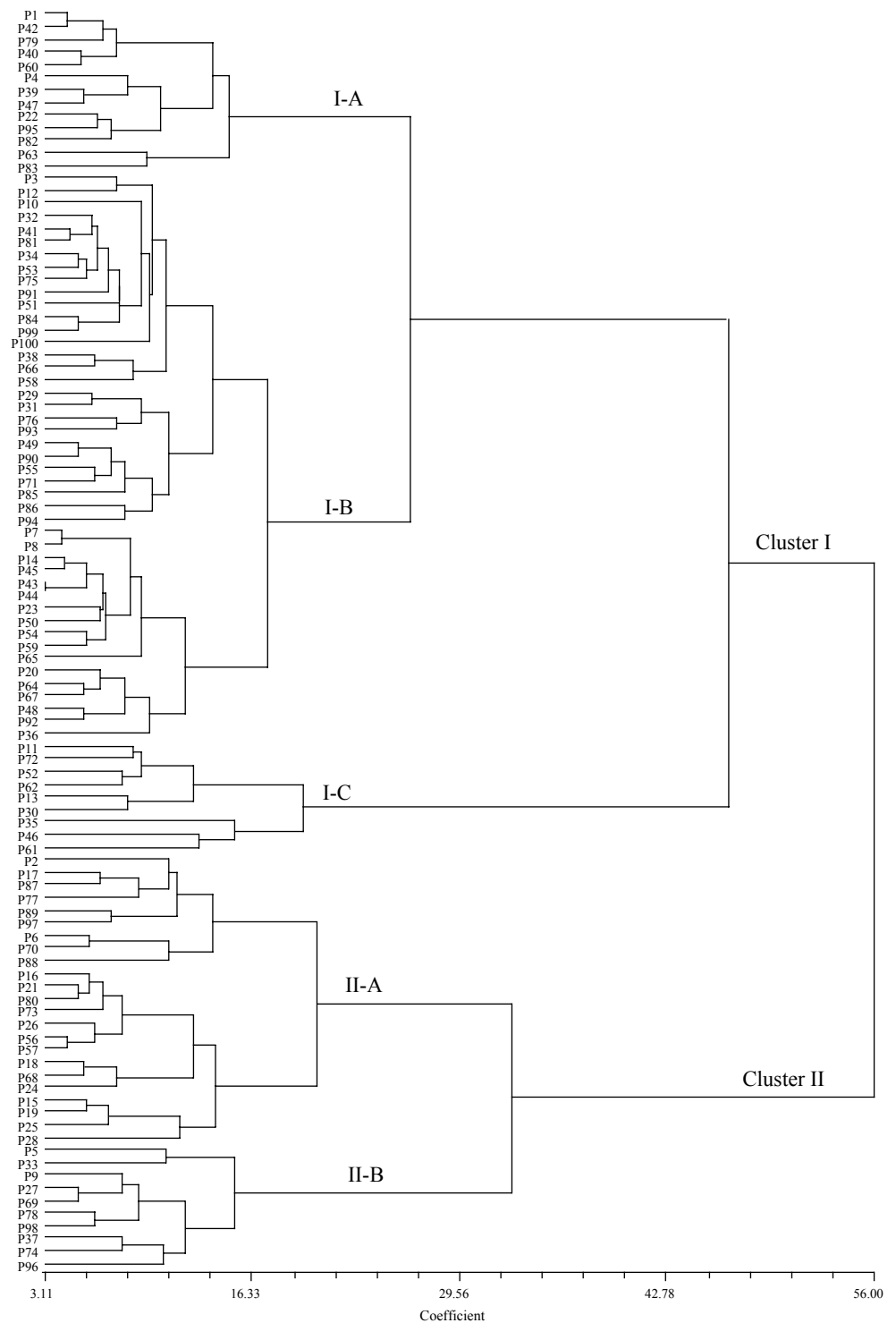
The dendrogram identified two major clusters with several sub-clusters (Fig. 1). The cluster I was divided into three sub-clusters, including predominantly the genotypes having higher values for leaf and fruit and the majority of these genotypes showed a medium-to-late flowering and ripening times, while other genotypes are grouped into the second major cluster. Into cluster I, sub-cluster I-A included 45 genotypes, the majority of which were characterized by rela-

tively high fruit, the presence of dark red or black skin, and a high firmness of the fruit. Sub-cluster I-B, which brought together 13 genotypes with medium fruits, dark red skin color of the fruit and medium firmness of the fruit, and sub-cluster I-C, which consisted of nine genotypes with medium fruit size, a red skin color of the fruit and soft firmness of the fruit. The cluster II was divided into two sub-clusters. Sub-cluster II-A included 23 genotypes which were charac-

Fig. 2 Scatter plot for the first two principal components (PCs) for the studied plum genotypes based on morphological characters
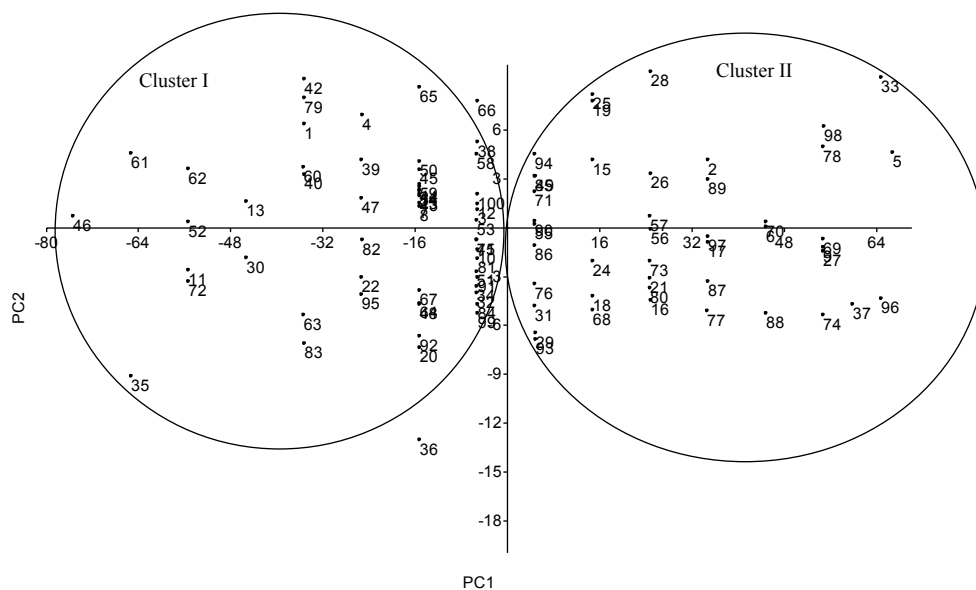
terized by relatively medium to small leaf and fruits, a red or pink red skin color, and medium flowering and ripening times. Sub-cluster II-B contained 10 genotypes which were characterized by small leaf and fruits, a pink red skin color, and medium flowering and ripening times.

Scatter plot was prepared according to the PC1 and PC2. Results of scatter plot supported the results of cluster analysis and genotypes were distributed into four sides of scatter plot with two major clusters (Fig. 2). Cluster I classified together the genotypes with high values for fruit and leaf descriptors, which had a large fruit size and large leaf. The genotypes included in cluster II were mainly those with the lowest values of leaf and fruit traits. The minimum discrepancy between cluster and scatter dendrograms can be explained by the variability considered for the analysis. The hierarchical cluster analysis based on the entire morphological data took into account the whole variability, while the cumulative variance explained by the first two principal components, creating scatter plot, was relatively low (18.09 %). These data emphasize the crucial question of how to choose the sampling strategy that maximizes the information present in germplasm collection.

Conclusions

Significant phenotypic diversity was detected between traditional plum genotypes from Iran. By using hierarchical cluster and PCA, two groups of genotypes were separated on the dendrograms obtained. The separation of the genotypes into groups was primary because of the leaf and fruit traits, but other characteristics also influenced the separation. The PCA identified highly discriminating variables, *i.e.* fruit and leaf traits which are important for the characterization of geno-

types groups. This result suggested a reduction in the number of traits to be studied in the local plum germplasm without causing a considerable loss of information, while making possible reductions in labor, time and cost. As an additional conclusion, the classification and misclassification of genotypes could provide information on the compactness of the cultivar. Our results, which were based on morphological analyses of genotypes, showed a level of mixing between the genotypes. It is clear that an appropriate sampling strategy is an important prerequisite in minimizing the influence of environmental factors which may cause diversity in desirable morphological traits. Moreover, certain genotypes may overlap each other. Large germplasm collections represent a massive investment of resources over time, while the increase in the number of samples tested and the accuracy of the samples, as well as the time and the methodology of the sampling (*i.e.*the cardinal direction, the position on the shoots) could constitute a valid system for reducing the level of overlap between the genotypes. Finally, examined germplasm of autochthonous plum genotypes consists of genotypes which can be recommended for fresh consumption and processing. Based on the fruit size, chemical and sensorial properties, genotypes P4, P19, P28, P34, P40 and P98 are recommended for fresh consumption, while genotypes P3, P46, P47, P50, P51, P80, P81 and P97 are recommended for drying. The conclusion of the present study confirmed the necessity of preserving these irreplaceable genetic resources.

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