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Original Article

Genetic diversity in a core collection of Iranian sour cherry

Diversidade genética em uma coleção central de ginja iraniana

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Abstract

The exploitation of plant genetic resources is an important and rapid strategy to release commercial cultivars. In this study, 234 sour cherry genotypes were collected from various locations of Iran and phenotypically assessed according to IPGRI and UPOV descriptors. The genotypes were grafted onto Mahaleb rootstock and were planted in Horticultural Science Research Institute (HSRI) core collection in Karaj, Iran. In this study, 22 different characteristics were measured in the sour cherry genotypes. The results showed that fruit and stone weights varied from 1.65 (G410) to 5.47 g (G125) and 0.13 (G428) to 0.59 g (G149), respectively. The fruit size index comprised average fruit length, width, and diameter, which varied from 10.57 to 19.13. The stalk length was less than 50 mm in 90.6% of the studied genotypes. Twelve of the 234 studied genotypes did not exhibit any symptoms of bacterial canker disease. Principle component analysis (PCA) and cluster analysis classified the studied genotypes into four main groups. Spearman's correlation analysis revealed that fruit size, stone shape, stone size, stalk thickness and weight, and fruit appearance correlated positively with stone and fruit weights. In contrast, fruit juice, fruit skin, and flesh color correlated negatively with the stone and fruit weights. The range of TSS varied between 12.66 (G251) and 26 (G427). Variations in pH value were between 3.66 (G236) and 5.63 (G352). In conclusion, a high level of genetic diversity was observed among the Iranian sour cherry genotypes. This diversity can be considered valuable and applicable for future breeding programs.

Keywords: correlation analysis, fruit weight, germplasm, genetic diversity.

Resumo

A exploração de recursos fitogenéticos é uma estratégia importante e rápida para liberar cultivares comerciais. Neste estudo, 234 genótipos de ginja foram coletados de vários locais do Irã e avaliados fenotipicamente conforme os descritores IPGRI e UPOV. Os genótipos foram enxertados no porta-enxerto Mahaleb e foram plantados na coleção principal do Horticultural Science Research Institute (HSRI) em Karaj, Irã. Neste estudo, 22 características diferentes foram medidas nos genótipos de acerola. Os resultados mostraram que os pesos dos frutos e caroços variaram de 1,65g (G410) a 5,47g (G125) e 0,13g (G428) a 0,59g (G149), respectivamente. O índice de tamanho do fruto compreendeu o comprimento médio, largura e diâmetro do fruto, que variou de 10,57 a 19,13. O comprimento do colmo foi inferior a 50 mm em 90,6% dos genótipos estudados. Doze dos 234 genótipos estudados não apresentaram nenhum sintoma de cancro bacteriano. A análise de componentes principais (PCA) e a análise de cluster classificaram os genótipos estudados em quatro grupos principais. Já a análise de correlação de Spearman revelou que o tamanho do fruto e do caroço, formato do caroço, espessura e peso do caule, e aparência do fruto correlacionaram-se positivamente com o peso do caroço e do fruto. Em contraste, suco de fruta, casca de fruta e cor de polpa correlacionaram-se negativamente com os pesos de caroço e fruta. A faixa de TSS variou entre 12,66 (G251) e 26 (G427). As variações no valor do pH ficaram entre 3,66 (G236) e 5,63 (G352). Em conclusão, um alto nível de diversidade genética foi observado entre os genótipos de ginja iraniana. Essa diversidade pode ser considerada valiosa e aplicável para futuros programas de melhoramento.

Palavras-chave: análise de correlação, peso do fruto, germoplasma, diversidade genética.

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1. Introduction

Among the thirty identified cherry species that mostly have been indigenous to Europe and Asia (Iezzoni and Hancock, 2008), only *cerasus* and *avium* of *Prunus* are found in global markets. Both species belong to the *Prunus* genus (subfamily *Amygdyloideae*, *Rosaceae*). Sour cherry (*Prunus cerasus* L. 2n=4x=32) is a natural allotetraploid hybridized from ground cherry (*P. fruticosa* 2n=4x=32) and sweet cherry (*P. avium* 2n=2x=16). Sour cherry is valuable for the production of jelly, jam, marmalade, stewed fruit, cakes, and syrup (Sabanci et al., 2022). Furthermore, it can be used as a dwarfing rootstock for sweet cherry.

The origins of this species go back to the Caspian and Black Sea. Cultivation and distribution of these plants takes place in temperate and cool regions especially in the Northern Hemisphere. Its features make it feasible for high volume production, such as in Russia, Turkey, Ukraine, USA, and Iran (Milošević et al., 2020; Blando and Oomah, 2019).

Sour cherry fruits have a low sugar content of approximately 8%, which means they are primarily used in the food industry for processing (Ferretti et al., 2010; Yilmaz et al., 2019). Despite their limited use as fresh fruits, sour cherries are highly valued for their rich nutrient and mineral content, making them a popular choice in many countries (Ivanova et al., 2018).

Genetic diversity is significant for breeding and provides the opportunity of releasing new cultivars during plant-breeding programs (Farajpour et al., 2011a, b). However, long breeding cycle of fruit trees is the major constraint for breeders. Introduction of superior genotypes is one of the basic strategies for reducing the length of breeding cycle (Moret et al., 2022). Parenting the genotypes and classifying the gene pool can largely assist in breeding programs (Whetten et al., 2023). The evaluation of plant germplasm is crucial for identifying informative values and characteristics that can be utilized for breeding purposes. In Iran, there is a vast range of sour cherry germplasm, which exhibits rich diversity that can be characterized for specific breeding purposes. In general, plant genetic resources (PGR) in this regard are characterized by quantitative and qualitative trait analysis (Ghamkhar et al., 2023).

Indigenous landraces and allelic diversity are important in characterizing germplasm collections. Phenotypic and morphological characterization are a suitable, quick approach for identifying gene variations in plant populations (Yilmaz et al., 2021) while laying out the constructs of future breeding programs (Nguyen et al., 2022). Various sour cherry populations have been examined for phenotypic diversity (Sánchez et al., 2008; Rodrigues et al., 2008; Khadivi-Khub, 2014). Sour cherries perform differently depending on climate, which makes them vary quantitatively (Ganopoulos et al., 2016).

To diversify plant populations and make use of available allelic richness, it is crucial to characterize and evaluate the morphological features of phenotypic variations. This information can be achieved through molecular methods and is paramount to achieving successful outcomes in plant breeding (Begna, 2021; Mishra et al., 2022).

Cluster and PCA analyses comprise multi-variate statistical methods in analyzing genetic relations from morphological characterization of genotypes (Wattimena et al., 2023; Moradi et al., 2023; Bhutia et al., 2022). In breeding cherry cultivars, fruit quality is one of the most important criteria when selecting genotypes as parents (Dondini et al., 2018).

The importance of horticultural biodiversity is widely documented, emphasizing alleviating the adverse effects of climate changes on the biodiversity. The introgression of local germplasms and their conservation helps obtain new varieties with a more comprehensive genetic background to enable suitable production under different conditions and elicit appropriate responses to various types of stress. Therefore, the present stusy aimed to assessment of the phenotypic variations and screeing of 234 sour cherry genotypes in a sour cherry collection.

2. Material and Methods

2.1. Plant material

This research was carried out on 234 sour cherry genotypes from different parts of Iran based on their main breeding traits. These genotypes were planted in the Horticultural Science Research Institute (HSRI) core collection, located in Karaj, Iran (35.754888° N and 50.952986° E). The studied genotypes were grafted onto Mahaleb rootstocks. The characteristics were studied on 10-year-old trees in early June.

2.2. The studied traits

The studied traits included stone weight, fruit weight, and fruit flesh: stone weight ratio, fruit width, diameter, and length, as well as fruit size index, fruit stalk length, thickness, and weight, number of leaf on the fruit stalk, canker percentage, fruit and stone shape, total soluble solid (TSS), fruit juice pH and color, flesh juiciness and color, fruit skin color and fruit appearance, which were evaluated for two consecutive years (2019-2021) based on IPGRI and UPOV descriptors. Twenty fruit per genotype were considered in four replications. The fruits were harvested when fully mature at the maturity stage and the chemical assessments were done. The fruits were relocated to the lab and physically analyzed at 20 °C. Stone and fruit weight (g) were measured as an average of twenty fruits in four replications for each genotype. By subtracting the stone weight and fruit weight, the flesh content (%) was measured. Fruit width, fruit length, fruit stalk diameter, fruit stalk length, fruit stone width, and fruit stone length were evaluated. Stone weight, fruit weight, and fruit-stalk weight were determined by an accuracy of 0.01 g. TSS content was measured with a hand refractometer at 20 °C. Tree height, trunk diameter, fruit skin color, fruit shape, fruit juice color, fruit flesh color, and flesh firmness were rated and coded.

2.3. Statistical analysis

Variations among the studied sour cherry genotypes were evaluated by SPSS (var. 19) software. R-packages,

including 'Hmisc', 'VGAM', 'MASS' 'gPlot' and 'graphics' for multivariate analysis. The heat-map clustrig was perfourmed by MetaboAnalyst 5.0 software. In this study, UPGMA was used as the clustering algorithm to analyze the genetic diversity of Iranian sour cherry genotypes based on their phenotypic traits..

3. Results and Discussion

According to the results of the measured traits, there was a high genetic diversity among the 234 sour cherry genotypes in the present study. The averages of fruit and stone weights were 2.65 and 0.29 g, respectively. Fruit and stone weights ranged from 1.65 (G410) to 5.47 g (G125) and 0.13 (G428) to 0.54 g (G149), respectively (Table 1, Figure 1a, b).

The fruit weight of the five studied genotypes i.e. G125, G133, G440, G102, and G122 were more than 5 g. In general, 21.37% of the studied genotypes (50 out of 234 genotypes) had fruit weights of more than 3 g. The variation of the fruit weight in the presend study was more than Di Matteo et al. (2017) and Grafe and Schuster (2014) reports. However, the highest fruit weight (7.8 g) in the studied

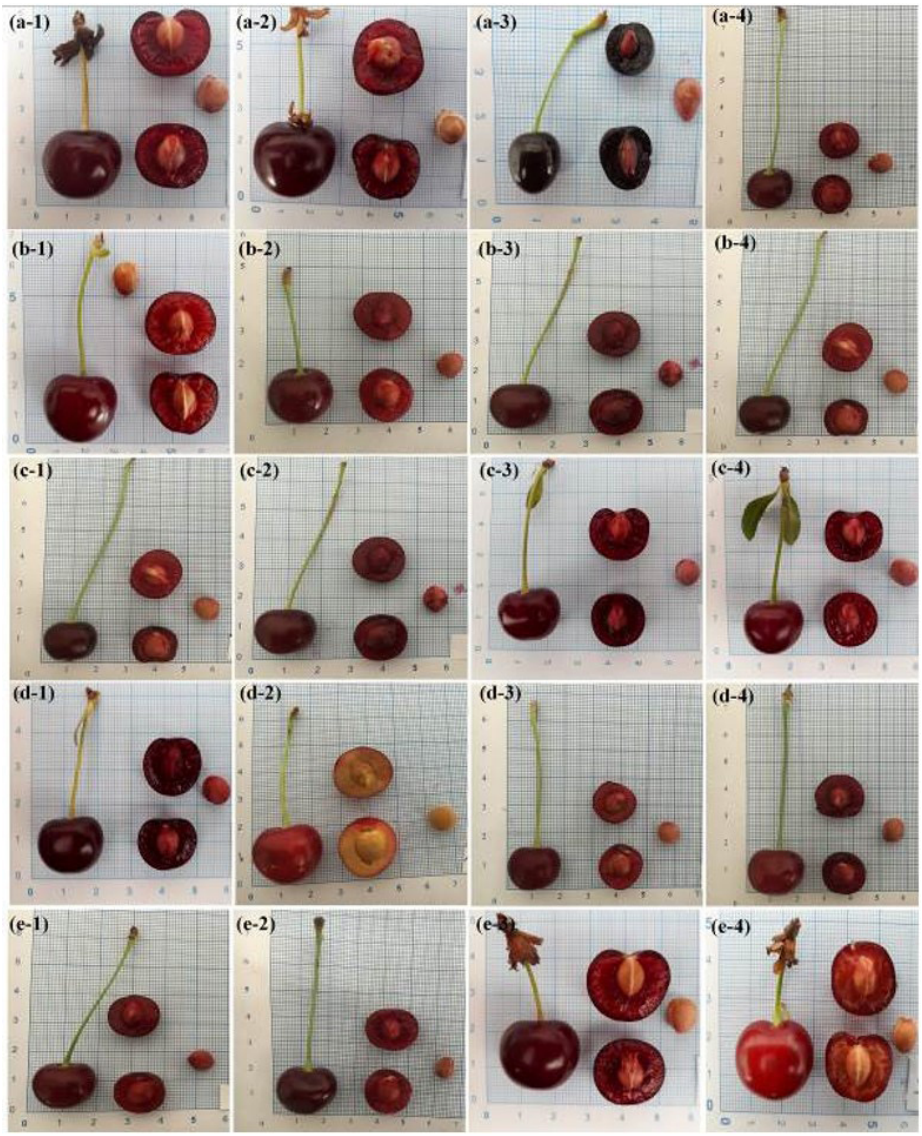

Figure 1. The fruits of some sour cherry genotypes with the highest and lowest values for fruit weight (a), stone weight (b), flesh: stone weight ratio (c), fruit size (d), and stalk length (e): (Highest fruit weight: a-1 (G125) and a-2 (G133); lowest fruit weight: a-3 (G410) and a-4 (G401); highest stone weight: b-1 (G149) and b-2 (G457); lowest stone weight: b-3 (G303) and b-4 (G428); highest flesh to stone weight ratio: c-1 (G428) and c-2 (G303); lowest flesh to stone weight ratio: c-3 (G239) and c-4 (G224); highest fruit size: d-1 (G234) and d-2 (G102); lowest fruit size: d-3 (G433) and d-4 (G418); highest fruit stalk length: e-1 (G320) and e-2 (G249); lowest fruit stalk length: e-3 (G158) and e-4 (G407)).

Table 1. Phenotypic diversity in some quantitative and qualitative traits of 234 sour cherry genotypes originated from Iran during 2018-2019.

Variable	Abbreviation	Mean	Min.	Max.	SD	CV%
Fruit weight (g)	FrW	2.65	1.65	5.47	0.77	28.96
Stone weight (g)	SW	0.29	0.13	0.54	0.05	18.56
Fruit flesh: stone weight ratio	FlSW	7.94	4.09	19.53	1.94	24.47
Fruit length (mm)	FrL	13.49	9.54	18.13	1.43	10.57
Fruit width (mm)	FrWi	14.85	11.01	18.62	1.27	8.53
Fruit diameter (mm)	FrD	15.91	11.08	21.37	1.71	10.75
Fruit size index	FrSI	14.74	10.57	19.13	1.38	9.41
Fruit stalk length (mm)	FrSL	43.70	28.22	66.70	5.58	12.77
Fruit stalk weight (g)	FrSW	0.07	0.03	0.15	0.02	29.53
Fruit stalk thickness (mm)	FrST	0.81	0.15	1.39	0.14	17.08
Canker percentage (%)	CaPe	36.38	0.00	100.00	26.00	71.48
Leaves on fruit stalk	LeFrSt	4.13	0.00	7.00	1.88	45.64
Fruit shape	FrSh	2.13	1.00	5.00	0.58	27.63
Stone shape	StSh	3.37	3.00	7.00	0.88	26.24
Stone size	StSi	4.29	2.00	7.00	1.20	27.97
pH	pH	4.48	3.66	5.63	0.26	5.90
TSS (°Brix)	TSS	18.6	12.67	26.00	2.27	12.22
Fruit juice color	JuCo	3.50	1.00	5.00	0.71	28.23
Fruit skin color	SkCo	5.79	4.00	7.00	0.55	9.51
Fruit flesh color	FlCo	3.55	1.00	6.00	0.74	20.86
Fruit appearance	FrApE	51.96	0.00	100	23.26	44.76
Flesh juiciness	FlJu	5.58	3.00	7.00	1.06	19.10

SD: standard deviation; CV: coefficient of variation.

sour cherries genotypes by Grafe and Schuster (2014) was more than the same value in the present study. Also, in the sour cherries genotypes of Turkey, the fruit weight was ranged from 1.91 to 4.81 g (Yaman, 2022). The higher variation of the fruit weight in the present study compare to previous reports could be due to the higher sample size in this study and different climate in Iran. Fruit flesh weight: stone weight ratio varied between 4.09 (G225) to 19.53 g (G428) (Figure 1c).

Based on the results, fruit length, width, and diameter varied between 9.54-18.13, 11.01-18.62, and 11.08-21.37 mm, respectively. The variation in sour cherries varieties of Republic of Macedonia for fruit length and width were 16.11 to 20.11 mm and 10.79 to 20.16 mm, respectively (Ristovski et al., 2015).

The fruit size index as the average fruit length, width, and diameter was a suitable parameter for grouping the genotypes based on fruit size. The results showed that the fruit size index varied between 10.57 to 19.13. Accordingly, G234 and G102 had the largest fruit size, whereas G418 and G433 had the smallest ones among the studied genotypes (Figure 1d). Thus, the averages fruit length, width, and diameter of the G234 genotype were 17.42, 18.62, and 21.37 mm, respectively. Based on the results, most of the studied genotypes (83.33%) had spherical stones with intermediate to large sizes. The length of the fruit stalk is an important trait in sour cherry breeding programs (Najafzadeh et al., 2014). Based on our results, the length of the fruit stalk in the studied sour cherry ranged from 28.22 (G407) to 66.70 mm (G320) (Figure 1e). The stalk length in 90.6% of the studied genotypes was less than 50 mm. Also, the stalk weight and thickness varied between 0.03-0.15 g and 0.15-1.39 mm, respectively.

Bacterial canker as a main sour and sweet cherry disease was caused by *Pseudomonas syringae* and *P. morsprunorum* (Gormez et al., 2023). One of the most important strategies for disease control is the screening and selection of resistant genotypes (Hulin et al., 2022). In the present study, 12 out of 234 studied genotypes (i.e. G28, G99, G98, G131, G148, G157, G158, G160, G164, G190, G198, G207, G208, and G213) did not show the symptoms of bacterial canker disease. In addition, the canker percentage of 98 studied genotypes was less than 25%. Based on the obtained results, different shape of fruit was observed in the studied population. Nevertheless, most of the studied genotypes (75.64%) had a flat-round fruit shape. After flat-round, round fruit shape (14.53%) was common in the studied sour cherry population. The results showed

that 17 out of 234 genotypes did not have leaves on the fruit stalk, however, 18.37% of the studied genotypes had many leaves on the fruit stalk.

The quantitative characteristics studied in this research generally indicated higher variation compared to the literature mentioned earlier. This could be due to the number of the genotypes used, and the different locations where the genotypes collected (Yaman, 2022).

The diversity of qualitative characteristics in the studied sour cherry population showed that the pH and TSS of fruit juice varied from 3.66 (G87) to 5.63 (G161), and 12.67 (G102) to 26.00 °Brix (G194), respectively. The results showed the fruit skin color varied from orange red in G453 to blackish in G342 and G410 genotypes (Figure 2). A high variation was observed in the studied genotypes in terms of fruit juice and flesh color. Also, 51.24% of the studied genotypes had fruit appearance more than 50%. The studied genotypes reveald a high diversity in their quality characters, however, the fruit quality of cherry is affected by some other factors shuch as rootstock, climate, and soil etc (Asghar et al., 2022).

Correlation coefficient analysis was widely used in plant breeding to estimate genetic/non-genetic association between some traits allowing the plant breeder to indirectly select genotypes with desired traits (Kafi et al., 2021). In this study, heatmap correlation analysis showed that fruit and stone weights had a positive and strong correlation with fruit size, stone shape, stone size, stalk thickness, and weight, and fruit appearance (Figure 3). In contrast, different negative correlation were observed between fruit and stone weights with fruit juice, skin, and flesh color ($P < 0.01$). According to the results, sour cherry genotypes with high fruit weights had high stone weight. Also, the results revealed a strong positive correlation between fruit length, width, and diameter. In addition, fruit size was positively correlated with fruit shape, stone weight, thickness, and fruit stalk weight.

Based on the correlation analysis, fruit juice pH had positively correlated with fruit weight, stone weight, stone

Figure 2. Variation in the studied sour cherry population in terms of skin and flesh color (left to right: G453, G343, G410).

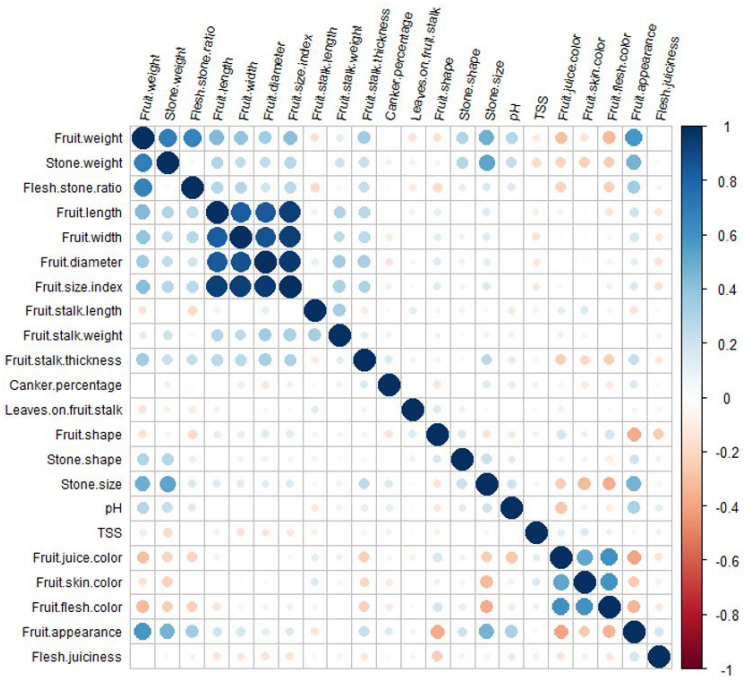

Figure 3. Heatmap of Spearman's correlations between some qualitative and quantitative traits of the studied sour cherry genotypes.

shape, and fruit appearance ($P < 0.01$). In contrast, a negative correlation was observed between the pH and color of fruit juice ($P < 0.01$). The TSS had a negative correlated with stone weight ($P < 0.01$) and positive correlated with juice color, fruit flesh, and skin color ($P < 0.05$). In addiation, different negative correlation were observed between fruit juice, skin, and flesh color with fruit and stone weights, stone shape and size, and fruit appearance. In contrast, fruit appearance was positively correlated with fruit and stone weight, stone shape and size, and flesh juiciness.

The principal component analysis (PCA) and cluster analysis are the two main approaches for grouping different plant population and genotypes (Ahmad and Noori, 2023; Ramezanpour and Farajpour, 2022). If these analyzes are conducted based on high-heritability traits, they can reveal the genetic distance between genotypes (Das et al., 2017). In other words, these techniques are the multivariate statistical analysis attempt to simplify the relationship among a large population (Ramezanpour et al., 2022). Based on the results, the four first PC explained more than 52% of the total variation in the studied sour cherry population (Table 2). The PC1 accounted for 23% of the total variation which is consisted of fruit size, fruit weight, stone weight, fruit appearance, stone size, fruit appearance, fruit stalk thickness, and fruit flesh: stone weight ratio (Figure 4; Table 2). In addition to fruit and stone size, fruit quality including fruit juice, flesh and skin color, and fruit appearance was the main component of PC2 which accounted for 15.1% of the total variation in the studied sour cherry population. The third (PC3) and fourth (PC4) components accounted for 7.3 and 7.1% of the total variation in the studied population, respectively.

The results of the cluster analysis classified the genotypes into four main groups (Figure S1). The first group consisted of five genotypes i.e. G430, G254, G3442, G237, and G410. This group had the heist mean values for StSh, FrSL, FrSh, TSS, FlCo, SkCo, and JuCo traits in compared with other groups (Table 3). For other characters (except for LeFrSt) the group had the lowest mean values. Many of the genotypes (188 genotypes) generated the scond group. The mean values of the measured characters in this group were in moderates values, however, the group had the lowest mean value for StSh. Third group was contained 17 genotypes. The group had the highest mean values for FrW, SW, FlSW, StSi, FrST, CaPe, pH, FlJu, FrApE. Also, the lowes mean value for LeFrSt was observed in this group. Based on the mean values of the quality traits, the genotypes in this group had better fruit quality than other groups. The fourth group included 24 genotypes. The highest mean values for FrL, FrWi, FrD, FrSW, LeFrSt, and FrSI were observed in this group. This group had bigger fruit siz in compared with the other groups.

Table 2. Prencipal components analysis for the studied traits for 234 sour cherry genotypes.

Traits	PC1	PC2	PC3	PC4
FSI	0.8	0.57	-0.01	-0.13
FrW	0.79	-0.26	0.34	0.19
FrL	0.78	0.47	0.01	-0.13
FrWi	0.74	0.54	0.04	-0.15
FrD	0.74	0.58	-0.07	-0.1
SW	0.6	-0.24	-0.11	0.53
FrApE	0.57	-0.5	0.18	0.07
StSi	0.51	-0.41	-0.09	0.3
FrST	0.5	-0.08	-0.1	-0.08
JuCo	-0.39	0.55	0.31	0.33
FlCo	-0.44	0.52	0.38	0.26
SkCo	-0.28	0.51	0.52	0.23
FlSW	0.48	-0.15	0.55	-0.28
FrSL	-0.1	0.26	-0.4	0.31
LeFrSt	-0.03	0.13	-0.35	-0.09
TSS	-0.19	-0.01	0.32	0.01
StSh	0.16	-0.26	0.16	0.54
FrSW	0.29	0.31	-0.26	0.37
FlJu	-0.05	-0.32	0.06	-0.28
FrSh	-0.08	0.44	-0.23	0.25
CaPe	0.05	-0.25	-0.11	0.16
pH	0.26	-0.33	0.15	0.16
% of variance	23	15.1	7.3	7.1
Cumulative (%)	23	38.1	45.4	52.5

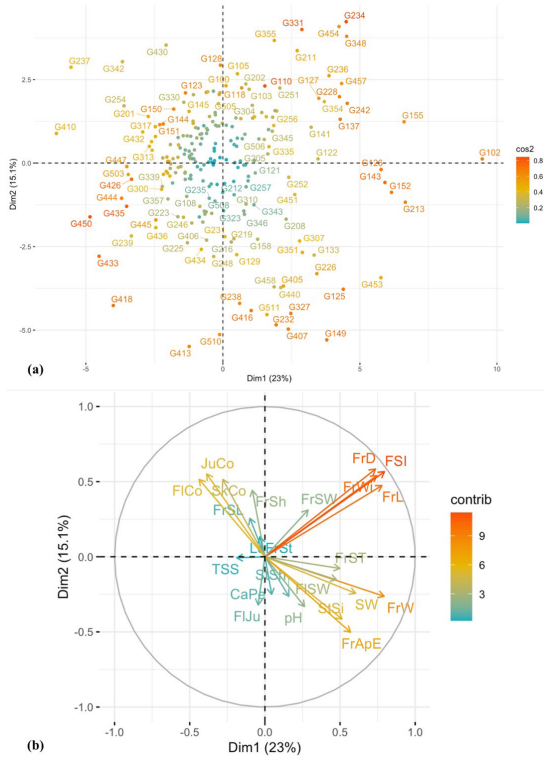

Figure 4. Scatter plot (a) and variables contribution plot (b) for 234 sour cherry genotypes originated from Iran.

Table 3. Mean values and standard error (SE) of the measured characters in the four gropus of heat-map clustering analysis.

Group	FrW (g)	SW (g)	FlSW	FrL (mm)	FrWi (mm)	FrD (mm)
G1	2.06 ± 0.12	0.28 ± 0.02	6.23 ± 0.46	12.07 ± 0.49	13.52 ± 0.48	14.13 ± 0.66
G2	2.39 ± 0.03	0.28 ± 0	7.49 ± 0.12	13.22 ± 0.08	14.66 ± 0.07	15.68 ± 0.1
G3	3.99 ± 0.24	0.35 ± 0.02	10.24 ± 0.55	12.74 ± 0.2	14.03 ± 0.27	14.72 ± 0.32
G4	3.97 ± 0.19	0.35 ± 0.01	10.19 ± 0.42	16.45 ± 0.27	17.23 ± 0.23	18.91 ± 0.35
Group	**StSi**	**StSh**	**FrSL (mm)**	**FrSW (g)**	**FrST (mm)**	**LeFrSt**
G1	2.2 ± 0.2	7 ± 0	46 ± 2.32	0.06 ± 0.01	0.6 ± 0.15	4.2 ± 0.81
G2	4.13 ± 0.08	3.14 ± 0.04	44.16 ± 0.44	0.07 ± 0	0.8 ± 0.01	4.13 ± 0.14
G3	5.71 ± 0.25	4.65 ± 0.2	40.66 ± 1.35	0.06 ± 0	0.91 ± 0.04	3.41 ± 0.56
G4	5.08 ± 0.35	3.58 ± 0.23	41.79 ± 1.03	0.08 ± 0.01	0.88 ± 0.03	4.63 ± 0.48
Group	**CaPe (%)**	**FrSh**	**TSS (°Brix)**	**pH**	**FlJu**	**FlCo**
G1	13.67 ± 3.95	3.8 ± 0.2	18.73 ± 1.41	4.32 ± 0.14	4.2 ± 0.5	5 ± 0
G2	36.18 ± 1.94	2.13 ± 0.03	18.63 ± 0.17	4.46 ± 0.02	5.6 ± 0.08	3.62 ± 0.05
G3	52.01 ± 8.07	1.18 ± 0.1	18.66 ± 0.53	4.69 ± 0.06	6.29 ± 0.25	2.65 ± 0.23
G4	31.56 ± 6.73	2.46 ± 0.23	18.34 ± 0.62	4.58 ± 0.1	5.25 ± 0.27	3.33 ± 0.25
Group	**FrApE**	**SkCo**	**JuCo**	**FrSI**	**-**	**-**
G1	2 ± 2.03	7 ± 0	4 ± 0	13.24 ± 0.53	-	-
G2	47.61 ± 1.36	5.79 ± 0.04	2.56 ± 0.05	14.52 ± 0.08	-	-
G3	92.35 ± 2.26	5.41 ± 0.18	1.65 ± 0.22	13.83 ± 0.23	-	-
G4	67.92 ± 6.59	5.79 ± 0.18	2.38 ± 0.21	17.53 ± 0.25	-	-

4. Conclusion

Plant genetic diversity is routinely evaluated by various techniques including morphological, biochemical, cytological, and molecular markers. Based on the results of present study, a high level of genetic diversity was observed among the studied sour cherry genotypes originated from Iran. In addition, among the studied genotypes, there were some superior genotypes with desirable pomological and phenological traits which have the potential to be introduced as commercial cultivars. Some of the genotypes had different valuable breeding traits which can be considered as valuable and evaluated plant material for future targeted breeding programs. However, important traits such as disease resistance and yield potential were not evaluated, leaving room for future research to explore these characteristics for targeted breeding programs.

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Supplementary Material

Supplementary material accompanies this paper.

Figure S1. Clustring of 234 sour cherry genotypes.

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