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ORIGINAL ARTICLE

Selection Almond Superior Genotypes Form F1 Segregated Population of ‘Tuono’ × ‘Shokoufe’ Cultivars

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ABSTRACT

The primary steps in breeding programs are identifying and selecting superior fruit trees genotypes. This study was conducted to achieve the most productive, self-compatible, and cold tolerated almond [*Prunus dulcis* (Mill.)D.A.webb] genotypes, by determining genetic variability of 103 progenies resulted by crossing ‘Tuono′ and ‛Shokoufe′ during two years, 2016-2017 at Meshkin Abad Horticulture Research Station in Karaj (50.9°E, 35. ° 7521 N, 1245 m height, with moderate and cold climates, shallow, calcareous soils, with a pH = 7) according to almond description (Gulcan, 1985) for selecting superior hybrids. The genetic relationship between selected hybrids was carried out by using genetic correlation. Minimum, maximum, and comparing mean results represented hybrids’ variability. Correlations indicated significant positive and negative variability. 20 components of effective traits justified 77.4% of the total variance. Hybrid separation was carried out by clustering analysis using 20 components. In 10th Euclidean distance, hybrids were separated into 17 groups. Fruit, nut, kernel, productivity, and vigor characteristics were the main factors in grouping clusters, respectively. In the first factor, traits including fruit size (0.70), fruit weight (0.880), fruit length (0.741), fruit width (0.769), fruit thickness (0.722), nut weight (0.872), nut length (0.729), nut width (0.795), nut thickness (0.673), kernel weight (0.849), kernel length (0.635) and kernel width (0.837). In the second factor, there were traits including productivity (0.797), number of nuts per tree (0.925), fruit weight per tree (0.932), and nut weight per tree (0.905). In the third factor, traits such as trunk diameter (0.60), the radius of expansion in two directions north-south (0.755) and east-west (0.804), leaf density (0.60), and growth habit (0.60). These third components could justify about 14%, 7%, and 5% of the total variance. The most variable traits were growth habit, high quality, bearing habit, flowering and leafing time, fruit size; date of harvesting, nut shape and the lowest variable trait was kernel taste.

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The almond belongs to the genus *Prunus*, family *Rosaceae*, and subfamily *Prunoideae*. The number of base chromosomes in plants of this genus is eight (n = 8), most of which are diploid (2 n = 16). Almond cultivars originate from wild populations in central Asia and are native to the arid mountainous regions of Central and West Asia, which has spread to the shores of the Mediterranean sea and wild species of this plant have been found in these areas (Kaster and Gardzil, 1996; Chaichi *et al*.,1999; Zeinalabedini *et al*., 2007). Genetic diversity is a pivotal requirement to allow future breeding in fruit trees (Imani *et al*., 2021; Soltani *et al.*, 2022; Vahdati *et al.*, 2019). Throughout the world, the narrow genetic background of commercial cultivars of almond faces breeding programs with many challenges (Ansari and Gharaghani, 2019). Iran is main region to the diversity of *Prunus* genetic resources in the world, as well as, present major achievements regarding identification, collection, evaluation, conservation, and utilization of this valuable genetic resource in the world (Gharaghani *et al*., 2017; Micke, 1996). In terms of almond production, Iran ranks third in the world after the United States and Spain (FAO, 2019). South Khorasan province is the first in Iran (Statistics of the Ministry of Jihad for Agriculture, 2017). Almonds are one of the fruit trees in the temperate zone of the world (Amani *et al*., 2017). On the other hand, the risk of late spring frosts in these areas is always a threat, so late flowering is one of the most important breeding traits in almonds (Eskandari *et al*., 2009). Also, flowering density, yield, fruit ripening time, and fruit quality traits are other important breeding traits in this plant (Kester and Gradziel, 1998; Dicenta and Garcia, 1992; Socias i Company. and Gradziel, 2017). Probably the most important feature of almonds in breeding programs is their flowering time. Flowering time depends on the chilling requirement and an inherited trait that is easily transferable, and many breeding and selection programs focus on this trait (Ajamgard *et al.*, 2017; Aslamarz *et al*., 2009; García *et al*., 1996; Kester *et al*., 1996; Dicenta *et al*., 2009). The actual flowering time varies by year and depending on the temperature before flowering and during it (Hassankhah *et al.*, 2017). Flowering sequence among different genotypes is almost constant, but flowering time may vary due to the different chilling requirements to overcome rest and the heat requirement for starting flowering (Aslamarz *et al.*, 2010). The opening time of the flower is often considered an index variety after or before flowering. Flowering time is a trait with quantitative inheritance (Vargas and Romero, 2001; Socias i Company, 1990).

Another important attribute in breeding programs is increasing yield. Genetically the concept of yield is the result of the interaction of separate parameters of yield, the number of nuts per tree, the average dry weight of the kernel, and the percentage of the kernel. Each of these parameters results in the action of a number of independent genetic traits, which often have many environmental and managerial components (Kester *et al*., 1996; Gradziel and Kester, 1999; Sanchez-Perez, *et al*., 2005). The number of fruits per tree is determined mainly by the density of flower buds that initiate during last fruiting year. This quantity depends on the characteristics of the bearing habit, the amount of yield and the amount of growth during the first part of the previous season. Yield should be considered in relation to some horticultural parameters. In almonds, this trait often appears to be related to growth and types of bearing habits. Therefore, almond trees are classified into three main groups according to bearing habit with the habit: on the annual branch, spur type and mixture. Therefore, in estimating yield, it will be important to pay attention to this attribute (bearing habit), which has a high correlation with yield (Kester *et al*., 1996; Kodad *et al*., 2008; Socias i Company. and Gradziel, 2017). Flower bud density and number of flower buds per spur and spur density were studied in 57 cultivars of almond selections in Spain to ensure its reproducibility and optimal commercial performance, which greatly varies between genotypes and year (Kodad *et al*., 2008 and 2010). The effect of location and the interaction of location and genotype were not significant for flower bud density. But this effect was significant on spur density and the number of flowers per spur. Flower bud density is often related to the number of flower buds in each spur and spurs density showed high reproducibility compared to the other two traits. The high number of flower buds is necessary for optimal production because the high number of flowers compensates for the damage caused by frost to some extent. In Croatia 7 phenotypes from the natural population of almonds were selected and evaluated their phenological and pomological traits in field conditions based on almond descriptor for three years (Strikic *et al*., 2010). Top phenotypes such as K1, K4, and K6 were selected among other phenotypes and compared with phenotypes that were in the same ecological conditions. The morphological diversity of 38 Iranian plum genotypes with some distinct growing characteristics were selected from the fruit-bearing orchards for qualitative and quantitative criteria based on IBPGR descriptor (Aazami *et al*., 2011; Ranjbar *et al*., 2018). There were significant differences ($p \leq 0.01$), between genotypes in respect to all studied traits. A number of these traits were included flower size, stone weight, titrable acidity, pH, Brix, bearing habit, and pulp to the stone ratio (Sarkhosh *et al*., 2007; Usenik *et al*., 2008). Ebadi *et al*. (2012) examined the morphological and molecular diversity of some Iranian almond genotypes and related *Prunus* species and their potential for rootstock breeding. They studied and showed the genetic diversity of 55 almond genotypes and 7 related *Prunus* species. The length, width, and surface of the leaves were correlated with each other and with growth vigor. A negative correlation was observed between traits such as leaf length to width ratio and growth vigor to determine the degree of polymorphism and similarities between almond genotypes, 19 almond genotypes were studied by Colic (2012) in Bosnia and Herzegovina. A great variety in phonological, morphological, and fruit quality traits was observed. The main and important correlation was observed between nut size (length, width, thickness, and weight) and leaf size (length, leaf, and surface). There was little correlation between kernel size and chemical composition, which makes it possible to create new almond cultivars with large kernel sizes and high quality. Parameters with contradictory values were related to nut, kernel, leaf size, harvest maturity, and tree growth habit. They suggested B-04, 1-03, 28-03 genotypes as superior genotypes for almond breeding. Estaji *et al*., (2013) evaluated the characteristics of 50 almond genotypes resulting from the crossing of some of the best Iranian genotypes with Tono cultivar to select the best genotypes. Finally, after evaluating the studied traits, genotypes 6, 15, 20, 25, 46 showed relative superiority over other genotypes in terms of traits such as average fruit and kernel weight, and genotype 6, in addition to having good fruit and kernel weight, it was also incompatible genotype. In 2014, the morphological diversity of 62 almond cultivars and top Iranian genotypes in Karaj city of Alborz province was studied by Arjmandi *et al*.,2014. The results showed that tree growth habits, number of flower buds, and fruit distribution varied greatly among the studied cultivars. The flowering time of ‘Sefid’, ‘Rabie’ and ‘Mamaie’ cultivars were very early flowering, and D-5 and D-11 genotypes were very late flowering. Khadivi- Khoob *et al*., (2016) studied the morphological diversity of 90 almond seed genotypes in Markazi province to evaluate the self-compatibility, flowering time, and morphological characteristics of some almond genotypes. By determining self-compatibility, flowering time, and yield, 13 genotypes were selected as the best genotypes. Tatari *et al*. (2016) studied five different ecotypes of Jujube (*Ziziphus jujuba* Mill.) were collected from different regions of Isfahan province, Iran, for evaluation of their morphological and pomological traits during 2011-13. Results showed that quantitative traits were more significant within ecotypes. ‘‘Najafabad’ ecotype had the highest dimensions of leaves (48×28 mm), fruit weight (2.1 g), and stone weight (0.35g). The largest fruit width (17mm) and peduncle length (13mm) was observed in ‘Ardestan’ ecotype, whereas the largest fruit length (22mm) was observed in ‘Dehaghan’ ecotype. Results showed that ‘Najafabad’, ‘Ardestan’, and ‘Dehaghan’ ecotypes are suitable for cultivation in Isfahan province for establishing commercial Jujube orchards. Agronomic and morphological characteristics of 50 passion fruit genotypes across two different elevations and agro-ecological sites as a base for germplasm enhancement was evaluated (Rodríguez Castillo *et al*., 2020). Results indicated that the mid-elevation site produced higher yields (kg fruit/plant) than the high elevation site, although some landraces were highly productive there. The ANOVAs showed high significance ($P < 0.001$) of genotypic effects for leaf area, days to flowering, longitudinal and transverse fruit diameters, fruit volume and fresh weight, fresh and dry weight of fruit pulp, number of fruits, and fruit weight harvested per plant, fresh and dry one hundred seed weight, and angles of seed vertices. Significant ($P < 0.05$) differences were still found for stipule length, diameter and length of the petioles, sepal length, the diameter of the floral peduncle, fruit lid or operculum diameter, dentate filament length, number of seed pits, seed area, volume, and germination of the petioles, sepal length, the diameter of the floral peduncle, fruit lid or operculum diameter, dentate filament length, number of seed pits, seed area, volume, and germination. This research aimed to study the diversity of morphological and pomological traits of some almond seedlings from the intersection of ‘Tuono' and ‘Shokoufeh' cultivars in order to achieve high-yield, cold-tolerant and self-compatible almond hybrids.

Materials and Methods

65 morphological and pomological traits including 39 quantitative and 26 qualitative traits of 103 progenies resulted from the crossing of Shokofeh and Tuono parental were studied at Meshkin Abad Horticulture Research Station in Karaj (50.9° E, 35. ° 7521 N, 1245 m height, with moderate and cold climates, shallow, calcareous soils, with a PH = 7) during two years, 2016-2017 according to almond description (Gulcan, 1985) for selecting superior hybrids. To perform the experiment, the entire population resulting from the crossing of labeling and the desired traits were prioritized and measured according to time constraints. Trunk diameter, trunk height, seedling height, length and diameter of one-year branch (in two directions north-south and east-west) and crown expansion radius (diameter of seedling crown in two directions north-south and east-west) are measured using a meter. Flower size, length and width of petals, sepals, hypanthium and ovary, length of peduncle, the thickness of the shell, length and width and thickness of fruit, nut, and kernel measured by caliper. Kernel percentage was resulted by kernel weight/fruit weight × 100 (Table 1).

Also, the evaluation of qualitative traits was performed according to Table 2. Data were recorded in Excel software and then SPSS software was used to calculate statistical indices, correlation coefficients, principal component analysis, dendrogram drawing, two and three-dimensional images. Factor analysis was performed using matrix rotation and cluster analysis by the Ward method. SAS software version 9.4 was used to compare the mean and standard deviation and standard error.

Results

Means comparison

The results of comparing the mean of traits with the assumption that the place effect is constant and the effect of hybrids are random showed that traits that have a high amplitude of variation have a wider range of trait quantity, which is a more selective domain for that trait. These traits include vigor, petiole length, flower size, sepal length and width, petal length and width, number of petals, number of sepals, number of stamens, female length, ovarian width, hypanthium length and width, fruit size, fruit weight, length and width and thickness of fruit, nut weight, nut length, nut width and nut thickness; kernel weight, kernel length kernel width and kernel thickness, fruit and nut weight per tree.

Table 1. Comparison of means of quantitative traits studied in hybrids, mean changes, minimum and maximum and standard deviation of traits

No.	Traits	Abbreviation	Unit	Mean	Minimum	Maximum	Standard deviation	Standard error
1	Trunk diameter	TD	cm	15.88	4	28	3.73	1.865
2	Trunk height	TH	cm	37.55	8	110	20.4	10.2
3	Tree height	THE	cm	226.75	135	322	37.5	18.75
4	Diameter one-year-old shoot	DOSE	mm	6.81	4	11	1.77	0.885
5	Diameter one-year-old shoot	DOSW	mm	7.07	4	15	1.9	0.95
6	Length of one-year-old shoot	LOSE	cm	47.09	15	80	13.9	6.65
7	Length of one-year-old shoot	LOSW	cm	53.09	10	110	16.7	8.35
8	Radius of spread	RSN	cm	144.49	23	260	40.7	20.35
9	Radius of spread	RSE	cm	141.50	23	260	40.7	20.35
10	Flower size	FLOSI	mm	30.70	15	41	4.9	2.45
11	Length of petal	LP	mm	13.64	7	20	2.35	1.18
12	Width of petal	WP	mm	11.29	5	15	1.9	0.95
13	Sepal length	SL	mm	4.92	3	7	0.82	0.41
14	Sepal width	SW	mm	4.01	3	7	0.79	0.4
15	Number of petals	NP	No.	5.09	4	7	0.34	0.17
16	Number of sepals	NS	No.	5.05	5	6	0.21	0.11
17	Number of stamens	NST	No.	36.68	10	55	8.1	4.1
18	Hypanthium length	HL	mm	6.08	5	8	0.99	0.5
19	Hypanthium width	HW	mm	4.30	3	6	0.84	0.42
20	Pistil length	PIL	mm	12.4	3	17	2.2	1.1
21	Ovary width	OW	mm	2.69	1	5	0.89	0.45
22	Peduncle length	PL	mm	3.93	1	12	1.87	0.94
23	Thickness of hull	THU	mm	3.81	1	7	1.13	0.57
24	Fruit weight	FEW	g	8.46	2.13	24.15	3.75	1.88
25	Fruit length	FL	mm	35.28	20	49	4.77	2.39
26	Fruit width	FWI	mm	27.29	13	43	4.69	2.35

27	Fruit thickness	FT	mm	20.82	8	32	3.41	1.71
28	Nut weight	NEW	g	2.99	0.7	9.37	1.5	0.75
29	Nut length	NL	mm	30.26	12	43	4	2
30	Nut width	NWI	mm	20.61	9	29	2.95	1.48
31	Nut thickness	NT	mm	13.32	5	23	2.76	1.38
32	Number of nut per tree	NNPT	No.	114.2	1	673	141	70.5
33	Kernel weight	KWE	g	1.10	0.4	2.64	0.39	0.2
34	Kernel length	KL	mm	22.95	8	30	2.99	1.5
35	Kernel width	KWI	mm	12.71	9	18	1.83	0.92
36	Kernel thickness	KTH	mm	7.99	5	15	1.82	0.91
37	Total fruit weight per tree	TFWPT	g	950.60	2.75	6025	1136.6	568.3
38	Total nut weight per tree	TNWPT	g	362.27	0.79	2410	482.8	241.4
39	Kernel Percentage= kernel weight/ Nut weight×100	KWE / NEW *100	%	41	20	90	13.13	0.211

Table 2. Evaluation and frequency of studied quality traits among the studied almond genotypes

No.	Quantity traits	Abbreviation	Coding quantity traits according to almond descriptor(Gulcan,1985)				
			1	3	5	7	9
1	Tree habit	THA	upright	Semi-spreading	spreading	Semi-weeping	weeping
	frequency		30	29	39	3	4
2	Productivity	P		poor	intermediate	well	Very well
	frequency			51	21	31	2
3	Foliage density	FD		low	intermediate	dense	
	frequency			7	28	70	
4	Location of flower buds	LFB	Shoot type	mixed	Spur type		
	frequency		13	67	25		
5	Flowering stage	FS	Before 11th March Extremely early blooming	11th-16th March Early blooming	16th – 21st March Intermediate blooming	21st-30th March Late blooming	After 30th of March Extremely late blooming
	frequency		8	22	46	20	9
6	Foliage stage	FOS	Before 11th March Extremely early	11th-16th March Early	16th – 21st March Intermediate	21st-30th March Late	After 30th of March Extremely late

	frequency		10	31	21	14	29
7	Color of petals	CP	white	Light pink	pink		
	frequency		9	19	77		
8	Notch of petal end	NPE	With notch	Without notch			
	frequency		89	16			
9	Position of pistil to stamen	PPS	Pistil and stamen at the same level	Pistil is higher than stamen	Stamen is higher than pistil		
	frequency		29	40	36		
10	Tomentose of pistil	TP	1/3 cracked	2/3 cracked	½ cracked	Completely cracked	
	frequency		21	77	4	3	
11	Softness of shell	SS		Extremely hard			soft
	frequency			48			57
12	Fruit size	FSI		small	medium	large	Extremely large
	frequency			16	27	60	2
13	Ease of harvesting	EHU		hard	intermediate	easy	
	frequency			20	9	76	
14	Ease of hulling	EHL		hard	intermediate	easy	
	frequency			9	2	94	
15	Harvest maturity	HM	11st of July	16th-19th July	21st July	23th-27th July	2nd -6th August
			Extremely early	Early	Medium	Late	Extremely Late
	Frequency		1	9	16	56	23
16	Date of harvest	DH	19th July	21st July	27th July		
	frequency		1	103	1		
17	Nut color	NC	Extremely light	light	intermediate	dark	Extremely dark
	frequency		3	29	7	53	4
18	Nut shape	NSH	round	ovate	oblong	cordate	Extremely narrow
	frequency		23	18	7	53	4
19	Kernel shape	KS	round	ovate	oblong	cordate	Extremely narrow
	frequency		25	10	23	22	25
20	Kernel color	KC	Extremely light	light	intermediate	dark	Extremely dark
	frequency		3	38	11	43	10
21	Kernel taste	KTA		sweet	intermediate	bitter	
	frequency			105			

22	Tomentose of kernel	TOK	Without tomentose	Semi tomentose	With tomentose	
	frequency		75	4	26	
23	Notch of kernel	NK	Without notch	With notch		
	frequency		54	51		
24	Twin kernel	TWK	one	One to tow	tow	One to three
	frequency			103		4
25	Blood aphid susceptibility	BAS		low	intermediate	high
	frequency			101	4	
26	Disease susceptibility	DS		low	intermediate	high
	frequency			102	3	

Qualitative traits of studied genotypes

Investigation of traits such as growth habit, productivity, foliage density, bearing habit, flowering habit, flowering stage, leaf emergence stage, flower color, the notch of petal end, pistil position to stamen, cracked of the pistil, the softness of shell, fruit size, ease of harvesting, ease of hulling, harvest maturity, harvest date, color and shape of nut, notch of nut, shape, color, taste, and corks of the kernel, twin kernel, susceptibility to blood aphids and gum showed high diversity in hybrids studied almonds. Out of 130 genotypes, 25 genotypes lost naturally and the number of genotypes under study was reduced to 105 hybrids. Evaluation and frequency of studied quality traits among the studied almond genotypes are shown in Table 2. Genotypes with the habit of vertical growth can be used in the development of almond orchards in sloping lands because these genotypes are tolerates to dehydration by reducing evaporation from the canopy. Among the studied genotypes, 30 genotypes with vertical growth habit were 33 high yielding genotypes and 29 genotypes were late flowering or very late flowering.

Factor analysis

In factor analysis (Table 3), 20 principal and independent factors which Eigen values were greater than 0.6 were able to explain a total of 77.432% of the total variance. In the first component, traits such as fruit size (0.70), fruit weight (0.880), fruit length (0.741), fruit width (0.769), fruit thickness (0.722), nut weight (0.872), nut Length (0.729), nut width (0.795), nut thickness (0.673), kernel weight (0.849), kernel length (0.635) and kernel width (0.837) were all positive. In the second component, there were traits such as productivity (0.797), number of nuts per tree (0.925), fruit weight per tree (0.932) and nut weight per tree (0.905) all with positive coefficients. In the third component, traits such as trunk diameter (0.60), radius of expansion in two directions north-south (0.755) and east-west (0.804), leaf density (0.60) and growth habit (0.60) were all positive. The first, second and third main components, which were mostly related to fruit characteristics and growth vigor of genotypes, were the most important in justifying traits. Therefore, in evaluating the traits of almonds, special attention should be paid to these traits and they should be given priority.

Table 3. Rotated Component Matrix and Total Variance Explained.

	component	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
Rotation Sums of Squared Loadings	Total	8.81	4.401	3.099	2.937	2.652	2.37	2.181	2.049	1.927	1.899	1.879	1.857	1.828	1.664	1.646	1.581	1.564	1.529	1.501	1.408
	% of Variance	13.984	6.986	4.919	4.662	4.209	3.762	3.462	3.252	3.059	3.015	2.983	2.947	2.902	2.641	2.613	2.509	2.482	2.428	2.383	2.235
	Cumulative %	13.984	20.97	25.889	30.551	34.76	38.52	41.98	45.24	48.3	51.31	54.29	57.24	60.14	62.78	65.4	67.91	70.39	72.81	75.2	77.43
Traits		Component																			
		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
TD		-0.154	0.315	0.547	-0.026	-0.05	0.113	0.026	-0.18	-0.05	-0.09	-0.12	0.075	-0.04	0.159	0.306	-0.11	0.086	-0.07	-0.02	0.26
TH		-0.039	0.087	-0.041	-0.139	0.008	0.087	-0.01	0.018	-0.05	0.136	0.215	0.134	0.02	0.068	-0.23	0.7	0	-0.01	0.197	0
THE		-0.06	0.262	0.423	-0.028	-0.02	0.263	-0.03	-0.13	0.071	0.048	-0.29	0.017	0.016	0.003	0.159	0.243	-0.02	0.206	0.098	0.247
DOSE		0.22	-0.02	-0.071	-0.083	0.202	-0.03	-0.17	-0.23	0.348	0.029	0.322	0.068	0.024	-0.14	0.274	-0.21	0.163	0.367	0.08	0.006
DOSW		-0.112	0.041	-0.126	-0.029	0.122	-0.06	0.007	-0.03	0.159	-0.1	0.776	0.127	0.065	-0	0.099	-0.01	-0.07	-0.1	0.09	0.057
LOSE		0.163	-0.017	0.025	-0.004	0	0.056	-0.16	-0	0.108	0.046	0.09	0.024	0.003	0.075	0.767	-0.04	0.073	0.068	0.116	0.027
LOSW		-0.017	0.115	0.122	0.093	-0.21	0.126	-0.08	0.077	-0.03	-0.03	0.73	-0.07	-0.03	-0.01	-0.02	0.088	0.018	0.251	-0.12	-0.02
RSN		-0.048	0.272	0.755	0.008	0.04	-0.01	0.077	0.058	-0.09	-0.04	0.056	0.095	-0.05	0.005	-0.04	0.008	0.013	-0	0.033	-0.02
RSE		-0.088	0.201	0.804	0.125	-0.02	-0.06	-0.13	0.014	-0.03	-0.03	-0.03	0.002	0.057	0.009	0.055	0.093	-0	-0.03	-0.07	-0.04
THA		-0.065	-0.123	0.59	-0.025	-0.09	-0.17	-0.04	0.227	0.076	-0.01	0.182	0.001	-0.15	-0.03	-0.09	0.115	-0.08	0.098	-0.02	-0.3
P		0.007	0.797	0.151	-0.043	-0.09	-0.02	0.061	0.067	0.119	0.123	-0.01	0.088	-0.09	0.078	-0.04	0.121	0.077	0.102	0.03	0.057
FD		-0.208	0.095	0.584	-0.081	0.16	-0.01	0.094	0.022	0.241	-0.08	-0.33	-0.1	0.238	-0	-0.12	-0.21	0.026	-0.07	0.044	-0.04
LFB		-0.193	0.196	0.013	-0.151	0.134	-0.22	-0.13	-0.21	0.061	0.055	-0.01	0.165	0.061	-0.44	-0.06	0.01	0.01	0.407	-0.17	0.27
FS		-0.145	-0.031	-0.015	-0.205	0.023	0.052	-0.01	0.123	0.031	0.062	0.031	0.042	-0.02	-0.8	-0.09	0.045	0.088	-0.16	-0.08	-0.06
FOS		0.102	0.115	0.174	-0.013	0.107	-0.07	-0.21	-0	0.104	-0.07	-0.21	0.001	-0.01	-0.16	0.225	0.632	0.131	0.131	-0.04	0.05
FLOSI		0.234	0.013	0.039	0.881	-0.03	0.037	-0.01	0.066	0.021	0.033	0.017	0.088	-0.09	0.002	0.048	-0.07	0.011	0.087	0.175	0.016
LP		0.108	-0.139	0.049	0.886	-0.03	-0.02	0.073	-0.08	-0	0.142	-0.01	0.098	-0.04	0.078	-0.02	-0.06	-0.01	-0.05	-0.01	-0.01
WP		0.113	-0.166	0.001	0.757	-0.07	-0.14	-0.05	-0.04	-0.01	-0.17	0.058	0.223	-0.01	0.144	-0.06	0.008	0.11	-0.05	-0.04	-0.03
SL		0.053	0.03	0.151	0.242	-0.01	0.018	-0.02	0.07	0.119	-0.1	-0.06	0.818	0.002	-0.05	0.035	0.102	0.112	-0.11	0.004	-0.01
SW		0.057	-0.059	-0.041	0.234	0.031	0.236	0.086	0.156	-0.07	-0.03	0.191	0.757	0.042	-0.03	0.003	0.011	0.001	0.018	0.152	-0.04

CP	-0.173	0.247	-0.163	-0.005	0	0.059	-0.13	-0.23	0.197	0.025	-0.16	-0.08	0.409	0.309	-0.23	0.058	0.296	-0.07	-0.07	0.003
NPE	-0.053	-0.202	0.18	-0.403	0.103	0.159	0.013	-0.16	-0.15	0.08	0.048	-0.1	0.168	-0.03	-0.31	-0.17	0.173	0.101	-0.33	0.066
NP	-0.036	0.095	0.06	0.045	0.1	-0.01	-0.04	0.823	0.045	-0.04	-0.03	0.06	-0.04	0.024	-0.04	0.032	0.104	0.041	-0.1	-0.01
NS	-0.037	0.006	0.031	-0.077	0.121	-0.14	0.009	0.81	-0.06	0	0.071	0.116	-0.03	-0.11	0.046	-0.03	-0.11	-0.08	0.142	0.052
NST	0.048	-0.069	0.036	0.189	-0.07	0.041	0.113	0.015	0.068	-0.17	-0.03	0.17	0.11	0.128	0.135	0.138	-0.11	0.06	0.692	-0.06
PPS	-0.016	0.07	0.034	-0.064	0.073	0.016	-0.06	-0.01	0.069	-0.17	0.067	-0.07	0	0.129	-0.05	-0.08	-0.77	0.105	0.108	0.032
HL	-0.111	-0.028	-0.07	-0.034	-0.02	0.918	-0.06	-0.05	0.035	0.064	0.026	0.083	-0.06	0	-0.04	0.028	0.039	0.015	0.029	-0.03
HW	-0.096	0.075	-0.015	-0.097	-0.01	0.915	-0.14	-0.09	0.054	0.01	0.011	0.084	-0.06	-0.01	0.099	0.008	-0.05	0.062	0.003	0.014
PIL	0.122	0.01	0.221	0.038	-0.05	0.03	0	-0.01	0.057	-0.08	0.16	0.138	-0.37	0.37	0.103	-0.03	0.492	-0.07	0.138	-0.1
OW	-0.183	0.013	-0.007	0.013	-0.04	0.116	0.008	0.009	-0.01	-0.05	0.078	-0.1	0.072	0.145	0.068	0.067	-0.14	0.813	0.051	-0.06
PL	-0.082	0.014	-0.007	0.088	0.057	0.171	-0.13	0.095	0.112	-0.11	-0.1	-0.11	-0.78	0.055	-0.02	-0.04	0.023	-0.12	-0.05	0.036
TP	-0.063	0.051	0.192	0.167	0.069	0.29	0.322	0.001	0.095	-0.11	0.2	-0.37	0.168	-0.11	-0.07	0.378	0.009	-0.23	-0.13	0.005
SS	-0.304	-0.086	0.034	-0.082	0.833	0.02	-0.01	0.139	-0.2	-0	-0.02	-0.02	-0.03	-0.03	-0.03	0.004	-0.07	-0.01	-0.04	-0.12
FSI	0.712	0.009	-0.076	0.194	-0.11	-0.06	-0.1	-0.06	-0.08	0.129	0.036	0.013	0.155	-0.06	-0.05	0.047	0.145	-0.09	0.114	0.166
EHU	-0.012	-0.278	0.017	-0.208	-0.25	-0.32	0.568	0.01	0.086	0.134	0.044	0.126	0.121	0.062	0.064	-0.05	0.13	-0.12	0.12	0.106
EHL	-0.06	-0.231	0.167	-0.116	0.14	-0.14	0.325	0.149	0.269	0.138	0.1	0.182	0.08	0.338	-0.09	0.01	0.175	0.138	-0.24	0.253
THU	0.552	0.166	-0.139	-0.108	0.275	0.028	0	-0.04	0.197	0.111	0.052	-0.05	-0.24	0.134	0.02	-0.08	0.055	0.045	0.402	0.024
HM	0.088	0.052	-0.232	0.117	-0.28	-0.14	0.571	0.07	0.056	0.239	-0.06	0.127	-0.38	0.046	-0.24	-0.04	0.07	-0.07	0.028	0.112
DH	0.002	0.072	-0.074	-0.011	-0.08	-0.02	0.049	0.05	-0.02	-0	0.036	-0.04	-0.03	0.018	0.018	0.028	-0.05	-0.02	-0.04	0.846
FEW	0.86	0.134	-0.106	0.093	-0.05	-0.06	-0.09	-0.01	0.117	0.017	0.045	0.031	-0.08	0.082	0.035	-0.06	-0.01	-0.1	0.024	-0.11
FL	0.837	-0.027	0.007	-0.02	0.094	-0.12	-0.16	-0.04	-0.04	-0.08	0.005	0.096	0.008	-0	-0.06	-0.04	0.137	0.04	0.103	-0.02
FWI	0.852	-0.021	-0.034	0.012	0.027	-0.08	0.017	0.047	0.077	-0.09	-0.09	-0.03	0.073	0.102	-0.07	-0.1	0.089	0.052	0.023	-0.06
FT	0.749	0.012	0.004	0.051	0.061	-0.08	-0.09	0.213	0.129	-0.06	-0.11	0.079	0.161	0.181	0.166	-0.12	0.009	-0.04	0.119	-0.14
NEW	0.796	0.159	-0.03	0.043	-0.41	-0.03	0.051	0.001	-0.02	-0	0.037	0.031	-0.16	-0.05	0.142	-0.01	0.006	0.026	-0.08	0.07
NL	0.828	-0.194	-0.018	0.026	-0.11	-0.09	0.011	0.074	-0.15	-0.08	-0.04	-0.02	-0.05	-0.07	-0.09	0.108	0.133	0.082	0.084	0.115
NWI	0.808	-0.137	0.082	0.106	-0.27	0.008	0.095	-0.02	0.047	-0.08	-0.01	-0.13	-0.01	-0.06	0.075	0.086	0.06	0.049	0.091	0.172
NT	0.667	-0.047	0.062	0.041	-0.35	0.105	0.063	0.056	0.018	-0.1	-0.13	0.078	0.009	-0.01	0.047	-0.17	-0.15	-0.06	-0.19	0.008
NC	-0.15	-0.205	0.028	-0.146	-0.15	0.039	-0.01	0.18	0.29	-0.09	-0.1	-0.17	0.485	0.309	0.017	-0.1	-0.11	-0.09	0.135	0.028
NSH	-0.108	-0.123	0.054	-0.199	0.36	-0.09	-0.01	0.01	-0.57	0.136	-0.07	-0.04	-0.17	0.185	0.091	0.119	-0.06	0.064	-0.3	-0.01

NNPT	-0.127	0.925	0.138	-0.096	-0.04	0.03	-0.06	0.018	0.022	0.046	0.042	0.019	-0.02	-0	-0.04	0.021	-0.06	0.021	-0.01	-0.03
KWE	0.781	0.172	-0.208	0.1	-0.12	0.047	0.017	-0.13	0.121	0.079	0.054	0.012	-0.07	0.088	0.202	0.119	-0.17	-0.11	-0.15	-0.1
KL	0.711	-0.057	-0.187	0.074	0.069	0.039	0.006	-0.09	-0.14	0.038	0.027	0.116	-0.03	-0.07	0.007	0.215	-0.23	-0.2	-0.25	-0.07
KWI	0.747	0.12	-0.063	0.142	-0.15	0.05	-0.02	-0.21	0.269	0.091	0.051	-0.03	-0.1	0.033	0.206	0.111	-0.21	-0.11	-0.03	-0.06
KTH	0.428	0.225	-0.371	0.069	-0.17	0	0.069	0.004	0.33	-0.02	-0.08	0.014	0.087	0.058	0.307	-0.13	-0.09	0.095	-0.26	-0.22
KS	-0.193	-0.077	-0.019	0.031	0.217	-0.08	0.098	0.003	-0.77	0.006	-0.1	-0.04	0.143	-0.07	-0.19	-0.14	0.107	-0.03	0.002	0.029
KC	-0.389	-0.3	0.077	-0.121	0.053	-0.08	0.509	0.149	-0.14	-0.16	-0.1	0.009	0.28	-0.1	0.058	0.106	-0.11	-0.06	-0.08	-0.06
TOK	-0.1	-0.054	-0.017	0.093	0.208	-0.06	0.805	-0.11	-0.12	-0.07	-0.06	-0.06	0.056	0.021	-0.14	-0.13	0.017	0.059	0.076	-0
NK	-0.286	-0.18	-0.011	-0.037	0.814	-0.04	0.104	0.157	-0.12	0.03	-0.04	0.053	-0.05	-0.05	0.017	0.066	-0.05	-0.02	-0.03	0.037
TWK	0.285	0.277	-0.117	-0.044	-0.28	-0.02	0.151	0.269	-0.15	-0.16	-0.08	-0	0.088	0.112	0.313	0	0.327	0.239	-0.12	0.194
TFWPT	0.107	0.932	0.126	-0.052	-0.01	0.048	-0.14	0.032	-0	0.045	0.025	-0.08	0.027	-0.04	0.037	0.008	-0.04	-0.02	-0.01	-0.06
TNWPT	0.121	0.905	0.133	-0.052	-0.11	-0	-0.08	0.006	0.002	0.04	0.064	-0.06	0.025	-0.06	0.069	0.021	-0.03	-0.05	-0.02	0.146
BAS	-0.08	0.079	-0.068	0.066	-0	0.018	-0.1	-0.03	0.046	0.832	-0.08	0.014	0.03	-0.1	0.037	0.028	0.081	-0.05	-0.11	0.03
DS	-0.012	0.12	-0.033	-0.047	0.043	0.043	0.104	-0.02	-0.09	0.834	-0.02	-0.11	0.03	0.033	-0.01	0.017	0.042	0.014	-0.01	-0.03

Plot analysis

Plot analysis can show a two or three-dimensional image of the distribution of genotypes based on two or three main factors resulting from factor analysis. Each dimension represents a major factor and each factor represents several traits influencing that factor. Therefore, the distribution of genotypes and the range of changes of these main factors can better show the distance and differences between genotypes.

Di Plot analysis

In this research, Di Plot was performed using the first and second main factors. This method is used to show a two-dimensional image of the distribution of genotypes based on the first and second main factors. The accumulation of genotypes in an area of the plot indicates a genetic similarity between the studied genotypes. Therefore, based on Di Plot analysis, hybrids that are similar in the first and second factors are close to each other and in a group.

For example, in Fig. 1, the distribution of promising hybrids in terms of prominent pomological traits (including size, weight, length and width, and high fruit thickness; weight, length, width and thickness of nut and weight and length and width of the kernel and high productivity, The large number of nut per tree, the high weight of fruit per tree and the high weight of nut per tree) in the positive part of the first and second factors show the similarity of pomological traits in those hybrids. In other words, if the goal is to select high-yield hybrids and it is quality based on this analysis, and can be selected from the hybrids that are distributed in that section. So that the two hybrids 38 and 124 with the highest performance among the studied hybrids and the highest similarity with each of the parents of Tuono and Shokoufeh are in this section.

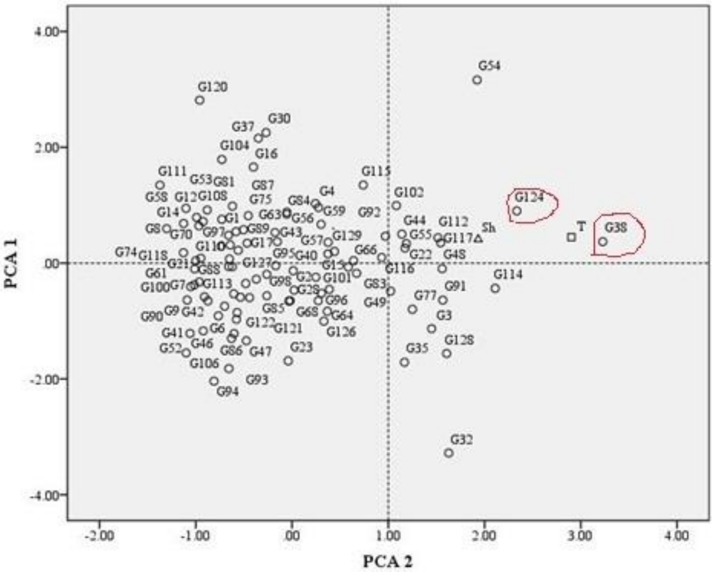

Fig.1. Distribution of studied hybrids based on two-dimensional analysis using the first two factors of fruit-related traits and the second factor of kernel-related traits that explained 20.97% of the total variance.

Tri-plot analysis

Three-plot analysis was performed using three main factors using SPSS software. These three factors account for 25.889% of the total variance. According to the results of three-dimensional analysis, genotypes were divided into three groups based on the first three factors. Due to the fact that in the effective traits in the first three factors, a positive correlation was often observed, these factors were also effective in separating the traits and most hybrids with high yield and vigor in the upper right and lower part of the plot are in the positive part. The hybrids in the middle part of the plot are often with medium productivity and vigor, and the hybrids on the lower left part of the plot are with low productivity and vigor (Fig. 2).

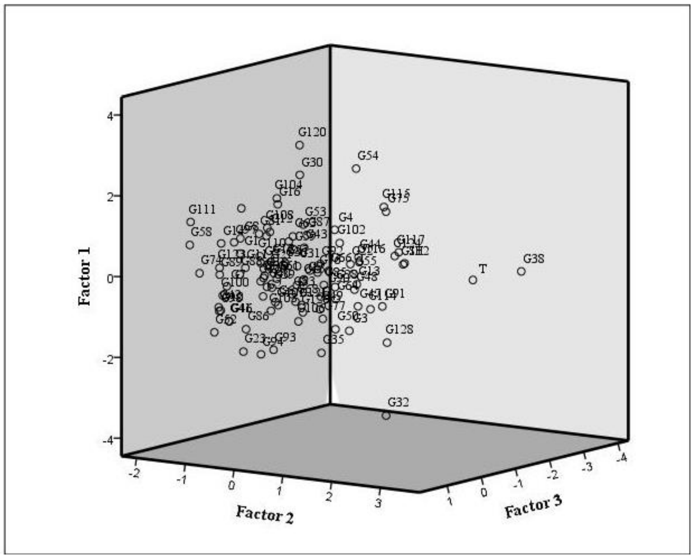

Fig.2. Distribution of studied hybrids based on three-dimensional analysis using three main factors. The first factor was related to fruit traits, the second factor was related to kernel traits and the third factor was related to the hybrid's vigor, which explained 25.889% of the total variance.

Discussion

Flowering time is an important agronomic trait in almonds since it is decisive to avoid the late frosts that affect production in early flowering cultivars (Socias i company *et al.*, 2017). Evaluation of this complex trait is a long process because of the prolonged juvenile period of trees and the influence of environmental conditions affecting gene expression year by year. Consequently, the flowering time has to be studied for several years to have statistically significant results. This trait is the result of the interaction between chilling and heat requirements (Raquel Sanchez-Perez et al., 2014). It is important to cross native Iranian almond with the self compatible, commercial variety in the world, in order to evaluate the morphological and fruit characteristics and introduce new cultivars. Almond Breeding program is one of the largest and oldest continually active almond improvement programs in the world. (Gradziel, 2017). Important issues in almond breeding are local adaptation, kernel quality, self-compatible and high yield. In this study, the morphological and pomological traits of 130 almond hybrids from the intersection of Tuono and Shokoufeh were evaluated. The results of this study showed high morphological diversity in almond genotypes. Regarding the qualitative traits, the highest diversity was obtained for traits such as growth habit, productivity, flowering stage, foliage stage, tomentose of the pistil, fruit size, nut shape, shape, color, weight and size of the kernel and the least variety in kernel taste (Figs 1, 2) Obtained. Because of the self incompatibility in almond, the results were expected. This high phenotypic diversity with previous reports on the study of molecular properties using different markers as simple reproducible nuclear and chloroplast sequences (Martinez-Gomez et al., 2003; Fathi et al., 2008; Zeinalabedini et al. , 2008; Slavica colic et al., 2012) or the polymorphism method is consistent with the length of the amplified fragments (Sorkhe et al., 2007). The relationship between some traits could help breeders to choose parent. Based on the comparison, the mean of the studied genotypes varied from vertical to hanging in terms of tree growth habit. Foliage density also varied from low to very high. Vegetative traits are effective to determine planting distance and tree's density. (Colic et al., 2012). Identifying and selecting superior genotypes in native germplasm is one method for breeding fruit trees (Tatari *et al*., 2016). Selecting superior ecotype which are adapted to different regions over many years, as well as identifying and preserving them could be allowed by diversity. Flowering time is a complex trait, and different regions of the genome have been identified as being involved in the control of this trait (Sanchez-Pérez *et al*., 2014). Obtaining late-flowering cultivars to avoid spring frosts is one of the main objectives of almond breeding programs. Like other temperate trees, the almond tree is at rest during the winter and usually without leaves. Almond has a high ability to withstand low temperature in these conditions, while it is very susceptible to cold during flowering and early fruit development stage. At this time, depending on numerous factors, particularly phonological stage, temperature, and exposure time, decreasing temperature to less than -1^{0}c or -2^{0}c leading to crop loss. Therefore breeders tend to achieve new late flowering almond cultivars which flower when the risk of the frost is minimal. (Federico Dicenta et al., 2017). Accumulation of chill and heat units in each cultivar determines the genetic aspect of flowering. In each environment, the amount of cold and heat that a tree receives is different and, consequently, its flowering date is also different. Nevertheless, the different cultivars usually maintain the same order of flowering. Flowering time is a complex trait that is largely controlled genetically and has High heritability , but temperature have an appreciable on this traits. Nevertheless, temperatures have an appreciable effect on this trait.

The progressive warming of the planet is a documented fact that is affecting many biological processes, including the flowering of the almond. Increasing temperatures will have important future implications for the distribution of almond cultivation, and problems could be alleviated by exploring variability and genetic breeding (Federico Dicenta *et al*., 2017).

Conclusions

The present study was carried out to select the late-blooming almond genotypes with high kernel quantity and quality. Significant differences were observed among the accessions based on all of the studied characters. The selected late-blooming genotypes showed significant morphological and pomological differences ($P < 0.05$). Fruit-related characters were the most effective traits for differentiating the studied accessions. Nut weight ranged from 0.7 to 9.37g with an average of 2.98g. Kernel weight ranged from 0.4 to 2.64g with an average of 1.1g. Nut weight and kernel weight with high standardized beta coefficients showed positive and significant associations with kernel percentage (3.44 to 13.41% with an average of 7.35%) and therefore they had a great impact on this key character and should be considered in breeding programs. Considering the ideal values of the important and commercial traits of almond, 2 genotypes were superior and thus they could be cultivated in orchards and/or to be used as a parent for crosses to create suitable populations or to improve blooming time, kernel quality, and nutritional values of almond cultivars.

In this study, morphological and pomological characteristics of 103 genotypes were evaluated. Results of morphopomological traits indicated that tree growth habit, buds, leaf, flowers, and fruit attributes were from a high diversity among studied genotypes. Also, the time of flowering among almond genotypes and cultivars varied widely from early, moderate and late blooming. Performances of almond genotypes based on their quantity and quality characteristics were different. Similar results have been reported by ardjmand *et al*., 2014, Asgari *et al*., 2021 to group and separating of almonds genotypes. Finally, among the late-blooming genotypes, 7 genotypes were promising according to the ideal values of commercial characters of almonds, including, yield, nut weight, and shell hardness, and can be used in breeding programs (Table 4).

Table 4. Promising genotypes according to the ideal values of commercial characters of almonds, including, yield, nut weight and shell hardness, which chosen in this study and can be used in breeding programs

Gynotype's name	Fruit weight(g/per tree)	Nut weight(g/ per tree)	Flowering stage	Self-(in) compatibility	Softness of shell
38	6025	2410	Moderate	Self-compatible	soft
124	3600	1300	Very late blooming	Self-in compatible	soft
114	3450	1750	moderate	Self-in compatible	hard
112	3300	1550	Late blooming	Self-in compatible	hard
117	3200	1150	moderate	Self-compatible	soft
54	2675	1250	moderate	Self-in compatible	hard
128	2550	1050	Late blooming	Self-compatible	hard

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