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Agronomic characters and traits correlation of Iranian purified melon populations in cold and dry conditions

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Abstract

In order to compare eighteen different melon genotypes belonging to two different populations, a two-year field experiment was carried in Khorasan-Razavi Research Centre for Agriculture and Natural Resources based on randomized complete blocks design with three replicates. The results indicated that selection and purification could improve studied traits. For instance, fruit yield, fruit weight and fruit number as well as sugar percentage and flesh thickness increased in purified genotypes. In addition, skin thickness and cavity dimeter decreased in purified genotypes. The maximum fruit yield (26.93 ton ha^{-1}) was related to Khatooni genotype, which is the most important cultivated genotype in Khorasan-Razavi province. By contrast the minimum yield was obtained from native Sooski genotype. Among exotic genotypes, purified Jajoo showed the best results. Fruit sugar percentage differ from 11.5 to 14.67 in different genotypes. The results showed that selection could improve fruit sugar percentage in some genotypes. The maximum fruit sugar percentage was recorded in purified Dargazi genotype, however native Dargazi was better than other genotypes. According to the cluster analysis the melon genotypes were divided into three different groups. The first group consist of seven genotypes i.e. Shadgan, purified Shadgan, Ananas, Khaghani, purified Sooski, Akila and Chah-Paliz. The second group consist of purified Khagani, purified Chah-Paliz, Jajoo, Khatooni and Dargazi and the third group consist of purified Chah-Paliz, purified Jajoo, native Bandi, purified Bandi and purified Khatooni.

Key words : Yield, Sugar percentage, Purified population, Cluster, Factor analysis

INTRODUCTION

According to the FAO statistics, 1,308,018-hectare land is under melon cultivation with total production of 28,321,159 tons (21.6-tonha-1 average yield). China produces the maximum melon in the world with 15,138,000 tons per annum, which is 53.5% of world production. Iran produces about 4.4% of the world's melon (1230000 tons) occupying 80,000 ha land. Native melons are not genetically uniform and have low production. Yield and yield components are considered as he most important traits in melon. Recent research projects on native melon populations have shown that native populations have great potential to be used in future breeding programs [1-2-3-4-5]. However, the status of each population in relation to their native or mother populations in different environments is not specified. Due to this fact that Iranian genotypes have wide diversity, study on modern populations in different regions is important. Melon is a sensitive species to environmental conditions, so its yield and quality should be evaluated in different conditions [6]. Plant breeders have always been paying more attention to genetic characteristics of Cucurbitaceae family. The most important traits in this family are growth habit, leaf shape, male sterility, fruit colour and shape, leaf area, leaf size, seed colour, fruit bitterness and pest and disease resistance [7]. Plants in this family are monoecious and although are known as cross-pollinated, some self-pollination may occur [8]. Most of the species in Cucurbitaceae family produce a lot of seeds, which are very important in genetic studies. Nonetheless, these species require too much space to be grown which increase production cost [8]. It has been reported that Gradner's mass selection is appropriate for maize [9]. In this method estimation of genetic and environmental effects are easy and inexpensive. [10] Feher has reported that commercial and North European varieties have been selected for the first time and crossed later according to their requirements[11] have stated that selection methods can be used to improve melon populations' traits such as fruit size, early maturity, seed size, fruit number and total soluble solids. It has been reported that increase in yield depends on fruit number and fruit weight, which has been observed in superior populations [10]. Genetic diversity of native watermelons and effects of environmental conditions have been studied by [12] who reported that environmental conditions such as temperature, rainfall and longitude have great impact on seed traits. Wild or native genotypes are important for being a good genetic sources of resistance to pests and diseases. Different resistance degree has been obtained using hybridization methods [13]. [14]Peterson have offered a method to select native mass and wild populations. According to his report, in initial experiments, the seeds should be sown in rows with replications. His reports on yield, early maturity and disease resistance is now accessible. Breeding methods have been defined by [15] who used mass selection for watermelon breeding. In his method seeds were sown in isolated plots and collected seeds were mixed to form a mass population. In each cycle final yield was compared with initial mass. Selection in Cucurbitaceae family can be done using mass selection. In this method, those individuals which have superior morphological characteristics are selected. In the next step, their seeds are sown and left them to be cross pollinated. Obtained seeds will be used for next year selection. This step will be repeated till the final goal is achieved [16]. Selection is one of the main and initial phenomena which causes genetic diversity in any population. This diversity depends on the genetic background of the individuals and selection intensity [15].Selection is one the main and most important steps to be taken into a consideration in breeding programs. Selection approaches are different based on propagation methods of plant species. For instance, selection methods in self or cross-pollinated species are different. Selection in self or cross-pollinated species improves traits [17]. Different Indian cantaloupe genotypes were studied in terms of disease resistance by [16] who reported that selection could improve disease resistance after couple of years. Mass selection could improve qualitative and quantitative traits such as average fruit weight, fruit number, ripening time and sugar percentage in melon genotypes after several selection cycles. [17]. The previous findings have shown that fruit number and weight correlate with final fruit yield so these two traits can be used in selection programs. Early mature genotype has also shown a positive correlation with plant length, initial branches number and fruit weight. In addition, negative correlation was found between maturity time and soluble sugar content and skin pattern [10].Economically important Iranian melon and cantaloupe populationswere studied by [18] who reported that there is 85-98% cross pollination in melon populations. Yield, fruit appearance, flesh quality and fruit storability have been considered as the most important traits in cantaloupe genotypes [6]. Since market's demand is most often defined as the combination of these traits, complex breeding programs should be undertaken to achieve a desired quality [19].Genetic screening for different traits is a time consuming process. In addition,there is no reports available about wild melons for these traits, however improvement in each traits considering the production priorities is not out of reach. Yield quality in cantaloupe and melon includes maturity time and fruit establishment on the plants [20]. Heredity of qualitative traits and yield such as maturity time and fruit establishment is highly complicated [21-11]. In addition to above mentioned traits, Iranian melons and cantaloupes are tolerant to low temperatures during germination period, which indirectly affect maturity time [22-23]. Most of these varieties have been released using selection and self-pollination methods [6].Breeding method used should be in accordance with the objectives of the program, for example, mass selection or recurrent selection can be used when the goal is creating inbred lines for F1 hybrids [24]. Fruit number and weight, main stem length, main stem node number and internode length correlate with final yield, hence can be used as a selection indexes [25]. [26] have studied 13 melon cultivars and found that there is a positive correlation between early maturity and plant length, initial and secondary branches number and fruit weight. In addition, negative correlation was found between early maturity and fruit soluble solid content [27]. Understanding the relationships and correlations between different traits is the first step in plant breeding, which could increase efficiency of the breeding programs through reducing selection time and individuals number in different populations.

MATERIAL AND METHODS

The current experiment was carried out in Khorasan-Razavi Research Centre for Agriculture and Natural Resources, Mashhad, Iran during 2011 and 2012 growing seasons. The experiment site was located approximately six km south east of Mashhad city (59° 38□ E, 36° 16□ N and 980 m above sea level). The site had silt loam soil with pH of 7.9, total nitrogen, phosphorus and potassium content of 0.06%, 12.8 ppm and 150 ppm, respectively. The experiment was laid out in randomized complete blocks design with 18 different melon genotypes and three replicates. The melon genotypes were belonged to two different populations, the first population consist of purified genotypes during previous years along with their mother (initial) populations (Sooski, Khaghani, Dargazi, Jajoo, Khatooni, Bandi, Chah-Paliz and Shadgan). The second population consist of foreign genotypes such as Ananas and Dorango. The filed was prepared by spreading 15ton ha^{-1} cattle manure in winter and ploughing by mouldboard and disk in spring. Melon seeds were manually sown on 11th of May. There was 3 m distance between rows and 0.7 m distance between plants. Chemical fertilizers were applied according to soil analysis. Irrigation and weed control were performed conventionally. At harvesting season, 10 plants were harvested and average fruit weight, fruit number per plant, plant length, fruit sugar percentage, flesh thickness, skin

Table 1: Comparison of means of different traits in native and purified melon genotypes.

Sugar percentage	Plant length (cm)	Fruit number	Fruit weight (g)	Yield (ton ha^{-1})	Genotype
11.83efg	164.333hi	2.07i	2.267L	16.467	Native Sooski
12def	167.667efg	2.2fghi	2.566IJ	18.533hij	Purified Sooski
11.67gf	170.333de	2.13hi	3.400c	17.633j	Native Khaghani
12def	173.667bc	2.33def	3.600ab	21.133g	Purified Khaghani
13.33b	169ef	2.07i	3.200d	22.267f	Native Dargazi
14.67a	172.333cd	2.37cde	3.533b	24.800bc	Purified Dargazi
11.5fg	164.667ghi	2.10hi	2.6332hi	22.933ef	Native Jajoo
12def	165.667ghi	2.30defg	2.867fg	24.367cd	Purified Jajoo
12def	176b	2.23efgh	3.167d	22.857ef	Native Khatooni
13bc	179.667a	2.90a	.3.6673a	26.933a	Purified Khatooni
11.67fg	167.667efg	2.17ghi	3e	23.800de	Native Bandi
12.5cd	168.333de	2.53b	3.333c	25.573b	Purified Bandi
11.67fg	164hi	2.17ghi	2.7002gh	19.100h	Native Chah-Paliz
12.33de	166fghi	2.50bc	3e	20.633g	Purified Chah-aliz
11.33g	167fghi	2.200fghi	2.8332f	17.950ij	Native Shadgan
12def	166.333fgh	2.40bcd	3e	18.900hi	Purified Shadgan
12def	164hi	2.90a	2.367kl	17.933ij	Ananas
12def	162.667i	2.87a	2.467jk	18.700hi	Akila

Tables 1: Continued

Cavity diameter (cm)	Fruit width (cm)	Fruit length (cm)	Skin thickness (cm)	Flesh thickness (cm)	Genotype
17.67efg	22.67bcde	29.17ef	0.5b	3/6d	Native Sooski
18.17 de	22.33abc	23.30/ de	0.47c	5.4 b	Purified Sooski
19.17abc	22.33abcde	36.13 c	0.40d	3fg	Native Khaghani
19bcd	24 a	35.73 c	0.5b	3.2ef	Purified Khaghani
18.5cde	23.67ab	40.67ab	0.3 e	3.5ed	Native Dargazi
17.67efg	23abcd	41 a	0.4 d	4.17c	Purified Dargazi
20 a	23abcd	32 d	0.51 b	3.6d	Native Jajoo
19.67ab	22.83abcdef	32 d	0.32 e	4.93a	Purified Jajoo
19bcd	21.67cdef	36.67 b	0.31 e	3fg	Native Khatooni
18.5cde	23abcd	41.33 a	0.31 e	3.23 de	Purified Khatooni
19bcd	22bcde	30def	0.30 e	4 c	Native Bandi
17.17fg	21.17ef	28.67ef	0.21 f	4.2bc	Purified Bandi
17gh	20.07 f	28.47ef	1 a	3.2ef	Native Chah-Paliz
16.17h	20.17f	29.63def	0.3 e	3.2ef	Purified Chah-Paliz
18ef	22bcde	27.33fg	0.32 e	3fg	Native Shadgan
17gh	21.67cdef	27.5efg	0.31 e	3fg	Purified Shadgan
13i	21.33def	24.67 h	0.31 e	2.2 h	Ananas
13i	22bcde	25.67gh	0.32 e	2.73 g	Akila

Table 2: Correlation between native and purified melon's traits.

Cavity diameter	fruit width	fruit length	Skin thickness	flesh diamater	sugar percentage	plant length	Fruit number	fruit weight	Yield	
									1	Yield
								1	0.618**	fruit weight
							1	0.117	0.184	Fruit number
						1	-0.025	0.674**	0.469**	plant length
					1	0.388**	0.197	0.460**	0.471**	sugar percentage
				1	0.061	- 0.095	.503** -0	- 0.046	0.304*	flesh diamater
			1	0.418**	0.070	0.009	-0.018	0.152	0.193	Skin thickness
		1	- 0.074	0.165	.575** 0	0.724**	-0.141	0.681**	0.522**	fruit length
	1	0.487**	0.032	0.192	0.244	0.232	-0.063	0.112	0.083	fruit width
1	0.275*	0.533**	0.105	0.551**	-0.026	0.23**	.665** -0	0.415**	0.381**	Cavity diameter

Table 3: Traits' correlation and obtained components from factor analysis

Component				
4	3	2	1	
-0.176	0.386	-0.164	0.732	**Yield**
-0.307	0.065	0.312	0.797	**fruit weight**
0.135	0.328	0.838	-0.162	**Fruit number**
-0.213	-0.235	0.249	0.776	**Plant length**
-0.334	0.191	0.415	0.592	**sugar percentage**
-0/168	0.385	-0.757	0.330	**flesh thickness**
0.054	0.797	-0.266	0.172	**Skin thickness**
0.126	-0.265	0.097	0.9	**fruit length**
0.781	-0.243	-0.110	0.431	**fruit width**
-0.227	-0.199	-0.623	0.669	**Cavity dimeter**

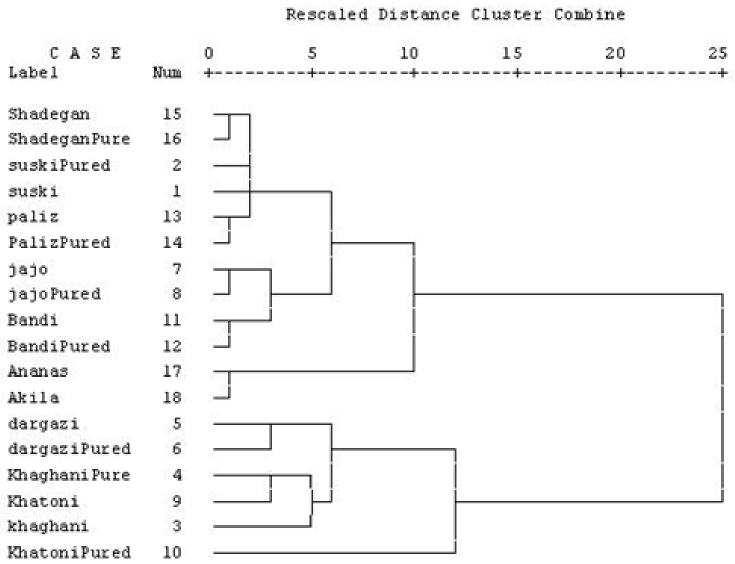

Fig 1: Cluster analysis based on all the traits.

thickness, fruit length, fruit width, cavity length and final yield were determined. The data were analysed using SAS software and means were compared using Duncan's' multiple range test.

RESULTS

Comparison of means indicted that there is a significant difference between genotypes in terms of fruit yield. The results indicated that selection and purification could increase fruit yield in all genotypes except for Shadgan genotype (Table 1). Khatooni genotyo, which is the most important genotype in Khorasan-Razavi Province produced higher fruit yield than other genotypes. The maximum fruit yield (26.93 ton. ha^{-1}) was obtained from purified Khatooni genotype. The minimum fruit yield was related to native Sooski genotype; however, purification could improve fruit yield in this genotype. Amongst foreign genotypes, Jajoo genotype showed a significant advantage (Table 1). There was significant difference between melon genotypes in terms of yield components (average fruit weight and fruit number per plant). From the results, selection and purification could increase average fruit weight in all genotypes. The maximum average fruit weight was obtained from purified Khatooni (3.60 kg) and purified (3.66 kg) Khaghani genotypes. By contrast, Sooski genotype showed the minimum average fruit weight (2.26 kg). Furthermore, foreign genotypes (Ananas and Akila) not only resulted in lower yield, but also showed lower average fruit weight (Table 1). Purification could improve fruit number per

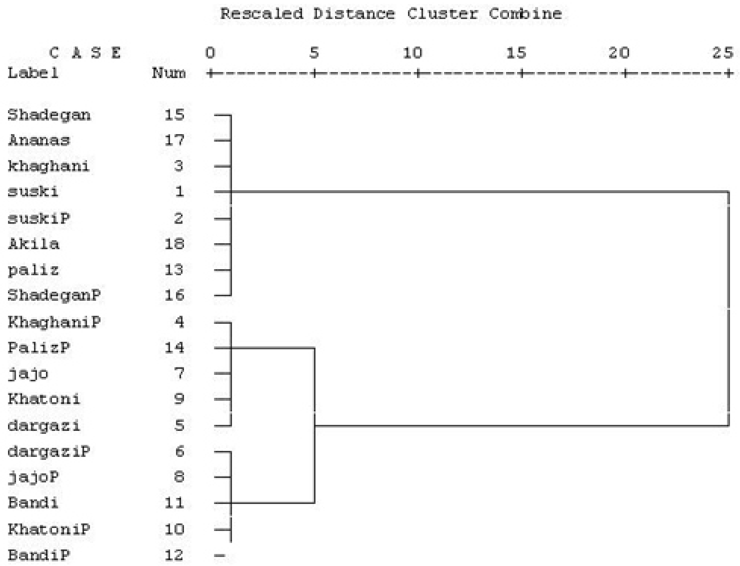

Fig 2: Cluster analysis based on fruit yield.

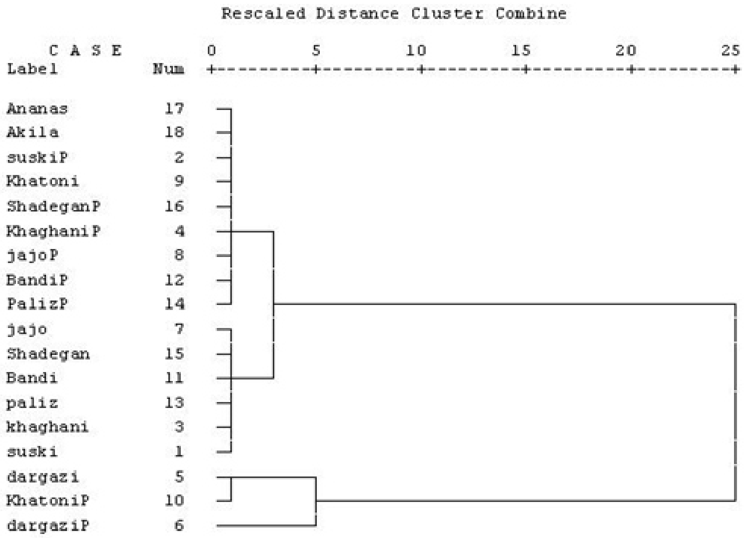

Fig 3: Cluster analysis based on sugar percentage

plant in all genotypes, except for Sooski genotype. The maximum fruit number per plant was observed in purified Khatooni, Ananas and Akila genotypes. Khatooni genotype produced the maximum fruit number per plant and average fruit weight which led to the maximum final fruit yield. Although Ananas and Akila produced more fruit, final fruit yield was lower due to less fruit weight (Table 1). The minimum and maximum plant length were related to Akila and Khatooni genotypes, respectively (Table 1). Sugar percentage ranges from 11.5 to 14.67% among the genotypes. Selection could improve sugar percentage in some genotypes. The maximum sugar percentage was observed in purified Dargazi genotype, however native Dargazi was found to be better than other genotypes (Table 1). There was significant difference between genotypes in terms of flesh dimeter. Purification could increase flesh dimeter in all genotypes except for Bandi, Chah-Paliz and Shadgan. Flesh diameter in Ananas genotype and Jajoo were registered as 2.2 cm and 4.93 cm, respectively. According to the results, skin thickness decreased on account of purification. However, there was no significant difference between native and purified Khatooni and Shagna genotypes in terms of skin thickness. The minimum (0.21 cm) and maximum (1.00 cm) skin thickness were related to purified Bandi and native Chah-Paliz genotypes, respectively. Only in Khatooni genotype fruit length was increased by selection process. The maximum (41.33 cm) and minimum (24.67 cm) fruit length were recorded from purified Khatooni and Ananas genotypes, respectively. Fruit width and cavity length were not affected by selection process, however cavity length decreased in Bandi and Shadgan genotypes (Table 1).. The correlations between the melon traits are shown in (Table 2). As can be seen, there is high correlation between fruit yield and average fruit weight as well as between fruit yield and fruit length. In addition, plant length and fruit length correlated with average fruit weight. There was also a significant correlation between cavity size and yield and average fruit weight (Table 2). We also found a significant correlation between fruit yield and fruit number per plant and also between fruit yield and average fruit weight. Therefore, fruit number per plant and average fruit weight can be considered as an important criterion for future selection programs. Early maturity showed a positive correlation with plant length, branches number and fruit weight. By contrast negative correlation was found between early maturity and soluble solid content and skin pattern [10]. Cluster analysis based on all traits has divided populations into four groups. The first group consist of Shadgan, Sooski, Chah-Paliz, Jajoo and Bandi and corresponding purified genotypes. The second group consist of Ananas and Akila genotypes. The third group consist of native and purified Dargazi and Khaghani and native Khatooni genotypes. The purified Khatooni was classified in the fourth group alone (Figure 1). Cluster analysis based on fruit yield has divided the genotypes in three groups. Native genotypes such as Shadgan, Paliz, Sooski, Khaghani, Ananas and Akila and purified genotypes such as Sooski and Shadgan were classified in the first group. In the second group, native genotypes such as Jajoo, Khatooni and Dargazi and purified genotype such as Paliz and Khaghani were classified. Purified Paliz, Jajoo, Dargazi and Bandi were placed in the third group (Figure 2). Cluster analysis basedon sugar content has divided the genotypes into four groups. The Ananas, Akila, Khatooni and purified Sooski, Shadgan, Khaghani, Paliz and Bandi were classified in the first group. The second group consist of Jajoo, Shadgan, Bandi, Paliz, Khaghani and Sooski. The third group consist of purified Dargazi and Khatooni and finally purified Paliz was placed in the fourth group (Figure 3). Factor analysis has divided the genotypes into four factors, which cover 81% of variations in melon genotypes. The first factor consists of yield, fruit weight, plant and fruit length, sugar percentage, fruit length and cavity diameter covered 37% of the variations.

According to cluster analysis based on all traits, melon genotypes were divided into six groups. The first group consist of native and purified Shadgan, native and purified Sooski and native and purified Paliz. The second group consist of native and purified Jajoo and native and purified Bandi. The thord group consist of Ananas and Akila. The fourth group consist of native and purified Dargazi. Th fifth group consist of native Khatooni and native and purified Khaghani. The purified Khatooni was placed in the sixth group. Cluster analysis based on fruit yield (Figure 2) has divided the genotypes in three groups. Native genotypes such as Shadgan, Paliz, Sooski, Khaghani, Ananas and Akila and purified genotypes such as Sooski and Shadgan were classified in the first group. In the second group, native genotypes such as Jajoo, Khatooni and Dargazi and purified genotype such as Paliz and Khaghani were classified. Purified Paliz, Jajoo, Dargazi and Bandi were placed in the third group (Figure 2).Cluster analysis based on sugar content has divided the genotypes into four groups. The Ananas, Akila, Khatooni and purified Sooski, Shadgan, Khaghani, Paliz and Bandi were classified in the first group. The second group consist of Jajoo, Shadgan, Bandi, Paliz, Khaghani and Sooski. The third group consist of purified Dargazi and Khatooni and finally purified Paliz was placed in the fourth group (Figure 3).

Factor analysis indicated that studied traits represent 81% of variations in melon genotypes and are palced in four main components. The first factor consists of yield, fruit weight, plant and fruit length, sugar percentage, fruit length and cavity diameter, covering 37% of the variations. Fruit number and flesh thickness were placed in the second component, covering 21% of the variations. Skin thickness was placed in the third component, covering 13% of the variations and fruit width as the fourth component covered 10% of the variations.

DISCUSSION

Increase in final fruit yield in superior populations depends on fruit number per plant and average fruit weight [10]. It has been reported that selection methods can be used to improve agronomic traits (fruit size, maturity time, seed size, fruit number per plant and soluble solid content) in melon in different populations [28]. The results indicated that plant length was slightly affected by purification. There was lees difference observed between genotypes in terms of plant length.Evaluating melon genotypes during several mass selection cycles indicated that qualitative and quantitative traits (average fruit weight, fruit number per plant, maturity time and sugar percentage) would improve in these populations [17]. The current study indicated that selection and purification have a positive impact on most of the traits in melon genotypes. Khatooni genotype, which is native to Khorasan-Razavi Province and is cultivated in 90% of the Province's field, showed the best performance compared with other genotypes.

It has been reported that traits such as early maturity, fruit size, flesh thickness, soluble solid content, seed size and fruit number per plant have an increasing effect [28]. Thus, it can be expected that selection based methods could be used to improve above mentioned traits in melon populations. In previous correlation studies, it has been noted that there is a positive correlation between fruit yield and fruit number, average fruit weight, leaves number on main stem, stem length, internode length and frit shape [26]. Fruit length significantly correlates with yield, fruit weight and fruit number. In addition, there is a high correlation between flesh weight and yield, average fruit weight and fruit length [29]. Studying on Khorasan-Razavi's genotypes revealed that there is a high level of diversity between them. The results demonstrated that there is positive correlation between fruit length and sugar content as well as between fruit weight and fruit length, fruit diameter, flesh thickness, skin thickness and sugar content. There was negative correlation found between fruit length and cavity width [30].

CONCLUSION

Genotypes in terms of yield, average fruit weight and number of fruits per plant, sugar content, fruit length and diameter showed significant differences meat. Khatooni melon, which is the country's primary function and characteristics of genotypes was better.The results indicated that the selection and purification of the melon can be effective in improving agronomic traits and yield of melon**.** This method can also be implemented in other populations melon and be considered in breeding programs. This study showed that genotypes of the melon has a high diversity of morphological characteristics areand this variation can be used to enhance desired traits in a high yielding varieties. It can also be purified with the masses, suitable for different areas selected.

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