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Variation of some *Diospyros* genotypes in Iran based on pomological characteristics

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A B S T R A C T

Purpose: Gaining knowledge about the genetic diversity is essential in terms of plant breeding and germplasm conservation. In this study, the genetic diversity of some persimmons was evaluated using pomological traits. **Research method:** 28 genotypes belonging to *D. lotus* and *D. kaki* species were evaluated from different regions of Iran. Nineteen fruit and seed traits were recorded for 15 fruits per genotype. **Findings:** Pomological characteristics showed high variations among the studied genotypes. Generally, the coefficient of variation in seed traits was higher than that in fruit traits. All of the *D. lotus* and some *D. kaki* genotypes were seeded, while the rest of *D. kaki* genotypes were seedless. Fruit weight ranged from 4.45–251.77g, and the most fruit weight was recorded in KBM1 genotype, also the biggest seeds and the most fruit length was detected in this genotype. The results indicated that a significant and positive correlation there was between fruit weight and length with seed dimensions. Various fruit shape was detected among the genotypes, but most of them were round-shaped. The genotypes ranged from strongly-astringent to completely non-astringent types. Cluster and principle component analysis showed that all the genotypes can be divided into three main groups, and some of the groups can be divided into distinct sub-groups. In PCA, first two components explained about 60.97% of total achieved variability. **Research limitations:** No limitations were encountered. **Originality/Value:** This study indicated that *Diospyros* germplasm resources in Iran are of noticeable diversities and can be promising for the utilization in the breeding programs.

INTRODUCTION

Diospyros genus, belonging to the Ebenaceae family, has over 500 species worldwide, some of which have considerable significance with respect to the persimmon production (Deng et al., 2015). The most important cultivated species of this genus is *D. kaki* Thunb., which is widely known as Japanese or oriental persimmon, typically a deciduous and subtropical crop (Yonemori et al., 2000). Phylogenetic study suggested that Japanese persimmon originated from southern of China and then, spread to Korea and Japan (Guan et al., 2020). Today, Japanese persimmon is one of the important fruit crops in the world, which is cultivated in different temperatures and subtropical regions in Asia, Oceania, Europa and South and Central America (Yesiloglu et al., 2018). Persimmon is naturally bestowed with bioactive molecules including phenolics, flavonoids, proanthocyanidins, tannins, carotenoids, dietary fiber, minerals (such as potassium, calcium, magnesium, iron, zinc, copper, manganese), and different vitamins such as ascorbic acid, etc. Owing to rich phytochemistry, persimmon and its products are considered effective in mitigating the oxidative damage induced by reactive oxygen species (Butt et al., 2015).

Worldwide persimmon production was 4,270,074 tons in 2019; the production in Asian countries was accounted for 96% of persimmon production (FAO, 2019). Although the origin and date of the introduction of Japanese persimmon to Iran have been unknown, it has been cultivated for more than 200 years in different regions of Iran. Commercial persimmon orchards are located in Northern provinces involving Alborz, Tehran and Isfahan. Iran's persimmon production was 25,272 tons from 1684 hectare in 2019. Date-plum (*D. lotus*) is one of the wild species of the *Diospyros* genus which is usually used as the rootstock for Japanese persimmon (Yang et al., 2015). Date-plum is wildly widespread in northern forests of Iran and the ripen fruits are used to produce syrup and jam. The seeds of date-plum can be used as medicine, and its fruits can be eaten directly after removal of astringency (Yang et al., 2015).

Investigation of genetic diversity is important for evaluating, conserving and utilizing plant genetic resources and for determining the uniqueness and distinctness of the genotypes, providing important basic information for genetic improvement (Hurtado et al., 2012). There are several different ways to measure genetic diversity, among which morphological characteristics are the strongest determinants of the agronomic value and taxonomic classification of plants (Jannatabadi et al., 2014). Evaluation of morphological traits is relatively easy and inexpensive; therefore, this type of markers is commonly used to analyze genetic diversity by breeders in terms of the selection of breeding materials (Geleta et al., 2006). In addition, these characters are often susceptible to phenotypic plasticity; conversely, this allows the assessment of diversity in the presence of environmental variation (Mondini et al., 2009). In persimmon, astringency and color are the main fruit traits used as indices in cultivar classification (del Mar Naval et al., 2010).

Persimmon breeding purposes have emphasized the enhanced fruit quality such as fruit weight, shape, color, soluble solids content, fruit cracking, fruit ripening time, high productivity, long shelf life, parthenocarpy and sex expression. Selective breeding is the most common breeding technique in persimmon due to the fact that persimmon breeding is mainly hindered by its high ploidy level and by its complex sex expression (Yesiloglu et al., 2018).

Gaining knowledge about the genetic diversity of a germplasm resource is important to support the breeding programs, botanical research and germplasm collection and conservation (Deng et al., 2015; Guan et al., 2020; Zarei & Erfani-Moghadam, 2021). The presence of great diversity in plant genetic resources provides an opportunity for the breeders to develop new cultivars with desirable traits such as high yield and resistance to biotic and abiotic

stresses (Houmanat et al., 2021; Govindaraj et al., 2015). Although in a study conducted by Fattahi Moghaddam et al. (2009), morphological and genetic diversity of some persimmon genotypes have been evaluated in Karaj and Varamin, Iran and it was shown that the genotypes were significantly different, however, there are few studies on the genetic diversity assessment in persimmon fruit in Iran. The wide geographical and climatic distributions are indicative of the fact that there is tremendous genetic diversity in persimmon in Iran, which needs to be identified and catalogued. In the present study, diversity of Iranian persimmons was investigated based on pomological traits.

MATERIALS AND METHODS

Plant materials and pomological traits

Twenty-eight wild and cultivated *Diospyros* genotypes belonging to *D. kaki* (25 accessions) and *D. lotus* (3 accessions) species have been evaluated from different geographical regions of Iran (Table 1 and Fig. 1). Since the origin of the samples was unknown and their degree of similarity or genetic distance from each other was not clear; therefore, each tree was considered as one genotype.

Nineteen morphological characters were recorded for 15 mature fruits per genotype (Table 2). The quantitative characters related to length and width of fruits, length, width and diameter of seeds and calyx size were determined using a Vernier caliper with accuracy of 0.1 mm. Fruit and seed weights were measured using analytical balance with sensitivity of ±0.01g. The content of total soluble solids (TSS) has been measured using juice samples of fruit pulp by a hand refractometer at room temperature. Fruit firmness was measured using an Effegi, FT 327 penetrometer equipped with an 8 mm tip and the results were reported as kg/cm². Moreover, other attributes including fruit shape, fruit color, astringency, attitude of calyx, grooving of apex, presence of brown specks and presence of brown specks in flesh have been evaluated as codes, described by Yilmaz et al. (2017).

Data analysis

Descriptive statistics analyses in terms of pomological traits were conducted using SAS software (ver., 9.3.1) to determine means, standard deviations, coefficients of variation (CV%) and minimum and maximum values of persimmon genotypes.

The correlation between the quantitative data was calculated by Pearson's correlation coefficient, and the correlation between the qualitative (ranking) data was calculated by Spearman's correlation coefficient. For calculating the Spearman's correlation coefficient between quantitative and qualitative data, the quantitative data have been transformed into ranking (qualitative) data, and then, all correlations were calculated using SPSS software (ver. 16).

According to the Ward's method, cluster analysis was carried out by SPSS software (ver. 16) based on the distances between the individuals estimated by Euclidean coefficients. The relationships between genotypes have been also determined by principal component analysis (PCA) using SPSS software (ver. 16).

Fig. 1. Map of Iran showing the provinces of the collection site (shown by yellow color) of the 28 *Diospyros* genotypes used in this experiment.

Fig. 2. Different fruit shape in *Diospyros* genotypes; A: round-shaped fruit of *D. lotus*, B: round-shaped fruit of *D. kaki*, C: oblong-shaped fruit of *D. kaki*, D: relatively oblong-shaped fruit of *D. kaki*, E: square-shaped fruit of *D. kaki*.

Table 1. List of studied persimmon accessions with their collection area in Iran

Number	Species	Collection site	Province	Accession Code	Ploidy level
1	*D. lotus*	Karaj	Alborz	LKA	2n = 2x = 30
2	*D. lotus*	Ramsar	Mazandaran	LRM	2n = 2x = 30
3	*D. lotus*	Isfahan	Isfahan	LII	2n = 2x = 30
4	*D. kaki*	Meshkindasht	Alborz	KMA1	*
5	*D. kaki*	Meshkindasht	Alborz	KMA2	*
6	*D. kaki*	Meshkindasht	Alborz	KMA3	*
7	*D. kaki*	Karaj	Alborz	KKA1	*
8	*D. kaki*	Karaj	Alborz	KKA2	*
9	*D. kaki*	Fardis	Alborz	KFA	*
10	*D. kaki*	Cheitgar	Tehran	KCT	*
11	*D. kaki*	Shahriar	Tehran	KST1	*
12	*D. kaki*	Shahriar	Tehran	KST2	*
13	*D. kaki*	Babol	Mazandaran	KBM1	*
14	*D. kaki*	Babol	Mazandaran	KBM2	*
15	*D. kaki*	Babol	Mazandaran	KBM3	*
16	*D. kaki*	Ramsar	Mazandaran	KRM1	*
17	*D. kaki*	Ramsar	Mazandaran	KRM2	*
18	*D. kaki*	Ramsar	Mazandaran	KRM3	*
19	*D. kaki*	Ramsar	Mazandaran	KRM4	*
20	*D. kaki*	Ramsar	Mazandaran	KRM5	*
21	*D. kaki*	Amlash	Guilan	KAG1	*
22	*D. kaki*	Amlash	Guilan	KAG2	*
23	*D. kaki*	Amlash	Guilan	KAG3	*
24	*D. kaki*	Rasht	Guilan	KRG	*
25	*D. kaki*	Isfahan	Isfahan	KII1	*
26	*D. kaki*	Isfahan	Isfahan	KII2	*
27	*D. kaki*	Khoramabad	Lorestan	KKL1	*
28	*D. kaki*	Khoramabad	Lorestan	KKL2	*

D. kaki ploidy level was described as 2n = 6x = 90 or 2n = 9x = 135

Table 2. Modified UPOV descriptors used for homological characterization in persimmon

No.	Characters	Unit
1	Fruit weight	gram (g)
2	Fruit length	Centimeter (cm)
3	Fruit width	cm
4	Length/width	cm
5	Firmness	Newton (N)
6	Fruit shape	1 (round), 2 relatively oblong, 3 (oblong)
7	Total soluble solids	%
8	Astringency	1 (non-astringent), 2 (astringent), 3 (strongly astringent)
9	Calyx size	Millimeters (mm)
10	Attitude of calyx	1 (horizontal), 2 (semi erect), 3 (erect)
11	Grooving of apex	1 (absent or weak), 2 (moderate), 3 (strong)
12	Fruit color at harvest	1 (green orange), 2 (orange), 3 (orange red), 4 (red), 5 (brown)
13	Presence of brown specks in flesh	1 (always absent), 2 (sometimes present), 3 (always present)
14	Presence of seeds	1 (absent), 2 (present)
15	Number of seeds	seed number per fruit
16	Seed weight	g
17	Seed length	mm
18	Seed width	mm
19	Seed diameter	mm

RESULTS

Descriptive statistics

A wide variation was achieved among the selected persimmon accessions according to pomological traits. The mean, maximum, minimum, standard deviation and coefficient of variation of traits are presented in Table 3. High variability was found among the samples for most of the traits, however, the CV values for seed traits were higher than those for fruit traits. The maximum of variations was respectively achieved in seed diameter (CV=147.22%) and seed weight (CV=126.85%). Generally, CV value for seed characters was more than 110% while CV value for fruit characters was less than 50%. Among the fruit characters, the highest variation was observed in severity of brown specks in flesh (CV=49.69%), followed by fruit weight (CV=49.62%) and fruit color (CV=48.22%). The lowest variation was also detected for TSS value (CV=17.22%).

Among the studied genotypes, 13 genotypes included all of the *D. lotus* genotypes and some of the *D. kaki* genotypes were seeded, but the rest of *D. kaki* genotypes (15 samples) were seedless. In seeded fruits, seed weight ranged from 0.235 g to 1.45 g with an average value of 0.38 g, the highest value of seed weight was recorded in KAG1 (*D. kaki*), and the lowest value of seed weight was recorded in LRM genotype (*D. lotus.*).

Fruit weight ranged from 4.45 g to 251.77 g with an average of 140.51 gr. The highest fruit weight value was recorded in KBM1 genotype, followed by KST1 (227.89 gr) and KAG2 (224.13) belonging to the *D. kaki* and the lowest fruit weight value was recorded in LII genotype (*D. lotus*).

Fruit length varied from 1.5 mm to 11.05 mm with an average of 5.45 mm while fruit width ranged from 1.5 mm to 7.78 mm with an average of 5.92 mm. The highest fruit length and fruit width were respectively recorded in KBM2 and KRM4 genotypes (*D. kaki*) while the lowest fruit length and fruit width were recorded in LII genotype (*D. lotus*).

Fruits of all *D. lotus* genotypes were round-shaped while in *D. kaki,* 14 genotypes included round-shaped fruits, 8 genotypes included relatively oblong-shaped fruits and 3 genotypes included oblong-shaped fruits (Fig. 2). All *D. lotus* genotypes and most of the *D. kaki* genotypes included strongly-astringent or astringent fruits, and only 4 genotypes included KBM2, KRM2, KAG2, KRG had completely non-astringent fruits (Fig. 3).

Fig. 3. Presence of brown specks in the fruit of *Diospyros* genotypes; A: always absent, B: sometimes present and C: always present

Table 3. The min, max, mean, standard deviation and coefficient of variation of evaluated characters among *Diospyros* genotypes

No.	Characters	Minimum	Maximum	Mean	SD	%CV
1	Fruit weight	4.45	251.77	140.51	69.73	49.62
2	Fruit length	1.50	11.05	5.45	2.29	42.02
3	Fruit width	1.50	7.78	5.92	1.67	28.22
4	Width/Length	0.59	1.62	0.92	0.28	30.65
5	Firmness	1.16	11.14	6.13	2.69	43.85
6	Fruit shape	1.00	3.00	1.5	0.69	46.26
7	Total soluble solids	12.53	24.00	17.4	2.99	17.22
8	Astringency	1.00	3.00	2.54	0.69	27.33
9	Calyx size	2.16	7.00	4.00	1.3	32.44
10	Attitude of calyx	1.00	3.00	1.75	0.65	36.88
11	Grooving of apex	1.00	3.00	1.64	0.73	44.5
12	Fruit color at harvest time	1.00	5.00	2.61	1.26	48.22
13	Brown specks in flesh	1.00	3.00	1.5	0.75	49.69
14	Presence of seeds	1.00	2.00	1.46	0.51	34.68
15	Number of seeds	0.00	6.00	2.43	2.67	110.05
16	Seed weight	0.00	1.45	0.44	0.55	126.85
17	Seed length	0.00	3.2	0.97	1.18	121.16
18	Seed width	0.00	1.28	0.47	0.53	113.38
19	Seed diameter	0.00	1.1	0.18	0.27	147.22

Correlation analysis

The correlation coefficients between the pomological traits were shown in Table 4. The results showed that there was a significant and positive correlation between fruit weight with seed diameter and seed weight. Also there was a significant and positive correlation between fruit length with seed diameter, seed width, seed weight and seed length. Similar trends were observed for the fruit length to fruit width ratio. No significant correlation was observed between fruit width and seed dimensions. There was also significant and positive correlation between fruit weight with fruit length and fruit width. Calyx size has not shown any significant correlation with fruit properties or seed dimensions.

In this study, significant and positive correlation was observed between fruit weight with fruit shape and fruit color. Similar results were observed between fruit length with fruit shape and fruit color. Fruit shape also showed significant and positive correlations with seed dimensions including seed weight, seed length, seed width and seed diameter while no significant correlation was observed between fruit color and seed dimensions.

Significant and positive correlation was observed between seed properties and presence of brown specks in the flesh while no significant correlations were observed between fruit properties and presence of brown specks in the flesh. There was a negative and significant correlation between astringency and presence of brown specks in the flesh: however, astringency has not shown any correlations with seed or fruit dimensions.

Principal component analysis

The results achieved from the PCA indicated that 85% of the observed variability was explained by the first four components (Table 5). The first two components explained about 60.97% of the total achieved variability. The most important variables which contributed to PC1 with positive coefficients (and values more than 0.7) were seed weight, seed length, seed width, presence of seed, seed diameter, number of seeds, fruit length to fruit width ratio, fruit shape, grooving of apex and fruit length. The most important variables which contributed to PC2 with positive values were fruit width and fruit weight, and the variable with negative coefficients was fruit color. This result clearly showed that the first PC was mainly explained by seed traits while the second PC was mainly explained by fruit traits. PC3 was influenced mainly by the attitude of calyx and PC4 was influenced mainly by calyx size.

Based on the first and second principal components, a two-dimensional scatter was depicted (Fig. 4). The Resulted bi plot showed that the genotypes could be divided into four distinct groups. In this trend, *D. lotus* genotypes were separated from the *D. kaki* genotypes and formed a distinct group. *D. kaki* genotypes were placed in 3 groups, where genotypes KRM1, KAG1 and KBM1 formed the first group, genotypes KBM2, KRM3, KRG1, KAG2, KRM2, KBM3 and KRM5 formed the second group and the rest genotypes formed the last group. First group contained the seeded and oblong-shaped fruits, second group contained the seeded round-shaped and relatively oblong-shaped fruits, and finally, third group contained the seedless round-shaped and relatively oblong-shaped fruits.

Table 4. The Pearson correlation among the pomological traits (quantitative data) of *Diospyros* genotypes

	Grooving of apex	Attitude of calyx	Brown specks	Fruit shape	Fruit color	Astringency	Presence of seeds	Fruit weight	Fruit length
Calyx size	0.051 ns	-0.112 ns	0.153 ns	0.376*	-0.386*	-0.147 ns	-0.27 ns	0.289ns	0.33ns
Soluble solids	-0.219 ns	0.357 ns	-0.35 ns	-0.081ns	-0.011 ns	0.252 ns	-0.435*	0.188ns	0.116ns
Seed diameter	0.610**	-0.096 ns	0.515**	0.523**	-0.262 ns	-0.2 ns	0.940**	0.412*	0.648**
Seed width	0.578**	-0.021 ns	0.447*	0.446*	-0.098 ns	-0.209 ns	0.940**	0.213ns	0.413*
Seed length	0.735**	0.025 ns	0.496**	0.660**	-0.171 ns	-0.175 ns	0.939**	0.361 ns	0.616**
Seed weight	0.728**	0.003 ns	0.505**	0.654**	-0.184 ns	-0.194 ns	0.940**	0.441*	0.680**
Number of seeds	0.646**	-0.248 ns	0.557**	0.321 ns	0.096 ns	-0.331 ns	0.966**	0.1ns	0.21ns
Firmness value	0.076 ns	-0.106 ns	0.115 ns	0.334 ns	-0.62**	0.13 ns	0.018 ns	0.606**	0.499**
Length to width	0.889**	-0.231 ns	0.434*	0.774**	-0.14 ns	-0.177 ns	0.665**	0.25ns	0.691**
Fruit width	-0.027 ns	0.152 ns	0.053 ns	0.289 ns	-0.64**	0.324 ns	0.1 ns	0.877**	0.634**
Fruit length	0.520**	0.186 ns	0.139 ns	0.781**	-0.54**	0.32 ns	0.255 ns	0.811**	1
Fruit weight	0.17 ns	-0.01 ns	0.278 ns	0.490**	-0.77**	0.345 ns	0.132 ns	1	
Presence of seeds	0.672**	-0.149 ns	0.532**	0.460*	-0.069 ns	-0.261 ns	1		
Astringency	-0.071 ns	0.458*	-0.49**	0.085 ns	-0.172 ns	1			
Fruit color	-0.2 ns	0.348 ns	-0.27 ns	-0.52**	1				
Fruit shape	0.857**	-0.048 ns	0.331 ns	1					
Brown specks	0.453*	-.613**	1						
Attitude of calyx	-0.202	1							
Grooving of apex	1								

ns, * and **: not significant, significant at 5% and 1% levels of probability, respectively

Table 4. Continue: The Pearson correlation among the pomological traits (quantitative data) of *Diospyros* genotypes

	Fruit width	Length to width	Firmness value	Number of seeds	Seed weight	Seed length	Seed width	Seed diamete	Soluble solids	Calyx size
Calyx size	0.343ns	0.034ns	0.145ns	-0.35ns	-0.034ns	-0.087ns	-0.266ns	-0.062ns	-0.216ns	1
Soluble solids	0.352ns	-0.146ns	0.14ns	-0.472*	-0.228ns	-0.247ns	-0.400*	-0.244ns	1	
Seed diameter	0.226ns	0.628**	0.416*	0.693**	0.854**	0.799**	0.813**	1		
Seed width	-0.096ns	0.657**	0.183ns	0.944**	0.907**	0.922**	1			
Seed length	0.039 ns	0.787**	0.281 ns	0.862**	0.980**	1				
Seed weight	0.162	0.755**	0.355 ns	0.808**	1					
Number of seeds	-0.328ns	0.603**	0.103ns	1						
Firmness value	0.594**	0.1	1							
Length to width	-0.102ns	1								
Fruit width	1									

ns, * and **: not significant, significant at 5% and 1% levels of probability, respectively

Cluster analysis

Cluster analysis using pomological data constructed by ward's method divided all the genotypes into 3 main clusters and 3 distinct sub clusters (Fig. 5). Cluster I included genotypes: LKA, LII and LRM belonging to *D. lotus* species, and those collected from Alborz, Isfahan and Mazandaran provinces, respectively. Cluster II included genotypes: KMA1, KST1, KMA2, KII1, KII2, KKA1, KRM4, KKA2, KST2, KMA3, KAG3, KFA, KCT, KKL1, and KKL2 collected from different regions belonging to *D. kaki* and containing seedless fruits regardless of the collection site and fruit shape. Finally, cluster III included all seeded *D. kaki* genotypes collected from Mazandaran and Guilan (Northern) provinces. In this cluster, genotypes KRM1, KAG1, KBM1 constructed sub cluster I including oblong shaped fruits, genotypes KBM3, KRM5, KRM3 constructed sub cluster II including round shaped fruits and genotypes KRM2, KAG2, KRG, KBM2 constructed sub cluster III including relatively oblong shaped fruits.

Table 5. Eigenvectors of principle component analysis (PCoA) for 19 fruit pomological traits in *Diospyros* genotypes, collected from different regions of Iran

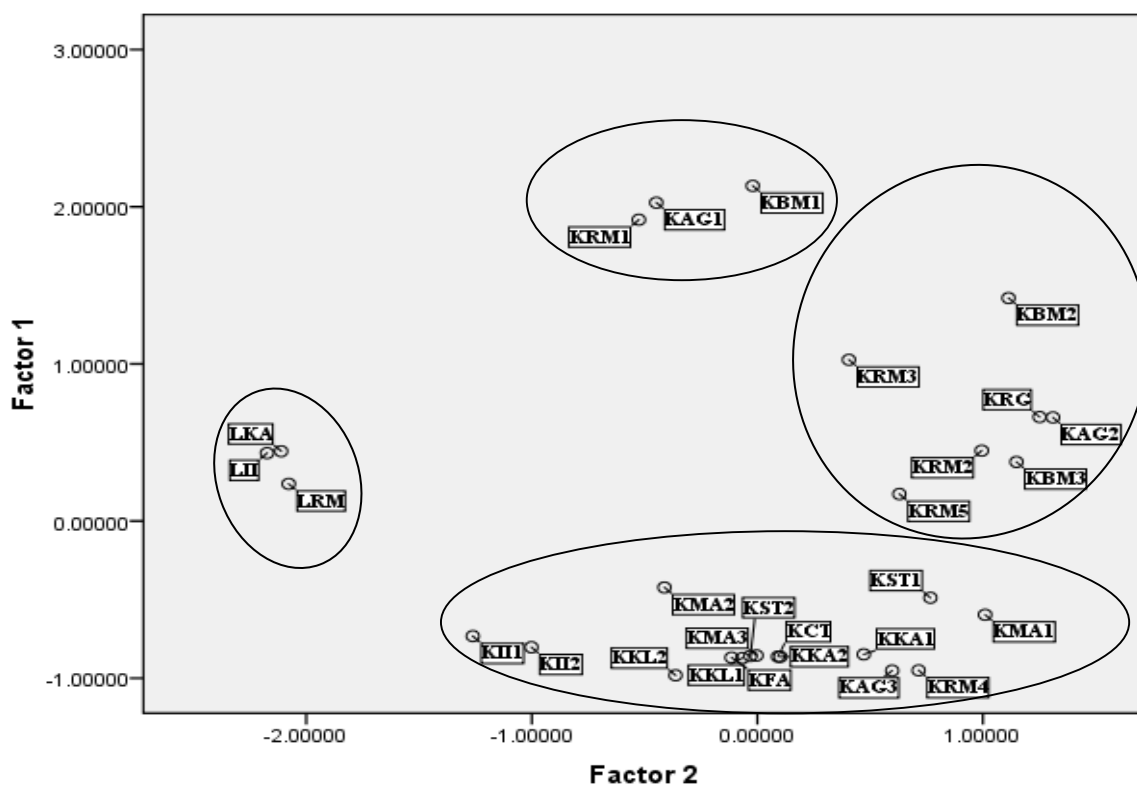| Traits	Component			
	1	2	3	4
Fruit weight	0.47	*0.816*	-0.042	-0.04
Fruit length	*0.712*	0.604	0.109	0.217
Fruit width	0.135	*0.94*	-0.112	-0.145
Length / Width	*0.817*	-0.089	0.285	0.358
Fruit Firmness	0.369	0.605	-0.377	-0.435
Fruit shape	*0.772*	0.259	0.318	0.376
Total soluble solids	-0.273	0.516	0.379	-0.227
Astringency	-0.271	0.399	0.631	-0.254
Calyx Size	-0.011	0.393	-0.35	*0.738*
Attitude of calyx	-0.009	0.272	*0.801*	-0.003
Grooving of apex	*0.769*	-0.14	0.328	0.279
Fruit color at harvest	-0.358	*-0.759*	0.378	0.083
Brown specks in flesh	0.602	-0.161	-0.623	0.071
Presence of seeds	*0.864*	-0.421	0.019	-0.23
Number of seeds	*0.818*	-0.508	0.013	-0.227
Seed weight	*0.97*	0.008	0.103	-0.073
Seed length	*0.966*	-0.105	0.132	-0.045
Seed width	*0.896*	-0.295	0.056	-0.238
Seed diameter	*0.861*	0.039	-0.173	-0.205
Total	8.204	4.167	2.357	1.49
% of Variance	39.328	21.645	15.147	9.238
Cumulative %	39.328	60.973	76.121	85.358

Fig. 4. The biplot derived from principal components analysis of 28 *Diospyros* genotypes based on the pomological traits. The number and accession code is the same in Table 1.
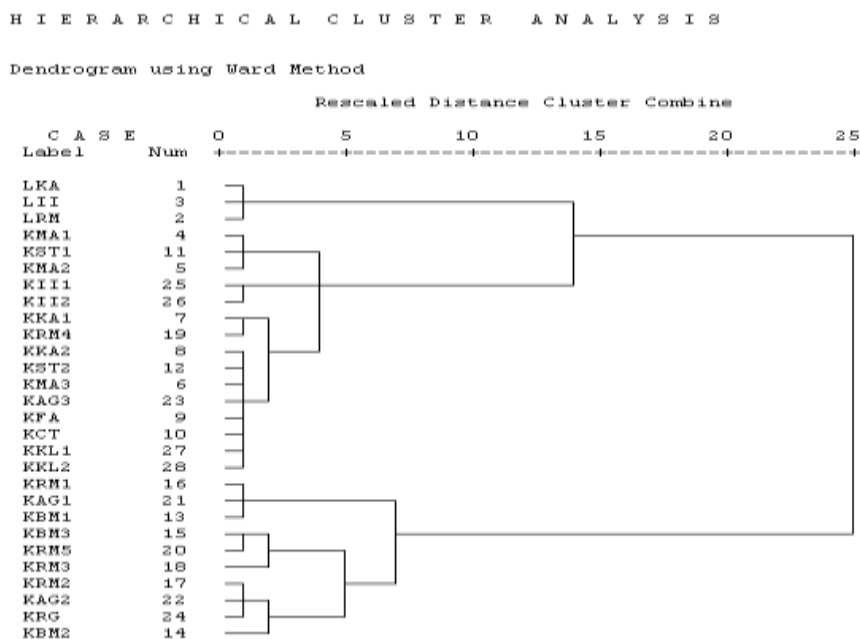

Fig. 5. Dendrogram generated based on Euclidean distance showing relationships among 28 *Diospyros* genotypes with pomological traits. The number and accession code is the same in Table 1.

DISCUSSION

In the present study, we attempted to characterize some Persimmon accessions, which were collected from different parts of Iran, using seed and fruit characteristics. Persimmons are well adapted to a wide range of climate conditions in Iran, ranging from north to south areas, but in spite of this distribution, there is little information about the genetic diversity of persimmon in Iran. Genetic diversity study is essential for support crop improvement as well as support conservation efforts (Zarei & Erfani-Moghadam, 2021). Our results showed there were high variations in pomological traits among the studied persimmon genotypes. The clustering and PCA results indicated that *D. lotus* genotypes were completely separated from *D. kaki* genotypes. Similar results were reported by Yilmaz et al. (2017) in analyzing morphological diversity of *Diosyros* genotypes in Turkey. The results also showed that *D. lotus* genotypes, regardless of the collection sites, were grouped together. This result can be explained by the fact that the genotypes probably have the similar origin because *D. lotus* is wildly widespread in northern forests of Iran and its seeds probably are distributed from northern forests to other parts of Iran. These species have small and inferior quality fruits and are usually used as rootstock for Japanese persimmon (Yang et al., 2015). It is possible that farmers share the seeds regardless of their origins (Houmanat et al., 2021).

Clustering and PCA results also showed that *D. kaki* genotypes can be divided into two main groups. First group mainly included seedless persimmons and the second group included seeded persimmons. In both groups, the sub groups were clearly distinguished, where round-shaped, relatively oblong-shaped and oblong-shaped fruits were clearly separated from each other. This result indicated that seed traits flowed by fruit traits (shape) were the main causes of grouping of *D. kaki* genotypes in this study. The research results concur with those achieved by Yilmaz et al. (2017) who reported that seedless genotypes were separated from the other genotypes based on seedlessness and a high tendency towards parthenocarpy; also, fruit characteristics such as fruit size, and fruit shape were the most important variables for classification of persimmon genotypes in Turkey.

The main point of our study was that all seeded Japanese persimmons belonged to the Northern provinces. These provinces have warm and humid summers and cold and humid winters, where usually subtropical fruits are cultivated. Other regions in this study have temperate climate, where Japanese persimmons become usually seedless. It is known that being seeded in Japanese persimmons is affected by climatic conditions, geographical region and nutritional status, those can influence the gender of flowers so that the same cultivar may be seeded or seedless according to the climate condition (Woodburn & Andersen, 1996); therefore, being seeded of some genotypes in Northern provinces probably was under the effect of environmental conditions, rather than genetic factors because clustering and PCA results indicated that seedless persimmons from Northern regions were grouped with the other seedless persimmons in the similar cluster.

The Japanese persimmon given the effect of seed presence on flesh color and taste is classified into four types including pollination constant astringent (PCA), pollination-constant non astringent (PCNA), pollination variant astringent (PVA) and pollination variant non-astringent (PVNA) (Yonemori et al., 2000). Considering the pomological observations in this study, Iranian edible persimmons were mostly astringent type because all seedless fruits, regardless of the collection site and fruit shape, were completely astringent. Among them, round-shaped and oblong-shaped persimmons were PCA type because the presence of seed had no impact on the flesh color and astringent taste, but the relatively oblong-shaped fruits were PVNA type because when the fruit was seeded, the flesh color was brown and the fruit

taste was non astringent; but when the fruit was seedless, the flesh color was not brown and the taste was astringent.

In this experiment, the largest fruit was obtained in KBM1 genotype; this genotype also contained the bigger seeds between the genotypes. Accordingly, the correlation result showed that the fruit size is positively correlated with seed size. With respect to the fact that the seeds supply the hormones and growth stimulant for the fruits, the production of big fruits in this genotype can be due to the impact of large seeds (Arteca, 2000). However, the second largest fruit was obtained in genotype KST1, which was seedless. It seems that appropriate environmental and soil conditions can be regarded as the elements of big fruit production with no seeds in persimmons. It is known that climatic conditions affect the color and size of fruits (Farahani et al., 2019). Since the consumers in Iran prefer the big, colored and seedless persimmons (Khademi et al., 2010), the genotype KST1 is more favored than the genotype KBM1.

The results of present study did not show a significant correlation between the sampling area and genotype background because all of the seedless persimmons regardless of their collection sites (including Meshkindasht, Karaj, Fardis, Cheitgar, Shahriar, Ramsar, Amlash, Isfahan, Khoramabad) were placed in the same cluster, and similar trends have been observed for the seeded persimmon even in the formation of the subgroup; the geographical area did not show any clear effect. In agreement with our results, Saboori et al. (2020) in evaluation of genetic structure of date palm cultivars did not find clear association between genotypes clustering pattern and geographical distribution. These results suggest that samples collected from different geographical locations may have the same origin and genetic structure (Yesiloglu et al., 2018).

CONCLUSION

Persimmon as one of the most important fruit crop in the world has been cultivated in different regions of Iran for more than two hundred years, the results of this study had suggested considerable diversity among the genotypes and provides a pathway for future crop variety identification and conservation. Our results suggested that Japanese persimmon in Iran may be divided into three types including round-shaped, relatively oblong-shaped and oblong-shaped persimmons. On the other hand, being seeded in some genotypes was under the effect of environmental conditions, rather than genetic factors. The results also showed that *D. lotus* genotypes regardless of the collection sites were not pomologically different, probably indicating the similar origin.

Conflict of interest
The authors declare that there is no conflict of interest to report.

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