Determination of genetic diversity among Arasbaran cornelian cherry (*Cornus mas* L.) genotypes based on quantitative and qualitative traits

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Abstract

Cornelian cherry is one of the most important small fruits in Arasbaran region, with wide applications in medicines and food products. In this study, the relationship among 28 quantitative and qualitative traits related to fruit, leaf, tree, and flower of 20 cornelian cherry genotypes was evaluated. Significant positive as well as negative correlations were found among some important quantitative and qualitative traits. Multivariate analysis method such as factor analysis was used to assign the number of main factors. It showed that the characteristics of fruit, leaf, petiole, and flower were the main traits. Effective traits were divided into 10 factors explaining 87.85% of the total variation. Factor loading values higher than 0.6 were considered significant. According to the cluster analysis of traits based on Squared Euclidean distance, all genotypes were divided into two main branches, but with decreasing of this distance from 25 to 5, the genotypes were placed into four main sub-clusters. Cluster analysis revealed that the traits of fruit length and its diameter, fruit stalk length and its diameter, fruit taste and color, leaf length and width, petiole length and its diameter, as well as pit length and its diameter were effective for clustering the genotypes.

***Key words*:** Arasbaran, Cluster analysis, Cornelian cherry, Correlation, Factor analysis.

INTRODUCTION

Arasbaran region is in the northwest of Iran and north of East Azerbaijan province. Most of Arasbaran jungles are located in four watersheds including Kaleybar-Chaei, Ilingeh-Chaei, Hajilar-Chaei, and Celen-Chaei (Alijanpour *et al.,* 2009). Cornelian cherry is one of the plant species with a wide distribution in Arasbaran region. Cornelian cherry (*Cornus mas* L.) belongs to *Cornus* genus and Cornaceae family. In this family there are about 10 genera and 120 species (Samiee Rad, 2011). Species of *Cornus* genus are perennial, mostly deciduous, and occur in the form of shrubs or small trees and native to Central and Southern Europe and parts of Western Asia (Hassanpour, 2012). The basic requirement for plant breeding programs is a diverse germplasm that provides necessary facilities for breeding species with desirable features. Therefore, accurate identification of genotypes is considered as a prerequisite in this manner. Phenotypic characteristics are the first markers that have been used for diversity research (Kiani *et al.,* 2010). High variation in morphological characteristics can be an important factor for germplasm collection. These characteristics are the first step for the identification and protection of genetic resources (Peng *et al.,* 2014). Ercisli *et al.* (2008) studied relationships among some cornelian cherry genotypes based on RAPD analysis in Turkey. Based on 56 random primers, seven showed a reliable polymorphism. The cophenetic correlation coefficient between similarity matrix and the cophenetic matrix of the dendrogram was relatively high. Therefore, their

results demonstrated high levels of polymorphism among cornelian cherry genotypes. Yilmaz *et al.* (2009) evaluated biodiversity, ex-situ conservation and characterization of cornelian cherry genotypes in Turkey. Twelve fruit parameters were studied and a wide variation was found among genotypes in fruit properties. Fruit weight varied from 1.4 to 9.2 g among genotypes. On average, the genotypes had 17% soluble solids content with the range of 11.3% (44-03) to 25.9% (44-27). Most of the genotypes had various degrees of red skin color, whereas two genotypes (44-03 and 44-17) had yellow skin color (Yilmaz *et al.,* 2009). Mert (2009) assessed pollen morphology and anatomy of cornelian cherry cultivars. Morphology and ultrastructure of pollen grain were described for six cornelian cherry cultivars using both light microscopy and transmission electron microscopy. Hence, two different pollen shapes were observed: oblate spheroidal and prolate spheroidal. Bijelic *et al.* (2011) studied morphological characteristics of best cornelian cherry genotypes selected in Serbia. Morphological characteristics of fruit, including fruit length, fruit diameter, fruit weight, fruit thickness, and weight to the stone ratios were measured. Hassanpour *et al.* (2012) evaluated some fruit characteristics of Iranian cornelian cherries. In their evaluation, fruit weight varied from 1.499 to 3.29 g, whereas seed weight ranged from 0.249 to 0.425 g. The mean length of fruits was between 15.22 and 22.31 mm, and their mean width was between 10.26 - 16.3 mm. The content of ascorbic acid ranged from 240 - 360 mg/100 g fresh weight, total soluble solids and total acidity were 5-12.2% and 0.43-1.86%, respectively. Grouping of cornelian cherry accessions based on 5 factors was performed and they were divided into three sub-clusters. Akbarinia *et al.* (2013) studied the amount of available compounds in cornelian cherry plants cultivated in Qazvin province. Cornelian cherry fruits were collected from Alamout and Gagazan villages in 2011. Dry matter content, acidity, vitamin C and total sugar were measured. Dry matter ranged from 14.8 to 25.4, acidity form 2.81 to 3.54, vitamin C from 27.55 to 81.7 mg in 100 g, sugar from 0.78 to 1.71% and total soluble solids from 12.33 to 21.66. Generally, Alamout cornelian cherry fruits were superior to Gagazan fruits in all characteristics except for total soluble solids amount.

Since Arasbaran region is the main cornelian cherry growing region in Iran and there is a wide distribution of this fruit tree in the Kaleybar-Chaei watershed (Figure 1), this investigation was carried out to determine the genetic diversity among cornelian cherry genotypes based on quantitative and qualitative traits, by descriptive statistics, correlation coefficients, and multivariate analysis.

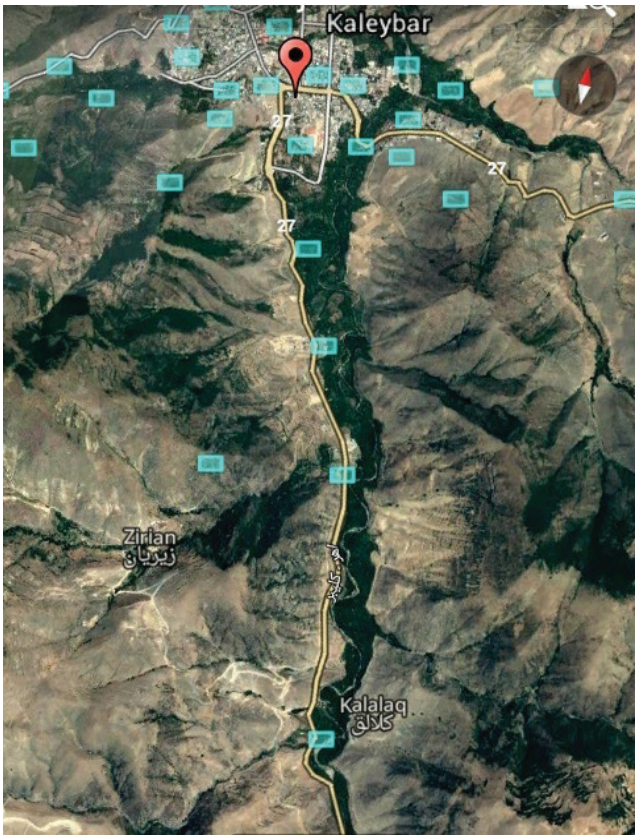

Figure 1. Satellite picture of regions from Kalalagh to Kaleybar in Kaleybar-Chaei watershed (from Kalalagh to Kaleybar, respectively: 1-Kalalagh 2-Dashli 3-Razoular 4-Chilakhaneh 5- Alkhoumlar).

MATERIALS AND METHODS

In this research, 20 cornelian cherry genotypes were chosen and studied for 28 qualitative and quantitative characteristics including fruit, leaf, and flower from different regions of Kaleybar-Chaei including genotypes from Kalalagh, Dashli, Razoular, Chilakhaneh, and Alkhoumlar (Table1). Qualitative and quantitative traits were measured, beginning from the flowering time to leaf appearance and full ripening of fruits in 2016. Flowering time and alternation were evaluated during three weeks in March 2016. Then, vegetative traits and growth habits of trees were evaluated from the end of the May, i.e from leaf growth to complete maturity. For leaf sample collection, leaves were chosen with matured, healthy, and bright green characteristics. Finally, fruits were harvested and fruit characteristics were measured (Figure 2).

Figure 2. Leaves and fruits of the selected cornelian cherry genotypes (KY1, KY2, KY3 and KY4: collected from Kalalagh; DH1, DH2, DH3 and DH4:collected from Dashli; RZ1, RZ2, RZ3 and RZ4: collected from Razoular; CH1, CH2, CH3 and CH4: collected from Chilakhaneh; AK1, AK2, AK3 and AK4: collected from Alkhoumlar).

Table 1. Genotype number, abbreviation, and region name.

Genotype number	Abbreviation	Region name
1	KY1	Kalalagh
2	KY2	Kalalagh
3	KY3	Kalalagh
4	KY4	Kalalagh
5	DH1	Dashli
6	DH2	Dashli
7	DH3	Dashli
8	DH4	Dashli
9	RZ1	Razoular
10	RZ2	Razoular
11	RZ3	Razoular
12	RZ4	Razoular
13	CH1	Chilakhaneh
14	CH2	Chilakhaneh
15	CH3	Chilakhaneh
16	CH4	Chilakhaneh
17	AK1	Alkhoumlar
18	AK2	Alkhoumlar
19	AK3	Alkhoumlar
20	AK4	Alkhoumlar

Data Analysis

Descriptive statistics, correlation of quantitative and qualitative traits, factor analysis and cluster analysis were carried out by SPSS 16. Two separate formulas were used for computing coefficient of variation in quantitative and qualitative traits:

$$(1) \qquad \text{C.V. For Quantitative Traits (\%)} = \frac{\text{Standard deviation}}{\text{Mean}} \times 100$$

$$(2) \qquad \text{C.V. For Qualitative Traits(\%)} = \frac{\text{Quartile(Q)}}{\text{Mean}} \times 100 = \frac{Q_3 - Q_1}{\text{Mean}} \times 100$$

The coefficient of variation (CV) refers to a statistical measure of the distribution of data points in a data series around the mean and can be used to compare the variation of traits in genotypes. Correlation of quantitative and qualitative traits was determined using Pearson and Spearman correlation coefficient, respectively. Factor analysis was used for the first time for measuring artificial intelligence by Karl Pearson (1901) and Charles Spearman (1904). Factor analysis used for the most effective variables if there are too many variables and relationship among them is unknown (Zarechahoki, 2010). For separation of factors, factor rotation and Varimax method were used. Factor loading values higher than 0.6 were considered significant in main and independent factors. Cluster analysis and classification of genotypes was performed using the Ward method based on Squared Euclidean distance.

RESULTS

Descriptive statistics and correlation

Important measured traits and descriptive statistics are listed in Tables 2 and 3, respectively. Some quantitative traits showed significant and positive correlations (Table 4). Among these traits, petiole diameter with leaf length ($r=0.476$, $p\leq0.05$) and petiole diameter with leaf width ($r=0.772$, $p\leq0.05$) had the lowest and highest correlations, respectively. This shows that when a positive correlation exists between two variables, the values of two variables change in the same direction. On the other hand, with using the Spearman rank correlation coefficient there were both significant positive and negative correlations between many qualitative traits (Table 5). Traits such as the number of fruits on a branch with fruit yield ($r=0.390$, $p\leq0.05$) and fruit yield with flower density ($r=0.894$, $p\leq0.01$) had the lowest and highest positive correlations, respectively. Also, the shape of tree crown

Table 2. Characteristics of traits in 20 cornelian cherry genotypes.

Trait	Abbreviation	Measurement unit	Measurement criterion
Fruit length	FrL	mm	ruler
Fruit diameter	FrD	mm	caliper
Tissue of fruit skin	TFrS	code	smooth (1), rough (2)
Fruit maturation	FrMa	code	early (1), medium maturity (2), delayed (3)
Fruit stalk length	FrSl	mm	ruler
Fruit stalk diameter	FrSD	mm	caliper
Fruit yield	FrYLD	code	few (1), middle (2), high (3)
Tissue of fruit flesh	TFF	code	tight (3), soft (5), watery (7)
Number of fruit on branch	CFrN	code	one (1), one & two (2), two (3), two & three (4), three (5), three & four (6), four & five (7)
Pit length	PL	mm	caliper
Pit diameter	PD	mm	caliper
Fruit color	FrCol	code	ruffous (1), red (2), scarlet (3), reddish-pink (4), reddish-black (5), black (6)
Fruit taste	FrT	code	sour (1), very sour (2), sour & astringent (3) , sour & very astringent (4), very sour & very astringent (5)
Leaf shape	LSh	code	oval (1), elliptic cylindrical (2), circular (3)
Leaf tip angle	LTA	code	slightly sharp (1), sharp (2), very sharp (3)
Leaf length	LL	mm	ruler
Leaf width	LW	mm	ruler
Flower density	FD	code	low (3), to high (7)
Flowering alternation	FAlt	code	extremely disordered (1), disordered (2), relatively disordered (3), orderly (4)
Fruit shape	FrSh	code	oval (1), cylindrical oval (2), circular (3), cylindrical circular (4), oblong (5), cylindrical (6), very cylindrical (7)
Fluff on fruit	FFr	code	glabrous (0), downy (1)
Petiole length	PeL	mm	ruler
Petiole diameter	PeD	mm	caliper
Fruit space on branch	FrSp	code	annual branch (1),both annual and biennial branch (2), perennial branch (3)
Leaves scattering on the crown of tree	TcLS	code	next to each other (1), scattered (2)
Fluff on leaf	Fle	code	very low (1), low (2), average (3), much (4), very much (5)
Shape of tree crown	ShTc	code	elongated (1), circular (2), oval (3), conical (4)
Tree height	TH	code	dwarf (1), average (2), tall (3)

with leaf tip angle (r=-0.381, p≤0.05) and color with leaf tip angle (r=-0.506, p≤0.05) had the lowest and highest negative correlations, respectively. Thus, when the value of rank correlation coefficient is positive, ranks are in the same direction but when the value of a correlation coefficient is negative, ranks are in the opposite directions.

Factor analysis

In this evaluation, effective traits were divided into 10 factors accounted for 87.85% of the total variances. Factor loading values higher than 0.6 were considered significant. Traits such as leaf width, petiole length, petiole diameter, and leaf shape related to the first factor explained 12.92% of variance; flower density, tissue of fruit flesh, and fruit yield related with the second factor explained 11.63% of variance; and fruit length and diameter related with the third factor explained 10.85% of variance. As a result, these three factors explained 35.4% of total variance. Also, traits such as fruit skin, fruit maturation, and the shape of tree crown with 9.18% of variance were the fourth

Table 3. Descriptive statistics and coefficient of variation in evaluated traits.

Genotype	FrL	FrD	TFrS	FrMa	FrSl	FrSD	FrYLD	TFF	CFrN	PL	PD	FrCol	FrT	LSh	LTA	LL	LW	FD	FAlt	FrSh	FFr	PeL	PeD	FrSp	TcLS	FLe	ShTc	TH
KY1	21.63	13.04	1	3	10.45	0.69	7	7	3	13.4	5.45	2	1	2	2	78.63	53.88	7	4	7	1	7.96	1.18	3	1	5	1	1
KY2	19.44	11.97	2	5	14.16	0.76	3	3	1	14.68	6.42	4	1	3	1	81.03	50.14	3	3	1	1	8.78	1.29	1	2	3	2	3
KY3	15.5	12.51	2	7	13.78	0.65	7	5	6	9.73	5.59	1	3	1	3	65.99	30.66	5	3	3	1	8.35	1.05	3	2	4	1	1
KY4	19	13.59	1	5	12.84	0.74	5	5	1	13.74	7.27	2	2	3	3	105.7	73.58	4	1	1	0	10.31	1.63	1	1	2	1	2
DH1	24.04	18.29	2	5	13.38	0.63	7	7	1	12.87	5.84	6	3	1	1	75.25	39.94	6	4	6	1	7.48	.88	2	2	2	3	3
DH2	17.55	14.14	1	3	16.19	0.61	3	3	3	12.26	6.01	2	5	2	2	67.96	42.83	3	2	4	1	7.01	.86	1	1	2	1	1
DH3	19.55	12.6	2	5	15.15	0.58	5	5	3	12.27	6.45	2	4	1	3	88.99	38.45	4	2	1	1	7.64	.89	1	1	1	1	2
DH4	19.43	13.74	2	7	12.2	0.64	7	5	5	12.05	6.68	6	3	2	1	81.52	35.57	5	3	4	1	8.6	.84	3	2	2	2	1
RZ1	21.23	11.71	2	7	12.57	0.53	5	5	5	15.34	5.25	4	3	3	1	67.29	41.95	4	4	7	0	7.6	1.24	3	1	1	3	1
RZ2	17.32	12.43	2	5	11.65	0.65	5	5	4	13.69	5.74	2	4	1	1	62.73	30.8	4	4	1	1	6.32	1.02	3	2	3	3	1
RZ3	17.98	14.81	2	7	17.29	0.71	5	3	2	13.74	7.01	2	1	2	3	92.34	51.31	5	2	3	1	8.17	1.49	1	1	1	4	1
RZ4	16.6	12.49	1	5	14.54	0.66	7	7	7	12.47	5.73	2	5	2	1	66.36	29.07	7	1	1	1	7.47	.95	3	2	2	1	2
CH1	19.11	14.42	2	3	16.01	0.76	7	7	4	14.53	7.27	1	3	3	2	84.05	59.26	6	2	2	1	10.18	1.73	2	2	2	1	1
CH2	19.03	12.31	2	5	13.49	0.79	3	5	3	13.07	5.85	2	2	2	1	79.79	33.21	4	2	1	1	6.07	1.03	3	2	2	3	3
CH3	21.69	14.88	1	3	12.57	0.68	7	5	7	17.46	7.62	3	3	1	2	81.9	39.45	5	3	6	1	7.09	1.25	1	1	3	1	2
CH4	19.55	12.9	2	7	15.95	0.69	3	3	4	19.47	6.43	4	1	2	2	82.24	31.01	3	1	2	1	7.17	1.08	2	2	1	1	1
AK1	18.43	13.54	1	3	12.07	0.6	5	5	1	12.53	6.26	5	3	3	2	75.48	50.43	4	1	1	1	11.15	1.48	2	2	1	1	3
AK2	17.32	12.29	2	7	14.72	0.63	7	3	4	14.66	7.89	3	4	1	1	60.82	39.35	6	3	2	1	8.52	1.12	3	1	2	1	1
AK3	17.51	11.45	2	5	16.8	0.67	7	3	3	12.92	5.89	2	3	2	2	77.48	40.37	5	4	1	1	10.14	1.29	3	1	1	3	1
AK4	20.77	14.9	1	7	15.74	0.76	7	5	3	13.51	6.18	2	5	2	2	66.39	37.21	7	3	5	1	9.06	1.2	3	1	2	1	2
Minimum	15.5	11.45	1	3	10.45	0.53	3	3	1	9.73	5.25	1	1	1	1	60.82	29.07	3	1	1	0	6.07	.84	1	1	1	1	1
Maximum	24.04	18.29	2	7	17.29	0.79	7	7	7	19.47	7.89	6	5	3	3	105.7	73.58	7	4	7	1	11.15	1.73	3	2	5	4	3
Mean	19.13	13.4	1.65	5.2	14.08	0.67	5.6	5.4	3.6	13.71	6.34	2.75	2.95	1.95	1.8	77.09	42.42	4.85	2.6	2.95	0/9	8.25	1.17	2.2	1..5	2.1	1.75	1.65
C.V. (%)	10.56	11.71	60.6	76.92	13.33	10.09	35.71	37.03	83.33	14.95	11.7	70.17	67.79	102.5	55.55	14.41	26.34	41.23	76.92	135.5	0	16.6	21.8	90.9	66.6	95.23	114.28	60.6

Note: LTA=Leaf tip angle, LL=Leaf length, LW=Leaf width, FD=Flower density, FAlt=Flowering alternation, FrSh=Fruit shape, FFr=Fluff on fruit, PeL=Petiole length, PeD=Petiole diameter, FrSp=Fruit space on branch, TcLS=Leaves scattering on the crown of tree, FLe=Fluff on leaf, ShTc=Shape of tree crown, TH=Tree height.

Table 4. Correlation coefficients of quantitative traits.

Trait	FrL	FrD	FrSl	FrSD	PL	PD	LL	LW	PeL	PeD
FrL	1									
FrD	0.573**	1								
FrSL	-0.310	0.050	1							
FrSD	0.001	0.086	0.203	1						
PL	0.377	0.006	0.093	0.161	1					
PD	-0.026	0.206	0.250	0.267	0.377	1				
LL	0.222	0.172	0.085	0.371	0.177	0.414	1			
LW	0.186	0.169	-0.063	0.279	0.045	0.380	0.659**	1		
PeL	-0.123	-0.001	0.113	0.117	-0.177	0.298	0.301	0.619**	1	
PeD	-0.021	-0.005	0.121	0.408	0.247	0.417	0.476*	0.772*	0.686**	1

*,**; significant at 0.05 and 0.01 probability level, respectively.
Note: FrL=Fruit length, FrD=Fruit diameter, FrSl=Fruit stalk length, FrSD=Fruit stalk diameter, PL=Pit length, PD=Pit diameter, LL=Leaf length, LW=Leaf width, PeL=Petiole length, PeD=Petiole diameter.

Table 5. Correlation coefficients of qualitative traits.

Trait	TFrS	FD	TFF	FrYLD	FrMa	FAlt	LTA	LSh	FrT	FFr	CFrN	FrSh	FrCol	FrSp	TcLS	FLe	ShTc	TH
TFrS	1																	
FD	-.196	1																
TFF	-.258	.558**	1															
FrYLD	-.119	.894**	.493*	1														
FrMa	.494*	.042	-.348	.033	1													
FAlt	.301	.277	.89	.395*	.109	1												
LTA	-.234	-.056	-.127	-.014	-.086	-.357	1											
LSh	-.195	-248	-.017	-.332	-.159	-.336	.000	1										
FrT	-.237	.248	.142	.305	-.030	.042	-.163	-.361	1									
FFr	.105	.237	-.063	.189	-.169	.015	-.062	-.465*	.150	1								
CFrN	.074	.248	.178	.390*	.221	.112	-.198	-.328	.343	.059	1							
FrSh	-.141	.358	.208	.364	.122	.471*	-.020	-.155	-.024	-.090	.248	1						
FrCol	.088	-.226	-.144	-.128	.153	.126	-.506*	.079	-.173	-.077	-.149	.201	1					
FrSp	.158	.462*	.261	.441*	.357	.437*	-.465*	-.147	.239	.063	.449*	.102	-.086	1				
TcLS	.314	-.116	.283	-.094	-.009	-.179	-.410*	.065	-.126	.333	.097	-.324	.177	.189	1			
FLe	-.213	.253	.323	.282	-.252	.352	-.169	-.278	-.014	.200	.213	.205	-.236	.159	.185	1		
ShTc	.580**	-.143	-.177	-.193	.279	.459*	-.381*	.009	-.283	-.082	-.210	-.014	.218	.150	.109	-.208	1	
TH	-.262	-.092	.243	-.187	-.290	-.257	-.158	.111	-.039	.032	-.472*	-.314	.296	-.296	.250	.025	-.019	1

*,**; significant at 0.05 and 0.01 probability level, respectively.
Note: TFrS=Tissue of fruit skin, FD=Flower density, TFF=Tissue of fruit flesh, FrYLD=Fruit yield, FrMa=Fruit maturation, FAlt=Flowering alternation, LTA=Leaf tip angle, LSh=Leaf shape, FrT=Fruit taste, FFr=Fluff on fruit, CFrN=Number of fruit on branch, FrSh=Fruit shape, FrCol=Fruit color, FrSp=Fruit space on branch, TcLS=Leaves scattering on the crown of tree, FLe=Fluff on leaf, ShTc=Shape of tree crown, TH=Tree height.

Table 6. Factor components loadings of 28 traits obtained from cornelian cherry genotypes.

Measured traits	Factors									
	1	2	3	4	5	6	7	8	9	10
FrL	0.015	0.044	**0.882**	0.013	-0.064	0.203	-0.090	0.191	-0.024	-0.180
FrD	-0.022	0.260	**0.808**	-0.088	0.243	-0.140	0.045	-0.016	0.001	0.221
FrSl	0.003	-0.067	-0.156	0.159	0.172	-0.776	-0.214	0.072	0.293	0.263
FrSD	0.253	0.018	0.026	0.016	0.089	0.041	0.216	0.174	**0.843**	0.155
PL	-0.038	-0.239	0.185	0.021	-0.094	-0.043	-0.091	**0.864**	0.151	-0.167
PD	0.312	0.092	-0.002	-0.093	0.365	-0.196	-0.031	**0.656**	-0.045	0.356
LL	0.394	-0.209	0.218	0.081	**0.731**	0.015	0.120	0.166	0.173	-0.168
LW	**0.798**	-0.084	0.168	-0.183	0.376	0.143	-0.157	0.035	0.122	-0.175
PeL	**0.887**	0.239	-0.138	-0.102	0.115	-0.142	0.057	-0.041	-0.163	0.058
PeD	**0.796**	0.063	-0.073	-0.042	0.212	-0.031	-0.077	0.230	0.307	-0.174
TFrS	-0.106	-0.100	-0.131	**0.863**	-0.028	-0.034	0.141	0.048	-0.056	0.146
FD	0.016	**0.891**	0.166	-0.107	-0.144	0.019	-0.094	-0.088	0.207	0.095
TFF	-0.072	**0.600**	0.333	-0.274	0.011	0.299	0.336	-0.255	0.102	-0.284
FrYLD	0.079	**0.933**	0.062	-0.011	-0.027	0.108	-0.140	-0.028	-0.151	0.158
FrMa	-0.201	0.155	-0.196	**0.676**	-0.028	-0.286	-0.028	0.124	-0.150	-0.163
FAlt	-0.094	0.201	0.219	0.408	-0.424	0.449	-0.477	-0.171	-0.091	0.147
LTA	0.152	0.022	-0.177	-0.116	**0.840**	-0.096	-0.278	-0.129	0.073	0.010
LSh	**0.693**	-0.234	-0.038	-0.120	-0.134	-0.096	0.158	0.050	0.162	-0.505
FrT	-0.308	0.318	-0.133	-0.439	-0.284	-0.441	-0.125	-0.281	-0.280	0.119
FFr	-0.294	0.096	-0.016	-0.044	-0.109	-0.025	0.205	-0.035	0.197	**0.808**
CFrN	-0.592	0.459	-0.376	-0.118	-0.108	0.069	-0.033	0.310	-0.062	-0.163
FrSh	-0.214	0.293	0.566	-0.020	-0.128	0.304	-0.481	0.088	-0.125	-0.235
FrCol	0.085	-0.141	0.530	0.212	-0.269	0.044	0.344	0.204	-0.595	0.006
FrSp	-0.164	0.511	-0.293	0.250	-0.607	0.147	0.083	-0.179	0.008	-0.154
TcLS	-0.107	-0.003	-0.059	0.151	-0.187	0.137	**0.882**	-0.052	0.053	0.103
FLe	-0.153	0.224	-0.064	-0.207	-0.024	**0.832**	-0.080	-0.090	0.250	0.181
ShTc	-0.004	-0.205	0.246	**0.746**	-0.179	-0.072	-0.092	-0.255	0.146	-0.076
TH	0.149	-0.270	0.488	-0.235	-0.079	-0.050	0.530	-0.199	0.081	0.092
Eigen values	3.61	3.25	3.03	2.57	2.53	2.18	2.14	1.84	1.71	1.69
% of Variance	12.92	11.63	10.85	9.18	9.06	7.80	7.64	6.58	6.11	6.03
% Cumulative	12.92	24.55	35.41	44.59	53.65	61.46	69.11	75.69	81.81	87.85

Note: Factor loading values more than 0.6 were considered as significant, i.e. the bold numbers are the highest loadings for each factors.

Note: FrL=Fruit length, FrD=Fruit diameter, FrSl=Fruit stalk length, FrSD=Fruit stalk diameter, PL=Pit length, PD=Pit diameter, LL=Leaf length, LW=Leaf width, PeL=Petiole length, PeD=Petiole diameter, TFrS=Tissue of fruit skin, FD=Flower density, TFF=Tissue of fruit flesh, FrYLD=Fruit yield, FrMa=Fruit maturation, FAlt=Flowering alternation, LTA=Leaf tip angle, LSh=Leaf shape, FrT=Fruit taste, FFr=Fluff on fruit, CFrN=Number of fruit on branch, FrSh=Fruit shape, FrCol=Fruit color, FrSp=Fruit space on branch, TcLS=Leaves scattering on the crown of tree, FLe=Fluff on leaf, ShTc=Shape of tree crown, TH=Tree height.

factor; leaf length and leaf tip angle with 9.06% of variance were the fifth factor; fluff on leaf with 7.80% of variance was the sixth factor. Leaf scattering on the crown of tree with 7.64% of variance was the seventh factor; pit length and diameter with 6.58% of variance was the eighth factor; fruit stalk diameter with 6.11% variance was the ninth factor; and fluff on fruit with 6.03% of variance was the tenth factor (Table 6). In general, each factor justifies the changes not stated by the previous factors. Since factors are independent, each factor represents different characteristics of the main data and must be interpreted independently.

Cluster analysis

Cluster analysis was carried out with the Ward method based on the measured traits and raw data. Generally, genotypes were divided into two main groups.

Important factors for the separation of main clusters were characteristics such as fruit length and diameter, fruit stalk length and diameter, pit length and diameter, leaf length and width, petiole length and diameter, fruit taste, fruit color, and etc. With a decrease in the Squared Euclidean distance from 25 to 5, the genotypes were divided into four main sub-clusters (Figure 3).

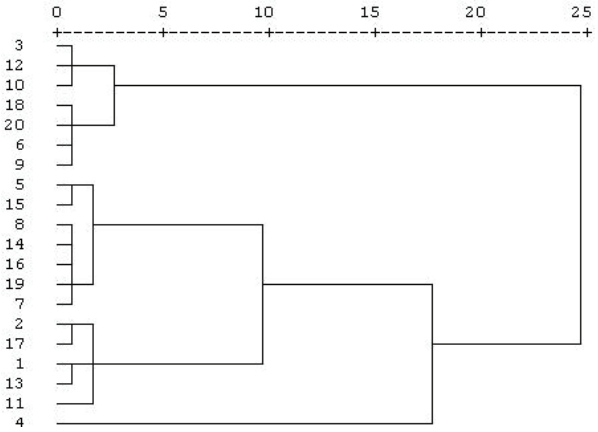

Figure 3. Cluster analysis dendrogram based on the evaluated traits.

First sub-cluster: KY3, RZ4, RZ2, AK2, AK4, DH2, and RZ1 genotypes were placed in this sub-cluster with low fruit length, average fruit diameter, average fruit stalk length, low fruit stalk diameter, low pit length and diameter, low leaf length and width, relatively soft tissue of fruit flesh, relatively average fruit yield, medium fruit maturation, red fruit color, elongated shape of tree crown, very sour and very astringent fruit taste.

Second sub-cluster: DH1, CH3, DH4, CH2, CH4, AK3, and DH3 are the member of this sub-cluster. These genotypes had a high fruit length and diameter, average fruit stalk length and fruit stalk diameter, high pit length and diameter, average leaf length and width, average petiole length and diameter, relatively high fruit yield, generally elliptic cylindrical leaf shape, red and black fruit color, oval shape of tree crown, and sour and astringent fruit taste.

Third sub-cluster: This sub-cluster included KY2, AK1, KY1, CH1, and RZ3 genotypes with the average fruit length and diameter, high fruit stalk length and diameter, average pit length and diameter, high leaf length and diameter, rough tissue of fruit skin, early fruit maturation, reddish-pink and reddish-black fruit color, scattered leaves on the crown of tree and sour fruit taste.

Fourth sub-cluster: KY4 genotype, with relatively high fruit length, average fruit diameter, low fruit stalk length, high fruit stalk diameter, low pit length, high stone diameter, high leaf length and width, high petiole length and diameter, soft fleshy fruit, average fruit yield, very sharp leaf tip angle, circular leaf shape, red fruit color, and very sour taste was placed in this sub-cluster. Consistent with some previous studies on cornelian cherry (Yaltirik 1981; Yilmaz *et al.,* 2009; Ersoy *et al.,* 2011), about cornelian cherry growing under the shade of tall trees, KY4 was the only genotype which had grown under the shade of walnut tree.

DISCUSSION

Main purpose of this study was determination of genetic diversity among cornelian cherry genotypes in Arasbaran region as a main planting and growing cornelian cherry region in Iran. Traits such as fruit shape, shape of tree crown, leaf shape, fluff on leaf, fruit space on branch, flowering alternation, fruit maturation, fruit color, fruit taste, leaves scattering on the crown of tree, tissue of fruit skin, leaf tip angle and tree height showed a high coefficient of variation. Hence, traits with high coefficients of variation had a high diversity among genotypes. Correlation coefficients of quantitative traits showed significant and positive correlations between fruit length and diameter. This was different with the results of Hadi (2015) and was in agreement with the results of Hassanpour *et al.* (2012). Also, there were significant and positive correlations between leaf length and width, petiole diameter and leaf length, petiole length and leaf width, petiole diameter and leaf width, and petiole diameter with petiole length. However, no correlation was found between pit length and pit diameter which was in contrast with the results of Hassanpour *et al.* (2012) but consistent with the results of Hadi (2015). Also, significant positive and negative correlations were obtained between different traits. According to the results, correlation coefficient of quantitative and qualitative traits facilitates measuring and analyzing the degree of relationship between two variables or in other words, it deals with the association between two or more variables. Results of factor analysis showed that the first, second, and third factors had the largest share in justifying variance and confirmed that the traits such as leaf width, petiole length and diameter, leaf shape flower density, tissue of fleshy fruit, fruit yield, fruit length, and fruit diameter had an effective role in causing variation among genotypes. Hassanpour *et al.* (2012) concluded that pit length and diameter had an important role in cornelian cherry genotypes

classification and considered them as effective traits in factor analysis, which was the same with the results of this study. It is essential to note that the main objective of factor analysis in this investigation was data reduction and determination of important variables. Based on the results of cluster analysis, traits such as fruit length and diameter, fruit stalk length and diameter, pit length and diameter, leaf length and width, petiole length and diameter, fruit taste and color were important traits for separating genotypes. Cornelian cherry is rich in nutrient components and is important in agriculture and medicine, therefore using both morphological and molecular diversity is essential for breeding these genotypes. Data analysis based on descriptive statistics, correlation, factor and cluster analysis indicated a large diversity among cornelian cherry genotypes in Arasbaran region.

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