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The morphological analysis of 'Shahrood1' × 'Shahrood12' population with their parents

Reza Tavakoli Banizi[1], Ali Imani[2*], Mehrshad Zeinalabedini[3], Assa Ebrahimi[4], Saeed Piri[5]

[1, 4]*Plant Breeding Department, Science and Research Branch of Islamic Azad University, Tehran, Iran*

[2]*Horticultural Department of Seed and Plant Improvement Institute (SPII), Iran*

[3]*Agricultural Biotechnology Research Institute of Iran (ABRII), Iran*

[5]*Horticultural Department of Abhar Islamic Azad University, Iran*

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Abstract

Genetic resources are sometimes called the "first resource" of the natural resources means attention to the vast diversity among and among the plant species. According to International Board for Plant Genetic Resources (IBPGR) descriptors , the 92 almond progenies variability from 'Shahrood1' × 'Shahrood12' with their parents, measure and compared. Principal component analysis (PCA) showed considerable to 30 phenotypic diversity among the almond progenies. The important traits frequency such as flowering time, tree size, resistance to frost, growth habit, flower density and leafing time in all hybrid population and compare them with their parents show their asymmetric distribution among them. The simple correlation coefficients traits showed that among the some of measured traits was a significant positive correlation. In other hand, the eigenvalue variance percentage and cumulative variance showed the among measure traits five independent factors that their eigenvalue were more than 14, they could justified 42.96% of total variance. Also the study population were separated into four different groups according to their height using cluster analysis performed by Ward's clustering method based on morphological data. some of progenies likes 'Shahrood12' in first group, some other likes 'Shahrood1'were in second group and some other that expression of phenotypic traits were additive mode, incomplete dominance or over dominance in third and fourth group.

* **Corresponding Author:** Ali Imani ✉ habel433@yahoo.com

Introduction

Almond [*Prunus dulcis* (Miller) D.A. Webb, syn. *Prunus amygdalus* Batsch] occupies a very peculiar place among fruit trees (Miller *et al*., 1989). An evaluation of economically valuable traits was performed to identify useful genotypes for almond producers and breeding programs(De Giorgio and Polignano, 2001). Phenotypic and genotypic variation studies are important for preliminary evaluation because they facilitate fast and simple evaluation and can be used as a general approach for assessing genetic diversity among phenotypical distinguishable accessions that they used in breeding programs(De Giorgio and Polignano, 2001; Baninasab and Rahemi, 2008). Iran is amongst the most important countries producing *Prunus* fruits, as its ranking regarding to production of almond is third in the world (Asma *et al.,* 2007; Sarkhosh *et al.,* 2006). Twenty-six almond species form a distinct and easily identified taxonomic group in the world (Gulcan, 1985). In Iran 21 almond species and 6 natural progenies have been described (De Giorgio *et al*., 2007). Today, for evaluate the cultivars and genotypes based on qualitative and quantitative characteristics and their relationships need to using multivariate statistics. This method can be an index between the independent and dependent traits (Mohammadi and Parmasa, 2003). In way that, Lansari *et al.* (1994) for diversity evaluation of almond cultivars and clones morphologically used Factor analysis. Their results showed that the kernel and fruit properties in variation of almond cultivars and clones are more important than leafing properties. Multivariate method can assistance to analysis large data sets and resolve several phenotypic and genotypic measurements into fewer more interpretable and more easily visualized groups. Factor analysis is a powerful method of multivariate statistical techniques that can group studied traits effetely. The PCA is useful before the cluster analysis because relative importance of specific traits role be determined (Jackson and Clarke, 1991). Therefore this method is useful for representing a set of variables with a much smaller set of composite variables that account for much of the variance among the original set. It facilitates visualization of differences among individuals and the identification of possible groups and relationships among individuals and variables (Martínez-Calvo *et al.,* 2008). This method has been used by Lansari *et al.* (1994), De Giorgio and Polidnano (2001), De Giorgio *et al.* (2007),Colic *et al.* (2012) and Chalak *et al.* (2007) in order to grouping and separating of almonds genotypes and cultivars. Also, Rasouli *et al.* (2013) in phenotype evolution some of 72 almond cultivars and genotypes using morphological markers showed that the 30 traits studied in 11 factors based on PCA were data reduction and classified with cluster analysis. In this study, 72 different varieties of almonds that collected in all over Iran were compared and correlated morphological traits and analyzed together. The 30 traits studied in11 factors based on PCA were data reduction and classified with cluster analysis. Colic *et al.* (2012) researched on morphological and biochemical evaluation of 19 almond genotypes in Serbia. Variation in traits related to phenology, morphology and fruit quality was observed, and the results indicated a high morphological diversity of almond genotypes. Also results showed the majority of important correlations were determined among nut size traits such as nut width, nut length, nut thickness, and nut weight and leaf size traits contain leaf length, leaf width, and leaf area. In other hands the lack of correlation between kernel size and chemical compounds enables the creation of a new almond cultivar with large kernels and improved quality. The PCA analysis showed considerable phenotypic variety among the study genotypes. Parameters within high discriminating values were those related to nut, kernel, and leaf size, ripening time and tree habit. Therefore, the purpose of at present study was to investigate the Phenotypic variation of 'Shahrood1' × 'Shahrood12' population and their compare them with the parents using morphological markers. The main cause of this present study was the identification and analysis of Phenotypic special charactistics of 'Shahrood1' × 'Shahrood12' population and their compare them with the parents using morphological markers in Karaj region almond collection, in order to reach to the

promising progenies with special features of performance.

Materials and methods

The study included 92 progenies from 'Shahrood1' × 'Shahrood12' and their parents selected from in northern Iran (Karaj). Their evaluated using 30 morphological features during 2013 and 2014. The 92 trees were selected after evaluation of over 500 trees on the basis of regular fruit production and observed phenotypic diversity. Selection of progenies was mainly conducted according to relevant morphological traits of the tree, nut and phenology. The trees from the examined progenies are 15-20 years old. They are mostly individual trees from private gardens that have been grown without applying any agricultural practices. Genotypes were evaluated for 30 traits. The study morphological traits such as tree size (TS), Growth habbit (GH), Bearing habbit (BH), Branches Number (BN), Leafing time (LET), Flowering time (FT), Flower size (FLS), Flower color (FC), Resistance to Frost (RF), Flower density (FD), Position of Pistil to stamen (SP), Fruit stage (FS), Color fruit (CF), Fruit fuzz (FF), Fruit shape (FSH), Kernel Color (KC) and Fruit Maturity (FM) were determined on the basis of the International almond descriptor (Gulcan, 1985).The other traits such as Leafing Size(LSI),Kernel Diagonal (KD), Kernel Wide (KW), Kernel Lengh (KL), Shell Wide(SWI), Shell Lengh (SL), Hull Wide (HWI)and Hull Lengh (HL) measered by caliper(cm) and the Shell Weight(SW), Hull Weight(HW), Weight Nut(WN) measured by balance (gr) an the other such as wood percentage(WP) and Duble kernel(DK) measured based on percent (Table1).

All observations were made on 20 ripe fruits sampled randomly from the periphery of the trees when the hull was fully desiccated and open along the suture. Leaves (20 per every hybrid) were sampled from the median section of 1-year-old branches during harvest time. Flowering time was figured by calculating days from the onset to the end of flowering. Fruit Maturity was the harvest date. For statistical analysis, Fruit Maturity was represented as the number of days from 1 July. The fruit stage period was expressed as the number of days from full bloom to ripening.

Statistical analysis

The frequency distribution of all 6 main traits was represented in histograms. Data analysis was performed using SPSS (Version 21.0) such as trait frequency, descriptive statistics, simple correlation, principal component analysis and cluster analysis. Correlation coefficients were determined as Spearman's coefficient. Categories registered for each parameter were used to perform the PCA and maximum of variance and in each Principal and independent factor, factor coefficient was considered 0.5 or higher as significant. This statistical procedure was applied to create a correlation matrix from which standardized principal component (PC) scores were extracted. Scatter plots of the first 2 PC scores were created. To determine which of the PC scores accounted for the greatest amount of variation for each trait, the eigenvalues of the 5 PC scores were compared for each trait. Data processing was performed using the statistical program Statistica (StatSoft , Inc., Tulsa, OK, USA). The Gower general similarity coefficient (Gower, 1971) was used in cluster analysis of morphological traits by Ward Method.

Results

Traits Frequency

Evaluated progenies in some of the traits had distribution of normal relatively. Frequency in of flowering time were mainly on 1-year-old shoots,according to IBPGR descriptors indicate about 23% hybrid population, from 'Shahrood1' × 'Shahrood12' close to one parent ('Shahrood1') and other hand about 8% for flowering time trait similar to other parent ('Shahrood12') and was late flowering. The leafing time in 92 progenies, 8% hybrid population from 'Shahrood1' × 'Shahrood12' close to one parent ('Shahrood1') and other hand about 12% for leafing time trait was super late that similar to other parent ('Shahrood12'). The tree size trait, 44% hybrid population from 'Shahrood1' × 'Shahrood12' close to one parent ('Shahrood1') and were

intermediate. In other hand about 54% were strong and similar to other parent (‘Shahrood12’).In growth habit 15% hybrid population from ‘Shahrood1’ × ‘Shahrood12’ close to one parent (‘Shahrood1’) and were Spreading. In other hand about 43% were Extremely upright and similar to other parent (‘Shahrood12’). Also about the 25% hybrid population were intermediate mode and were upright. resistance to frost23% hybrid population from ‘Shahrood1’ × ‘Shahrood12’ close to one parent (‘Shahrood1’) and were sensitive. In other hand about 55% were resistance and similar to other parent (‘Shahrood12’). For flower density or fruit density trait on 1-year-old shoots, 40% hybrid population from ‘Shahrood1’ × ‘Shahrood12’ close to one parent (‘Shahrood1’) and were large. In other hand about 35% were medium large and similar to other parent (‘Shahrood12’)(Figure 1).

Table 1. The traits evaluation methods according to International Board for Plant Genetic Resources (IBPGR) descriptors (Gülcan, 1985).

Trait	Obrivation	Measure method
Tree size	TS	3=Weak،5=Intermediate ،7=Strong
Growth habbit	GH	1= Extremely upright ،3= upright ،5= Spreading ،7= Dropping ،9= Weeping
uy habbit	BH	1= Most flower buds on one year old shoots ،2= Most flower ،3= Mixed
Branches Number	BN	0= without ،3= low ،5= medium ، 7= large ،9= very large
Leafing time	LET	1= extra early ،2= very early ،3= early ،4= early medium ،5= medium ،6= medium late ،7= late ، 8= very late ، 9= super late
Flowering time	FT	1= extra early ،2= very early ،3= early ،4= early medium ،5= medium ،6= medium late ،7= late ، 8= very late ، 9= super late
Flower size	FLS	3= small ،5= medium ،7= large
Flower color	FC	1= white ،2= white pink ، 3= pink
Resistance to Frost	RF	1= sensitive ، 3= medium sensitive، 5= medium ، 7= medium resistance ،9= resistance
Flower density	FD	1= low ، 3= low medium ، 5= medium large, 7= large
Position of Pistil to stamen	SP	1= Pistil equal with stamen ، 3= Pistil to stamen ، 5= Pistil taller and equal with stamen ، 7= Pistil shorter and equal with stamen ، 9= Pistil shorterl with stamen
Fruit stage	FS	1= extra early ،3= early ،5= medium ، 7= late ، 9= super late
Color fruit	CF	3= white ، 5= white green ،7= green
Fruit fuzz	FF	1= low ، 3= low medium ، 5= medium large, 7= large
Fruit shape	FSH	1= round ، 2= ovate ، 3= oblong ، 4= cordate ، 5= extremely narrow
Leafing Size	LSI	Cliper
Kernel Color	KC	1= Extremely light, 3= light, 5= Intermediate, 7= Dark, 9= Extremely dark
Wood Percent	WP	Percentage
Double Kernel	DK	Percentage
Weight Nut	WN	Balance
Kernel Diagonal	KD	Cliper
Kernel Wide	KW	Cliper
Kernel Lengh	KL	Cliper
Shell Weight	SW	Balance
Shell Wide	SWI	Cliper
Shell Lengh	SL	Cliper
Hull Weight	HW	Balance
Hull Wide	HWI	Cliper
Hull Lengh	HL	Cliper
Fruit Maturity	FM	1= extra early ،3= early ،5= medium ،7= late ، 9= Super late

Traits simple correlation coefficients

At present study, the table 2 shows only the signifi cant correlations ($P < 0.05$) with an r-value over 0.5 between variables studied. There is a positive correlation for the branches number(BN) with fruit fuzz(FF) (r=0.52), tree size(TS) (r=0.66), bearing habit(BH) (r=0.50), leafing time(LET) (r=0.52), flower size(FLS)(r=0.50), flower density(FD)

(r=0.58) and fruit color(FC) (r=0.66). Furthermore flower density have positive correlated with leafing time (r =0.54), branches number (r =0.58), tree size(r =0.58), bearing habit(r =0.52), fruit fuzz(r =0.52) and fruit color(r =0.54). On the other hand tree size correlated with fruit fuzz, (r = 0.54), bearing habit(r=0.57), branches number (r = 0.66) flower size(r = 0.72), flower density(r=0.58), fruit size(r=0.50) and fruit color (r = 0.65). Also flower size with fruit color (r = 0.58), branches number (r = 0.50), bearing habit(r=0.50) and tree size (r = 0.72) has correlated positively. Also fruit size has correlated with flower color (r = 0.55), leafing time (r = 0.50), and tree size (r = 0.50). in other hand Hull Weight(HW) crrolated with Weight Nut(WN) (r = 0.65), Kernel Wide (KW) (r = 0.55), Kernel Lengh (KL) (r = 0.66), Shell Wide(SWI) (r = 0.63), Shell Lengh (SL) (r = 0.63), Hull Wide (HWI) (r = 0.61), Hull Lengh (HL) and the Shell Weight(r = 0.63).

Table 2. The simple double correlation of 15 measured almond progenies traits in this study.

	FSH	FF	CF	FS	SP	FD	RF	FC	FLS	FT	LET	BN	GH	BH	TS	LSI	KC	WP	DK	WN	KD	KW	KL	SW	SWI	SL	HW	HWI	HL	FM
FSH	1																													
FF	.09	1																												
CF	.35	.45	1																											
FS	.35	.38	.55**	1																										
SP	.24	.10	.31	.16	1																									
FD	.27	.52**	.54**	.38**	.32	1																								
RF	.14	.36	.40	.35	.01	.27	1																							
FC	.12	.30	.41	.17	.08	.17	.29	1																						
FLS	.27	.42	.58**	.33	.15	.37	.25	.46	1																					
FT	.38	.30	.34	.30	.33	.34	.29	.10	.10	1																				
LET	.34	.52**	.66**	.50**	.30	.54**	.48	.37	.45	.58**	1																			
BN	.26	.52**	.64**	.44	.21	.58**	.35	.35	.50**	.20	.52**	1																		
GH	.31	.53**	.64**	.40	.20	.52**	.37	.31	.50**	.32	.66**	.50**	1																	
BH	.12	.30	.31	.12	.10	.23	.17	.20	.37	.23	.22	.42	.36	1																
TS	.43	.59**	.62**	.48	.2	.58**	.29	.43	.72	.32	.59**	.66**	.57**	.36	1															
LSI	-.08	-.11	-.07	-.10	-.29	-.12	-.17	.009	.02	-.25	-.22	-.23	-.17	-.01	-.15	1														
KC	-.06	-.07	-.12	-.09	.02	-.16	-.21	.04	.07	.001	-.006	-.19	-.14	-.12	-.01	-.09	1													
WP	.06	-.04	-.03	-.02	-.11	-.06	.08	.000	-.03	.03	-.13	-.06	.05	.20	-.06	.25	-.06	1												
DK	-.21	.06	-.02	-.04	-.008	-.13	.12	-.04	-.006	-.04	-.02	-.03	.0	.10	-.01	-.06	-.10	.07	1											
WN	-.16	-.21	-.02	-.16	.11	-.10	-.10	-.13	-.14	.08	.07	-.19	.04	-.11	-.24	-.24	.12	-.26	.11	1										
KD	-.09	-.08	-.06	-.08	.008	-.14	.05	.10	-.07	.04	-.04	-.07	.02	.07	-.16	.06	.04	.24	0	.35	1									
KW	-.05	-.19	-.07	-.13	.05	-.13	-.10	-.001	-.14	-.03	-.14	-.21	-.04	-.11	-.19	.05	.14	.23	.05	.42	.55**	1								
KL	-.10	-.08	-.10	-.25	.15	-.20	-.08	-.06	-.06	-.04	-.09	-.18	-.01	-.06	-.24	-.20	.25	-.08	.14	.60*	.41	.54**	1							
SW	.05	-.17	-.08	-.006	-.11	-.03	-.19	-.01	-.13	.07	.02	-.02	.03	.05	-.07	-.03	.005	-.03	-.005	.37	.31	.48	.39	1						
SWI	.001	-.28	-.18	-.14	.13	-.13	-.18	-.13	-.15	-.09	-.14	-.30	-.12	-.18	-.23	-.04	.23*	-.03	.07	.47	.46	.64**	.60**	.55**	1					
SL	-.01	-.09	-.03	-.16	.15	-.07	-.17	-.11	-.02	.06	-.02	-.20	.07	-.15	-.08	-.19	.41	-.09	.06	.44	.23	.40	.67**	.52**	.65**	1				
HW	-.03	-.21	-.05	-.11	.20	-.12	-.23	-.09	-.16	-.003	-.04	-.17	.01	-.17	-.25	-.13	.27	-.09	.07	.67**	.52**	.55**	.66**	.51**	.61**	.63*	1			
HWI	-.17	-.13	-.03	-.10	.18	-.12	-.10	-.06	-.14	.06	.11	-.19	.03	-.15	-.23	-.18	.28	-.13	.08	.76**	.38	.53**	.65**	.39	.60**	.66*	.79*	1		
HL	-.06	-.04	.04	-.070	.25	-.06	-.10	-.08	-.11	.10	.07	-.14	.10	-.16	-.16	-.27	.34	-.17	.12	.64**	.24	.33	.70**	.18	.50**	.76*	.84*	.78*	1	
FM	-.15	.07	.12	-.10	.04	.04	.11	.19	.20	-.05	.05	.05	.09	.03	.00	.06	.03	-.28	.10	.07	-.10	-.03	.2	-.02	-.06	.05	.05	.05	.19	1

Factor analysis

The PCA results presented in Table 2 shows that the first 4 components explained 42.96% of the total variability observed; PC1, PC2, PC3 and PC4 accounted for 21.06%, 7.83%, 7.22 and 6.84 of variance, respectively. PC1 showed 8 variables with

higher scores (over 0.50 absolute value) related to WN, KW, KL, SW, SWI, SL, HW, HWI and FM (Fruit Dimension). In other hand the highest contribution of PC2 corresponded to FT and LET (Time Dimension) indicate 7.8% of the total variance. The separation along PC3 were FSH,WP and FM (Fruit Dimension) indicate 7.2% of the total variance. Finally the highest contribution of PC4 corresponded to RF,FLS and TS (Resistance and Size Dimension).

The eigenvalue indicates percentage of variance and cumulative variance that (pc1) to (pc4) represent the largest variance. In other hand, the eigenvalue, variance percentage and cumulative variance showed the among measure traits four independent factors that their eigenvalue were about 13 (Table 3).

Table 3. Eigenvalues, proportion of total variability, and correlations among the original variables and the first 4 principal components (PCs).

Traits	PC1	PC2	PC3	PC4
FSH	-.006	-.373	.510	.426
FF	-.123	.090	-.285	-.381
CF	.110	-.140	.127	.177
FS	-.106	-.369	.302	.060
SP	.298	-.389	-.056	.223
FD	-.033	-.360	-.033	-.010
RF	-.092	-.039	.080	-.535
FC	-.019	.432	-.011	.151
FLS	-.083	.430	-.107	.578
FT	.187	-.556	.240	-.151
LET	.247	-.519	.018	-.125
BN	-.212	-.006	.003	.084
BH	.276	-.025	.149	-.179
GH	-.118	.275	.235	-.056
TS	-.240	-.004	.069	.675
LSI	-.278	.450	.249	.062
KC	.303	.043	-.243	.425
WP	-.087	.291	.629	-.206
DK	.089	.173	-.157	-.312
WN	.767	-.106	-.109	-.108
KD	.472	.362	.476	-.239
KW	.662	.292	.405	-.018
KL	.809	.221	-.125	-.037
SW	.534	.095	.349	.050
SWI	.773	.133	.227	.129
SL	.795	.033	-.126	.187
HW	.866	-.029	-.024	.082
HWI	.894	-.040	-.088	-.057
HL	.846	-.121	-.268	.008
FM	.137	.313	-.573	-.055
Eigenvalue	6.31	2.35	2.16	2.05
Var%	21.06	7.83	7.22	6.84
Cum%	21.06	28.89	36.11	42.96

Cluster analysis

In this study, cluster analysis based on all traits measured (Table1) done Ward method (Figure 2). The cultivars were divided two main groups at distance of 20, so both parents ('Shahrood12' and 'Shahrood1') were at a cluster. From important factors to separation varieties in this traits distance were FSH, CF, KC, WP, BH, LET, HW,HWI and HL. The

cultivars were divided four main groups at the 10 distance. In this distance 'Shahrood12' was in a cluster and other parent ('Shahrood1') was in other. The important traits for separating this clusters were, CF, FF, FS, FD, RF,FT, LET, KC,KW and KD. The 'Shahrood12' in group 1 was teammate with varieties number 30, 26 and 25. Also the 'Shahrood1' in group 2 was teammate with only the variety number 1. At the third and fourth groups with about 65 progenies were variations in studied traits.

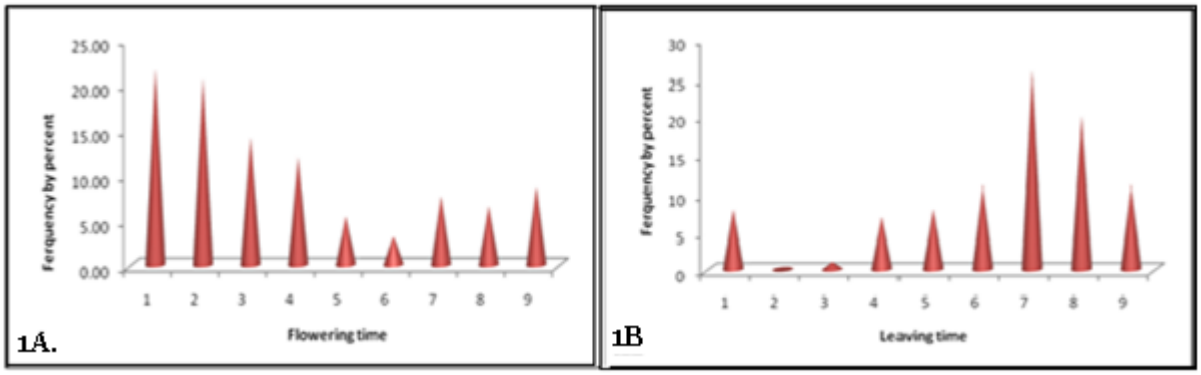

Fig. 1A. Frequency of leafing time in study progenies (early=1 ،very early=2 ،earl=3 ،early medium=4 ، medium=5 ،medium late=6 ،late=7،very late=8،extra late=9).

Fig. 1B. Frequency of flowering time in study progenies (early=1 ،very early=2 ،earl=3 ،early medium=4 ، medium=5 ،medium late=6 ،late=7،very late=8، extra late=9).

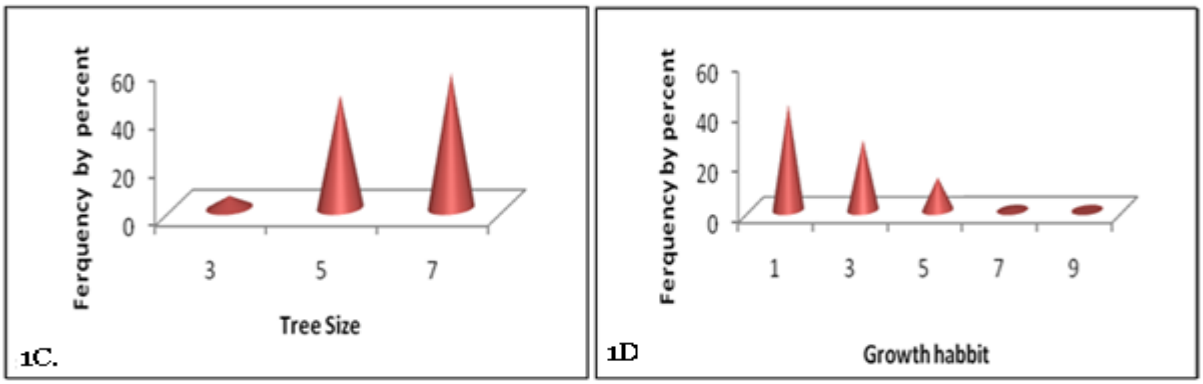

Fig. 1C. Frequency of tree size in study progenies (3=Weak،5=Intermediate ،7=Strong).

Fig. 1D. Frequency of growth habit in study progenies (1= extremely upright ،3= upright ،5= Spreading ،7= Dropping ،9= Weeping).

Discussion

All the hybrid progenies from'Shahrood1' × 'Shahrood12' population are highly adapted to the environmental conditions in northern Iran and could be a very interesting source of genetic diversity. The results of this study indicated a high morphological diversity of almond population. Regarding study traits, the highest variability was established for Growth habit, tree size, resistance to frost,Time dimension (FT,LET), Flower Dimension(WN, KW, KL, SW, SWI, SL, HW, HWI and FM)(Figure 1; Table 3). These results were expected since the almond is self-incompatible. Variation in traits related to phenology, morphology and fruit quality was observed and the results indicated a high morphological diversity of almond genotypes. This high phenotypic variability corresponds with recent reports on molecular description by using different markers as nuclear and chloroplast simple sequence repeats (Martinez- Gomez *et al.,* 2003; Fathi *et al.,* 2008; Zeinalabedini *et al.,* 2008,) or AFLP marker (Sorkheh *et al.,* 2007). Appointed relationships between some traits can help breeders in setting goals for parental partner selection and breeding.

Significant correlation coefficients positive between flower density with leafing time (r =0.54), branches number (r =0.58), tree size(r =0.58), bearing habit(r =0.52), fruit fuzz(r =0.52) and fruit color(r =0.54) (Table 2) indicate that this trait can be direct effect in yield Increased product. Also this research indicated, a positive correlation existed among most variables related to hull, shel and kernel size (r = 0.50-0.65), which is in accordance with the findings of Thakur *et al.* in 2005, Tavassolian in 2008 and Rasouli *et al.* in 2013. Therefore, these parameters can be used to predict each other. The other research established significant correlations between nut weight and kernel weight(Talhouk *et al.,* 2000; Ledbetter, 2008; Tavassolian, 2008; Sorkheh *et al.*, 2010). our results revealed a lack of correlation between these 2 traits. Sanchez-Perez *et al.* in 2007 concluded that shell hardness does not affect the weight of a kernel, which was also confirmed by our results. Significant correlation coefficients were determined between leaf length and leaf width (r = 0.57) and between leaf width and leaf area (r = 0.93), which corresponds with results obtained by Talhouk *et al.* in 2000 and Sorkheh *et al.* in 2009.

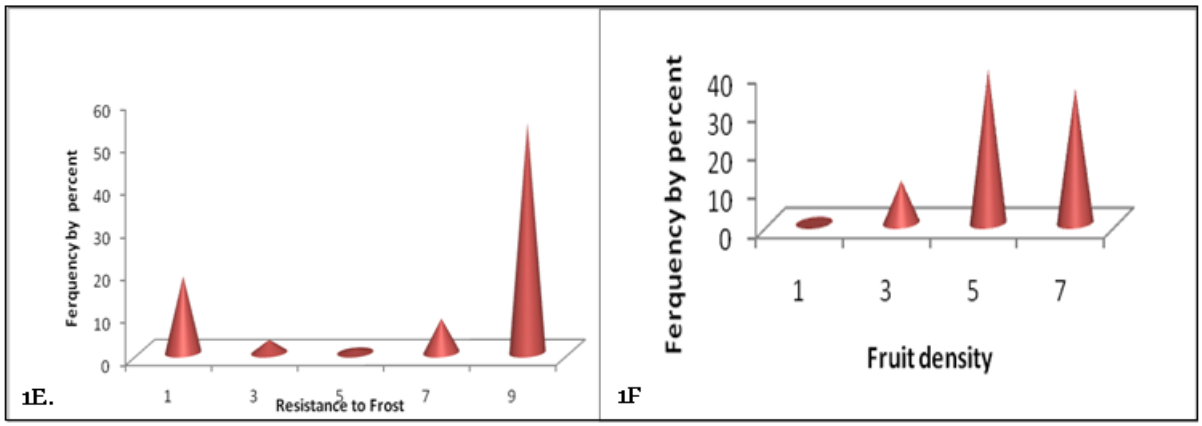

Fig. 1E. Frequency of resistance to frost in study progenies (1= sensitive ، 3= medium sensitive، 5= medium، 7= medium resistance ،9= resistance).

Fig. 1F. Chart frequency of fruit density in study progenies (1= low ، 3= low medium ، 5= medium large, 7= large).

This results correspond with those of Lansari *et al.* in 1994, Talhouk *et al.* in 2000, and Sorkheh *et al.* in 2009, that showed the kernel and fruit properties in variation of almond cultivars and clones are more important than leafing properties. Also the similar results have been reported by Ledbetter and Shonnard in 1992, Lansari *et al.* in 1994, Karl *et al.* in 1998, Talhouk in 2000, De Giorgio and Polidnano in 2001, Fatahi *et al.* in 2004, Sarkhosh *et al.* in 2006, De Giorgio *et al.* in 2007, Asma *et al.* in 2007, Chalak *et al.* in 2007, Colic *et al.* in 2012, in order to grouping and separating of almonds genotypes and cultivars. High absolute values of correlations between variables related to fruit, nut, and leaf size; phenology; and PC1 or PC2 were also established in other species of the genus Prunus, such as apricots (Badenes *et al,*. 1998; Ruiz and Egea, 2008), peaches (Nikolić *et al.,* 2010), sour cherries (Krahl *et al.*, 1991), and sweet cherries (Hjalmarsson and Ortiz, 2000). This indicates that these traits could be sufficient for reliable germplasm characterization. At the same time, these are the most important traits in agricultural practice and breeding.

Moreover, PCA results indicated that the observed variability in the studied almond population was more influenced by quantitative than qualitative traits. As quantitative traits, apart from genotype, are influenced by environmental factors, a combination of molecular markers and morphological data is the best choice for genetic variability analysis. The study population with high PC1 scores could be good genitors for increasing hull, shell and kernel size. On the other hand, Flower Time and Leafing Time (Time

Dimension) could be attained using those population with higher PC2 scores as genitors. Therefore progenies teammate with 'Shahrood1' and 'Shahrood12' to be used in breeding programs as parents in hybridization crosses.

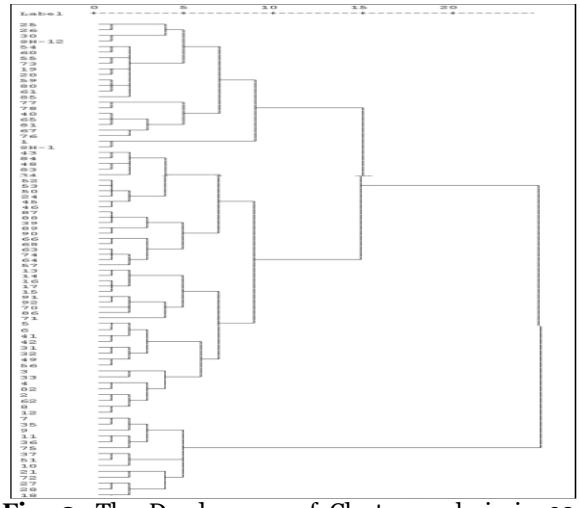

Fig. 2. The Dendrogram of Cluster analysis in 92 study progenies ($Sh_1 \times Sh_{12}$) with their parents using Ward method.

According to Cluster analysis in 10 distance. the progenies in some traits were like 'Shahrood1' and for some other traits like 'Shahrood12', or the expression of phenotypic traits were additive mode, incomplete dominance or over dominance. For example, in number of 84 progenies for FSH trait was like one parent ('Shahrood1'), for RF was like other parent ('Shahrood12') and for LET was like additive mode and in FLS was like over dominance(Figure 2).

The results of pomological traits indicated that tree habit growth, buds, leaf, flowers and fruit attributes were from a high diversity among studied progenies. Also time of flowering among almond progenies varied widely and as early flowering, middle flowering and late. Performances of almond progenies base on their quantity and quality characteristics were different. The success of breeding programs is dependent the availability of diversity genetic resources, and using hybridization can be generated variation based on scientific requirements(Kester and Gradziel, 1996). Therefore, studies on morphology of almond hybrids and their compare by their parents are important due have valuable genes for using heterosis and hybridization (Garcia *et al.,* 1996).

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