International Journal of Horticultural Science and Technology
Journal homepage: http://ijhst.ut.ac.ir

Diversity and Broad Sense Heritability of Phenotypic Characteristic in Almond Cultivars and Genotypes

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ARTICLE INFO

Article history:

Received: 27 May 2020
Received in revised form: 21 December 2021
Accepted: 10 February 2021

Article type:

Research paper

Keywords:

Compost,
Almond,
Flowering,
Genotypic diversity,
Phenotypic diversity.

ABSTRACT

Phenotypic and genetic diversity are mandatory aspects to allow future breeding in fruit trees. This work was aimed to study the genetic diversity and heritability of important phenological traits in several almond genotypes. The seedlings were planted in randomized complete block design with 3 replications (two trees in each replication). Phenological traits including flower size, petal length, petal width, sepal length, sepal width, pistil length, pistil thickness were evaluated. Furthermore, number of stamens, first flowering, 10% flowering, 50% flowering, 90% flowering, date of flowering among 33 selected almond cultivars and genotypes were also evaluated using almond descriptors during 27 February to 29 March 2017. The results showed the existence of genetic variation among the studied cultivars and genotypes. A great phenotypic variation was observed for pistil length, petal width and flowering time. The exact and extended characterizations of all the new materials of almond could provide breeders new opportunities to develop future crosses and to obtain more resistant seedlings that can be better adapted to extreme and changing weather conditions in this area and in other regions of the world.

Introduction

Limitations in soil and water resources and ever-increasing world population, has forced agricultural researchers to improve crop production and quality. The improvement of fruit trees species has been carried out through selection, which depends largely on phenotypic variation. Phenotypic variation is the basic feature of life system, it is required for populations to evolve in response to environmental changes, and its maintenance is crucial for long-term survival of the species (Kester et al., 1996; De Giorgio and Polignano 2001). The observed phenotypic variation between individuals of a population could be attributable to genetic and/or environmental sources.

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Genetic, environmental, and phenotypic diversity coefficients are used to determine whether or not diversity exists. The higher the ratio of genotypic to phenotypic variation, the better the selection efficiency is, and easier to identify the desired genotypes (Burton and Devan, 1953). The rate of selection efficiency is expressed by inheritance ability, which is an important factor in determining the appropriate method for improving the traits in the breeding program, which depends on the relative effect of the genetic and non-genetic factors on detection of the phenotypic differences of those traits.

Plant germplasm collections preserve rare or endangered species, vulnerable landraces or commercially important fruit cultivars and their wild relatives could provide reservoirs of genetic traits of unanticipated importance in the present (Karl et al., 1998; Kester, 1966; Kester and Asay, 1975). Almond germplasm collections have provided raw material to breed new cultivars via hybridization (Dicenta et al., 2007) or selection (Rasouli et al., 2014).

Almond is one of the main fruit trees in the majority of temperate regions of the world and is threatened by late spring frost. To overcome these problems, almond breeders are developing new late-flowering, self-compatible and high yielding cultivars (Kester et al., 1996; Dicenta et al., 2009; Oručević and Aliman, 2018). To obtain such elite cultivars several approaches such as screening of germplasm diversity and in large populations of seedlings can be exploited (Kester and Asay, 1975; Ebrahimi et al., 2015, Kester et al., 1996; Gradziel and Kester, 1999).

Therefore, the future success in breeding programs depends on the presence of genetic resources (Kester and Asay, 1975). Indeed, understanding the genetic diversity and genetic structure of the specie and the inheritance of the main traits of interest should be mandatory in fruit tree breeding (Gradziel and Kester, 1999). The first step to characterize local populations is to evaluate morphological and phenological traits.

Phenology is the study of the timing of recurring biological events in plants (Le Roux et al., 1984), which seems to be modulated by biotic and abiotic forces. For example, flowering time can vary between few hours to several days, which is temperature and species dependent (Oručević and Aliman, 2018). The effects of the environment on important traits, such as flowering time, should be assessed to guarantee an optimal adaptability of new cultivars to new growing regions (Oručević and Aliman, 2018).

Variation in flowering and Morpho-pomological parameters has been reported in almond genotypes through phenological and morphological evaluations (Kester and Asay, 1975; Stansfield, 1991; Gradziel and Kester, 1999). Lansari et al. (1994) used multivariate method to evaluate morphological variation of almonds and stated that nut and kernel traits take an important role in genotype differentiation. De Giorgio et al. (2007) divided almond varieties to separate groups based on morphological traits. Besides, it has been reported that one of the most important prerequisites for the improvement of almond production is good biological and phenological characteristics (Kester et al., 1996; Oručević and Aliman; 2018). In the present study, different parameters such as the heritability and the genetic variation of important phenological characteristics from interesting genotypes and cultivars of almond were evaluated.

Material and methods

This study was carried out to investigate the morphological and phenological traits of several genotypes and cultivars of almond. The work was carried out at Meshkin Abad Horticulture Research Station in Karaj (50.9° E, 35. ° 7521 N, 1245 m height, with moderate and cold climates, shallow and calcareous soils, PH=7) during two successive years, 2016-2017. The origin of studied genotypes and cultivars are presented in Table 1.

Table 1. Almond cultivars and genotypes that were studied in this research

Code	Cultivar/ genotype	Origin	Country	Code	Cultivar/ genotype	Origin	Country
A1	12-26 C-10	Hybrid	Iran	A18	5-17 C-5	Hybrid	Iran
A2	4-4 C-12	Hybrid	Iran	A19	NO.10	Hybrid	Iran
A3	5-27 C-17	Hybrid	Iran	A20	Sh-15 C-7	selection	Iran
A4	9-7 C-18	Hybrid	Iran	A21	Nonpareil	selection	USA
A5	Ne Plus Ultra	selection	USA	A22	Narengi-54	selection	Iran
A6	3-19 C-20	Hybrid	Iran	A23	Narengi-89	selection	Iran
A7	1-32 C-23	Hybrid	Iran	A24	Narengi-94	selection	Iran
A8	151 C-2	Hybrid	Iran	A25	17FM	Hybrid	Iran
A9	102-2 C-1	Hybrid	Iran	A26	Narengi-55	selection	Iran
A10	17- 2 B-17	Hybrid	Iran	A27	Tosi 21-1-3	selection	Iran
A11	18-1 B-5	Hybrid	Iran	A28	Narengi-21	selection	Iran
A12	4-14 B-21	Hybrid	Iran	A29	Azar	Hybrid	Iran
A13	1-5 B-22	Hybrid	Iran	A30	Abi-1-7	selection	Iran
A14	1-25 B-23	Hybrid	Iran	A31	2-7 C-4	Hybrid	Iran
A15	Rabie	selection	Iran	A32	5-17 C-5	Hybrid	Iran
A16	Mamaie	selection	Iran	A33	Narengi-943	Hybrid	Iran
A17	2-7 C-4	Hybrid					

The seedlings were planted in randomized complete block design with 3 replications (two trees in each replication). Phenological traits including flower size, petal length, petal width, sepal length, sepal width, pistil length, pistil thickness were measured using a ruler and vernier caliper. In addition, number of stamens, first flowering, 10% flowering, 50% flowering, 90% flowering, date of flowering of the 33 selected (five-year-old) almond cultivars and genotypes were evaluated using almond descriptors during 27 February to 29 March 2017 (Gulcan, 1985). The flowering date was counted from the starting time, February 19 for all genotypes at different stages.

The data were statistically analyzed based on the analysis of variance. Mean comparison was done by Duncan test. Multivariate statistics were used to determine the relationships between some important traits using MSTATC Version 1.2 and Excel version 13. Environmental, genotypic, and phenotypic variances, general heritability and also phenotypic, genotypic, and environmental variation coefficients were calculated using the equations 1-6 (Pistorale, 2008).

$$V_E = \frac{\mathrm{MSe}}{\mathrm{r}} \quad (1)$$

$$V_{\mathrm{p}=} V_G + V_E \quad (2)$$

$$H_b = \frac{V_G}{V_P} \quad (3)$$

$$CV_P = \frac{\sqrt{V_P}}{\bar{\mathrm{X}}} \times 100 \quad (4)$$

$$CV_G = \frac{\sqrt{V_G}}{\bar{\mathrm{X}}} \times 100 \quad (5)$$

$$CV_E = \frac{\sqrt{V_E}}{\bar{\mathrm{X}}} \times 100 \quad (6)$$

Where, V_G, V_E and V_P are genotypic, environmental, and phenotypic variances, respectively. MSg, MSe, r and x are treatment variance, error variance, number of replications and mean value. *Hb* is broad sense heritability; CV_G, CV_P and CV_E are coefficients of genetic, phenotypic and environmental variation, respectively.

Results

In general, significant differences were observed for the majority of the studied traits (Table 2 and 3). Table 2 shows different stages of flowering and flowering period in the 33 studied genotypes. The starting time of flowering was February 19. The results showed a wide range of flowering time, from an early flowering, 5 days after the starting time (A15) to late flowering 26 days after the starting time (A1) (Table 2). The longest flowering period with 16 days was related to A5.

According to the obtained results, flower size, was significantly different among genotypes. The largest flower size was observed in A4 and A16 genotypes and the smallest flower size in A14 genotype (Table 3). Large flower size is more effective in attracting insects for better pollination and fruit setting. Large flowers usually have large petals, which were obtained in A4 and A16 genotypes. The results showed that A16 genotype had the largest sepals (Table 3). The pistils of flowers with large sepals are good for better protection against early spring frosts in the early stages of flowering. The number of stamens was significantly different among genotypes. A5 and A19 genotypes had the highest number of stamens and A22 and A1 had lower number of stamens (Table3). Flowers with more stamens can also produce more pollen, which can be effective for better pollination, although pollen viability should be also considered. A6 and A32 genotypes presented the highest pistil length. In contrast, A29 and the A26 had the lowest pistil length (Table 3). In almond genotypes, flowers with less style length are more likely to succeed in pollination, a trait which is related to the length of pistil. The longest pistil diameter was belonged to A14 (0.5 cm), while the shortest pistil diameter was observed at A29 (0.1 cm). Chances of fruit formation increases in almond genotypes with larger pistil diameter and thickness.

Table 2. Mean comparison for phenological flowering period for 33 almond genotypes/cultivars

Genotype/Cultivar	First flowering (day)[ǂ] (Start from 19 February)	10% flowering (day)[ǂ]	50% flowering (day)[ǂ]	90% flowering (day)[ǂ]	Flowering period(day)[ǂ]
A1	26.00 a[ǂ]	29.00 a	31.00 a	35.00 a	9.00 d
A2	11.00 h	22.00 c-f	24.00 c-e	24.00 fg	13 a-d
A3	17.00 de	21.00 d-g	24.00 c-e	28.00 de	11.00 bcd
A4	22.00 b	25.00 bc	27.00 bc	32.00 a-c	10.00 cd
A5	18.00 c-e	24.00 b-d	27.00 bc	34.00 ab	16.00 ab
A6	15.00 e-g	20.00 e-g	23.00 de	27.00 ef	12.00 a-d
A7	11.00h	16.00 h-j	18.00 g	22.00 g	11.00 b-d
A8	20.00 b-d	23.00 b-e	24.00 c-e	29.00 de	9.00 d
A9	16.00 ef	19.00 f-h	22.00 ef	26.00 ef	10.00 b-d
A10	12.00 gh	16.00 h-j	18.00 g	23.00 g	11.000 a-d
A11	17.00de	21.00 d-g	23.00 de	28.00 de	11.00 a-d
A12	13.00 f-h	18.00 g-i	19.00 fg	24.00 fg	11.00 a-d
A13	18.00 c-e	21.00 d-g	23.00 de	28.00 de	10.00 b-d
A14	10.00 hi	14.00 j	17.00 g	21.00 gh	11.00 a-d
A15	5.00 j	9.00 k	12.00 h	16.00 i	11.00 a-d
A16	7.00 ij	10.00 k	12.00 h	18.00 hi	11.00 a-d
A17	22.00 b	26.00 ab	28.00 ab	32.00 a-c	10.00 b-d
A18	10.00 hi	15.00 ij	17.00 g	24.00 fg	14.00 ab
A19	20.00 b cd	23.00 b-e	26.00 b-d	29.00 c-e	9.00 d
A20	22.00 b	25.00 bc	27.00 bc	31.00 b-d	9.00 d
A21	22.00 b	26.00 ab	29.00 ab	33.00 ab	11.00 a-d
A22	13.00 f-h	16.00 h-j	19.00 fg	24.00 fg	11.00 a-d
A23	17.00 de	21.00 d-g	23.00 de	27.00 ef	10.00 b-d
A24	13.00 f-h	16.00 h-g	19.00 fg	24.00 fg	9.00 d
A25	16.00 ef	19.00 f-h	23.00 de	27.00 ef	11.00 a-d
A26	11.00 h	15.00 ij	18.00 g	22.00 g	11.00 a-d
A27	20.00 b-d	24.00 b-d	28.00 ab	34.00 ab	14.00 ab
A28	21.00 b c	25.00 bc	29.00 ab	33.00 ab	12.00 a-d
A29	15.00 e-g	19.00 f-h	22.00 ef	27.00 ef	12.00 a-d
A30	10.00 hi	14.00 j	18.00 g	23.00 g	13.00 ab
A31	10.00 hi	15.00 ij	16.00 g	21.00 gh	11.00 a-d
A32	12.00 gh	16.00 h-j	18.00 g	23.00 g	11.00 a-d
A33	10.00 hi	14.00 j	19.00 fg	24.00 fg	14.00 ab

[ǂ]Means followed by similar letters in each column are not significantly different

Table 3. Mean comparison for flower parameters of 33 almond genotypes/cultivars

Genotype/ Cultivar	Flower size (cm)[1]	Petal length (cm)	Petal width (cm)[1]	sepal length (cm)[1]	sepal width (cm)[1]	Pistil length (cm)[1]	Pistil thickness (mm)[1]	Number of stamens[1]
A1	3.5000 g	1.50 h-j	1.16 gh	0.46 de	0.30 a-c	1.46 d	.43 a-c	15.00 e
A2	4.1667 ef	1.53 g-j	1.23 d-g	0.56 b-e	0.30 a-c	1.53 c	0.26 b-e	30.00 b
A3	3.9667 f	1.53 g-j	1.02 h	0.50 c-e	0.36 a-c	1.50 c	0.30 a-e	25.00 c
A4	5.5000 a	2.2000 a-d	1.96 b	0.56 b-e	0.36 a-c	1.50 c	0.20 de	30.00 b
A5	5.0333 b	2.3333ab	1.53 c-e	0.600 b-e	0.36 a-c	1.66 b	0.30 a-e	35.00 a
A6	5.0333 a	2.5000 a	1.70 b-d	0.60 b-e	0.40 a-c	1.70 a	0.50 a	30.00 b
A7	4.0333 f	1.40 j	1.00 hi	0.50 c-e	0.30 a-c	1.53 c	0.40 a-d	24.66 c
A8	4.7000 bc	2.10 b-d	2.60 a	0.56 b-e	0.44 ab	1.36 e	0.30 a-e	30.00 b
A9	4.9333 b	1.96 b-f	1.43 d-g	0.40 e	0.33 a-c	1.26 f	0.21 c-e	20.00 d
A10	3.9667 f	1.60 e-j	1.50 c-f	0.50 c-e	0.26 bc	1.66 b	0.46 ab	30.00 b
A11	4.5000 c-e	1.96 b-f	1.50 c-f	0.600 b-e	0.30 a-c	1.50 c	0.30 a-e	25.00 c
A12	5.0333 b	2.06 b-e	1.70 b-d	0.60 b-e	0.50 a	1.50 c	0.40 a-d	25.00 c
A13	5.0333b	2.03 b-e	1.80 bc	0.46 de	0.30 a-c	1.70 a	0.36 a-d	30.00 b
A14	1.5000 i	1.00 k	0.50 j	0.53 b-e	0.33 a-c	1.20 f	0.50 a	30.00 b
A15	4.5333 cd	2.00 b-e	1.23 e-h	0.53 b-e	0.30 a-c	1.46 d	0.10 e	25.00 c
A16	5.5000 a	2.5000 a	2.00 b	1.00 a	0.50 a	1.50 c	0.20 de	25.00 c
A17	3.5333 g	1.50 h-j	1.20 f-h	0.60 b-e	0.40 a-c	1.36 e	0.30 a-e	25.00 c
A18	4.0000 f	1.50 h-j	1.50 c-f	0.63 b-e	0.40 a-c	1.53 c	0.50 a	25.00 c
A19	4.2000 d-f	1.70 e-j	1.50 c-f	0.76 ab	0.30 a-c	1.20 f	0.23 c-e	35.00 a
A20	3.0000 h	1.00 k	0.70 ij	0.50 c-e	0.30 a-c	1.40 d	0.23 c-e	25.00 c
A21	3.5000 g	1.46 ij	1.20 f-h	0.40 e	0.20 c	1.20 f	0.30 a-e	20.00 d
A22	4.5000 c-e	2.00 b-e	1.73 b-d	0.50 c-e	0.20 c	1.46 d	0.23 c-e	15.00 e
A23	4.0000 f	1.50 h-j	1.20 f-h	0.50 c-e	0.20 c	1.43 d	0.20 de	20.00 d
A24	4.2000 d-f	2.03 b-e	1.80 bc	0.50 c-e	0.20 c	1.36 e	0.30 a-e	25.00 c
A25	4.0333 f	1.80 d-i	1.50 c-f	0.40 e	0.30 a-c	1.50 c	0.40 a-d	25.00 c
A26	4.2000 d-f	1.80 d-i	1.56 cd	0.50 c-e	0.40 a-c	1.12 g	0.20 de	20.00 d
A27	5.0000 b	2.03 b-e	1.50 c-f	0.50 c-e	0.30 a-c	1.50 c	0.43 a-c	20.00 d
A28	3.5333 g	1.46 ij	1.00 hi	0.50 c-e	0.33 a-c	1.66 b	0.23 c-e	20.00 d
A29	4.0000 f	1.86 c-h	1.56 cd	0.73 bc	0.46 ab	1.13 g	0.10 e	20.00 d
A30	4.2000 d-f	1.900 c-g	1.10 h	0.600 b-e	0.36 a-c	1.53 c	0.23 c-e	20.00 d
A31	4.2000 d-f	1.80 d-i	1.50 c-f	0.46 de	0.30 a-c	1.46 d	0.30 a-e	30.00 b
A32	4.2333 d-f	2.00 c-e	1.20 f-h	0.70 b-d	0.46 ab	1.75 a	0.30 a-e	20.00 d
A33	4.9667 b	2.03 b-e	1.56 cd	0.46 de	0.26 bc	1.36 e	0.36 a-d	30.00 b

[1] Means followed by similar letters in each column are not significantly different

Based on the obtained results, in 48.4% of genotype the stamen was longer than the stigma, in 45% of genotype, stamen and stigma were in the same size, while in the rest of them the stigma was longer than the stamen. Also, results of coefficient of variation and heritability evaluation in Table 4 showed that minimum, maximum, mean, components of variance (phenotypic, genetic and environmental), coefficient of variation and broad sense heritability are different among 13 almond characteristics. For instance, the lowest broad sense heritability value was assigned to sepal length (83%), while average broad sense heritability was associated with the characteristics of flowering period and width of the pistil with broad sense heritability of 85.1% and 90%, respectively.

Table 4. Range, standard error, variance components, coefficient of variation and heritability to the studied traits of almond genotypes/cultivars

Traits	Range		Genotype related to range		S.E	Means	Diversity index	Variance components			Coefficient of variation			Broad sense heritability (%)
	Min	Max	Min	Max				Vp	Vg	Ve	CVp	CVg	CVp	
Flower size	1.50	5.50	A14	A4	0.794	4.267	537.40	0.623	0.62	0.003	18.52	18.48	1.28	99
Petal length	1.00	2.500	A20	A6	0.3513	1.7970	511.52	0.124	0.12	0.004	7.62	7.49	3.53	96
Petal width	0.50	2.60	A14	A8	18.38	4.62	25.13	0.152	0.15	0.002	47.54	47.23	0.96	98
sepal length	0.40	1.00	A25	A16	1.649	0.827	50.15	0.012	0.01	0.002	32.21	29.41	0.96	83
sepal width	0.20	0.50	A23	A12	0.0879	0.3409	387.82	0.061	0.06	0.001	17.03	16.89	9.30	98
Pistil length	0.86	2.03	A29	A6	0.2250	1.4576	647.82	0.81	0.12	0.69	62.06	23.89	57.28	94
Pistil thickness	0.10	0.50	A29	A14	0.1121	0.3045	271.63	0.011	0.01	0.001	34.96	33.33	10.54	90
Number of stamens	15.00	35.00	A1	A5	5.154	25.000	485.06	26.48	26	0.48	20.58	20.39	2.77	98
First flowering (day)	5.00	26.00	A15	A1	5.051	15.031	269.58	25.79	25.46	0.336	33.38	33.17	22.03	98.72
10% flowering (day)	9.00	29.00	A15	A1	4.877	19.303	395.79	23.77	23.44	0.336	25.26	25.08	3	98.61
Date of 50% flowering(day)	12.00	31.00	A15	A1	4.876	21.909	269.54	23.76	23.43	0.336	22.3	22.1	2.64	94.4
Date of 90% flowering(day)	16.00	35.00	A15	A1	4.770	26.455	345.03	22.74	22.42	0.327	17.9	17.9	2.16	98.6
Flowering period (day)	11.00	17.00	A1	A33	1.489	13.697	914.96	2.21	1.88	0.336	10.9	10	4.23	85.1

Discussion

In the present study, diversity and broad sense heritability of phenotypic characteristic were studied in detail in several almond cultivars and genotypes. Genetic diversity can be used as an effective tool to improve important phenological parameters such as flowering time. According to the obtained results, both genetic and phenotypic variation coefficients showed the existence of diversity in the studied individuals. Some of these individuals can be selected as superior genotypes for future almond breeding.

The small difference between phenotypic and genotypic variation coefficients for the studied characteristics showed that the major part of the existing diversity is due to genetic variation and that environment seems to have small effect. With a higher ratio of genotypic to phenotypic variation, an increase of efficiency in selection can be reached, which can help to detect superior genotypes more accurately.

According to the obtained results, the largest flower size was observed in A4 and A16 cultivars. Also, the smallest flower size was observed in A14 genotype (Table 3). Studies on the inheritance of almond flowers have shown that larger flowers are dominant over small flowers (Grasselly, 1985; Kester and Asay, 1975). In small flowers, the tip of the stigma, especially in late flowering cultivars, emerges from the flower buds before the full opening of the flower. In this case, the probability of the risk of frost damage is higher for these types of cultivars (Kester and Asay, 1975; Viti and Loreti, 1994). Rasouli et al. (2014) reported heritability of some important traits such as flowering time, leafing date and bearing habit as 0.70, 0.80, and 0.75 respectively. They indicated close relationship between flowering time and leafing date (Rasouli et al., 2014), which is in agreement with the results of present study.

The results of Table 3 show that the number of stamens is significantly different among the studied population. The presence of a large number of stamens in each flower

genotypes makes it possible for the pistil to have enough pollen to fertilize the egg. Also, these genotypes and cultivars can be used as pollinators for incompatible genotypes (Kester et al., 1996; Socias i Company and Gradziel, 2017).

The length of the pistil was significantly different among the studied population. (Table 3). The short length of the pistil in each flower in the almond cultivars, especially in self-incompatible cultivars, makes it possible for pollination to be carried out easily, because these almonds have shorter pistil length than the stamens, because of that the pollen is sufficiently and easily can access to the stigma (Socias i company, 1990; Kester et al., 1996). There was a significant difference among the cultivars and genotypes regarding the thickness of the pistil. As shown in Table 3, the longest diameter of the pistil belonged to A14 (0.5 cm), while the shortest pistil diameter was observed in A29 (0.1 cm). Studies showed that the greater the diameter of the pistil in almonds when the flower is opened, the more probability of the percentage of the fruit set (Kester et al., 1996).

Taking into account the results of genotypic, phenotypic, and environmental variances associated with genetic diversity, phenotypic diversity coefficient and broad sense heritability, which are presented in Table 4, it can be detected that the genetic variance between genotypes for all of the measured characteristics was less than the phenotypic variance, with the exception for the first flowering trait. Other characteristics measured in the range of phenotypic variation were 20.58 and 62.7%, respectively. For all the measured properties, except for the length of the sepal (the genetic and phenotypic variation coefficients were approximately equal), the phenotypic coefficient of variation is greater than the genetic diversity coefficient. As the phenotypic diversity is greater than genetic diversity, the feature is more affected by the environment and the selection efficiency was detected to be low. On the other hand, a slight difference between the genetic and phenotypic variation coefficients for features such as the beginning of flowering indicates that the genotype has a greater role than the environment. A large part of the phenotypic variation can be caused by the effect of the environment on the features and especially on the polygenic features. The values of the coefficients of the estimated broad sense heritability are shown in Table 4. If the range of heritability is divided into four categories: very low (less than 25%), low (between 25 and 52%), medium (between 52 and 55%) and high (more than 55%), the lowest inheritance value can be assigned to sepal length (83%), which indicates that this trait is not strongly influenced by environmental factors. Thereafter, the average inheritance was associated with the characteristics of flowering period and width of the pistil with inheritance, which was 85.1% and 90%, respectively. Therefore, the efficiency of the selection for these features in the breeding programs would be low. The inheritance of other measured characteristics was high. The most heritability was belonged to the flower size with inheritance of 99% (Table 4), indicating the very low impact of these characteristics on the environmental factors. Basically, quantitative characteristics have variable heritability, as some of them have high heritability due to genetic control (Asma et al., 2007; Socias i Company and Gradziel, 2017). Heritability values for these genotypes showed that, the genetic variance is more than the environmental variance, because high heritability values were estimated for most of the characteristics. Therefore, the first step in identifying local populations is to identify their morphological and phenological characteristics, because these characteristics are easily measurable and have a great practical application (Rotondi et al., 2003).

According to Stansfield's theory (1991), if the inheritance of a traits is more than 50%,

attribute have high heritability, if the broad sense heritability is between 20 and 50%, the inheritance property is moderate and if the broad sense heritability of the considered attribute is less than 20%, the attribute has low inheritance. According to this theory, all characteristics were highly heritable and the average broad sense heritability for the studied characteristics was between 83% and 99%. Heredity for some of the attributes was low because of the largeness of their phenotypic variance, which is due to environmental influences. Some scientists believe that selection would be relatively easy if the inheritance of a trait is very high (more than 80%).

Conclusion

In this study, a wide phenotypic diversity in all evaluated traits was detected. The presence of such diversity and the maintenance of genetic diversity are important for future breeding of almond. Interested genotypes were evaluated and can be used as a great gene pool for breeding purposes. These materials will be available for breeders to design new future crosses in order to obtain new seedlings with better adaptation to extreme weather conditions.

Acknowledgements

The authors thankfully acknowledge for Iran National Science Foundation (INF) the financial support.

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