



Assessment of Melon Genetic Diversity Based on Fruit Phenotypic Traits and Flowering Habits

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ABSTRACT

Understanding genetic diversity and germplasm classification are the keys for selection of right parents for breeding purposes. In the present study, the genetic diversity and classification of 45 Iranian and 15 foreign melons were evaluated. A greenhouse experiment was laid out as a randomized completely block design with three replications and five plants in each replicates. Fruit number had a positive correlation with female flower numbers, fruit number, and fruit yield. The fruit number, however, correlated negatively with the leaf area. Genotypes with monoicous flowering habit produced female flowers in lower nodes and formed longer fruit. The number of the female flower, fruit number, yield, high total soluble solids (TSS), leaf area, the first node of female appearance, and flesh firmness were amongst the high weighted and more coefficient in the component analysis. For the breeding purpose, all accessions of cluster 4 were andromonoecious and obtained high TSS, leaf area, and flesh firmness. From the first three clusters, 11 accessions were monoecious, which belonged to TN-93-5, TN 92100, TN 921071, TN 922025 (Cluster1), FLTM 27, and FLTM35 (Cluster2), TN921026, TN-94-21, TN- 94-44, TN-94-28, and TN-94-3 (Cluster3). The characteristic of cluster 3 included melons with high female flower and fruit number and fewer number of the first node of female flower. In conclusion, good genetic resources and foreign types for selection are available for improving the breeding of melons based on the evaluated traits.

Introduction

The study of genetic diversity and rescue germplasm is important not only for the organization and conservation of plant material but also for the heterosis and the production of hybrid seed and tolerance to biological and abiotic stresses (Fabriki et al., 2009; Staub et al. 2004). Increasing genetic

diversity with a major concern in jeopardizing destroying germplasm plants is vital due to hybrid seeds (Zargar Shooshtari et al. 2020). Genetic variability of the species and breeders' skills choice are important for the selection in breeding plans. Among the methods of morphological marker, molecular, and biochemical methods, are the most important features for plant improvement (Escribano and Lázaro, 2009; Gazafrodi, 2008; Nasrabadi,

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2012; Szamosi et al. 2009; Adhikari et al. 2018; Kandel et al. 2018).

Cucumis melo L. ($2n=2x=24$) has been cultivated in various geographical areas of Iran from historical times. Iran is one of the main origins of this melon group (Munger and Robinson, 1991) and has the third world rank of production quantity (FAO, 2018). It is recorded that melon was cultivated in Iran about 3000 years B.C. (Walters, 1989). In Iran's ancient culture, dried fruits have been an important and valuable source of providing sugar to the people. It has been well documented that Iran has an important place for the melon gene pool. Throughout ancient history and ample evidence, melon is a well-known fruit that recognized among people (Pitrat, 2008).

More than half of the produced vegetables in Iran belongs to cucurbits. There are five known melon groups, including 'Kharboze,' 'Talebi,' 'Garmak,' 'Dastanbou,' and 'Khiarchanbar' (in Persian word). According to the classification proposed by Pitrat et al. (2000), characters of 'Talebi,' 'Garmak,' 'Dastanbou' and 'Khiarchanbar' belong to the cantalupensis, reticulates, dudaim, and flexuosus, respectively. However, 'Kharboze' (inodorus type of Iranian accessions) is the most known melon fruit in Iran. "Kharboze" is the common name of a group of melons that have been cultivated in different parts of Iran. "Khatouni" (*Cucumis melo* var. *inodorus*) is the most famous cultivated group of melons, which is produced in Iran during the warm season (Pourranjbari Saghaiesh et al. 2018). Hence, determining the distribution of genetic relationships between popular and commercial Iranian melon accessions and foreign accessions could improve the proficiency of melon genetics in Iran (Danesh et al. 2015).

Melons have a high polymorphism in a leaf shape, flower sex, plant habits, and fruit morphology traits for their size, shape, color, texture, and flavor. Pourranjbari et al. (2018) and Obando U. et al. (2009) subdivided melon species into the eight groups: Agrestist (wild

melon), Flexuous (snake melon), Conomon (pickling melon), Cantalupensis (Cantaloupe or musk melon), Inodorous (winter melon, honeydew, casaba), Chito (mango melon), and Momordica (phoot or snap-melon). Darrudi (2018) reported that between 21 accession of *Cucurbita pepo* there is a significant positive correlation between fruit weight, fruit flesh thickness, fruit cavity diameter, seed length, seed width, and seed weight. However, there is a negative correlation between fruit weight and seed weight in 11 accessions of *Cucurbita moschata*. Interestingly, it is evidenced that there is a positive association between TSS and fruit flesh thickness, fruit weight, and fruit yield. From the genetic diversity of Iranian melons, ten morphological markers including fruit shape, immature primary color fruit, the main color of flesh, fruit ribbing, days to first mature fruit, average fruit weight per bush, skin thickness, total soluble solids, and flesh thickness were related to plant growth habits (Maleki et al. 2018).

Bartaula, et al. (2019) concluded that characteristics such as weight per fruit, days of germination, number of flowers, and days to flowering had high genotypic coefficients of variation. Phenotypic coefficient of variation and heritability and high genetic advance could be used effectively in the crop enhancement program's selection process. As fruit diameter is positively and highly correlated with fruit yield, selection for this trait might enhance grain yield. Days to flowering had a highly significant negative correlation with fruit yield, and selected accessions with fewer days to flowering may result in improved fruit yield.

The first and main step in a genetic resource is morphological description (Obando et al. 2007). Geographical and climate changes induce variation in morphology and adaption mechanisms of melon germplasm (Pourranjbari Saghaiesh et al. 2018). Therefore, evaluating and classifying local and foreign melon groups help conserve the

valuable germplasm and use them to introduce the superior accession and breeding program. The current study aimed to investigate the key information of different melon groups based on their fruit traits and flowering habits for selecting a breeding plan.

Material and methods

Plant material

Sixty melon accessions included 45 Iranian germplasm, and 15 common foreign types were used in this project. The information of the melon populations used in this study is illustrated in Table 1.

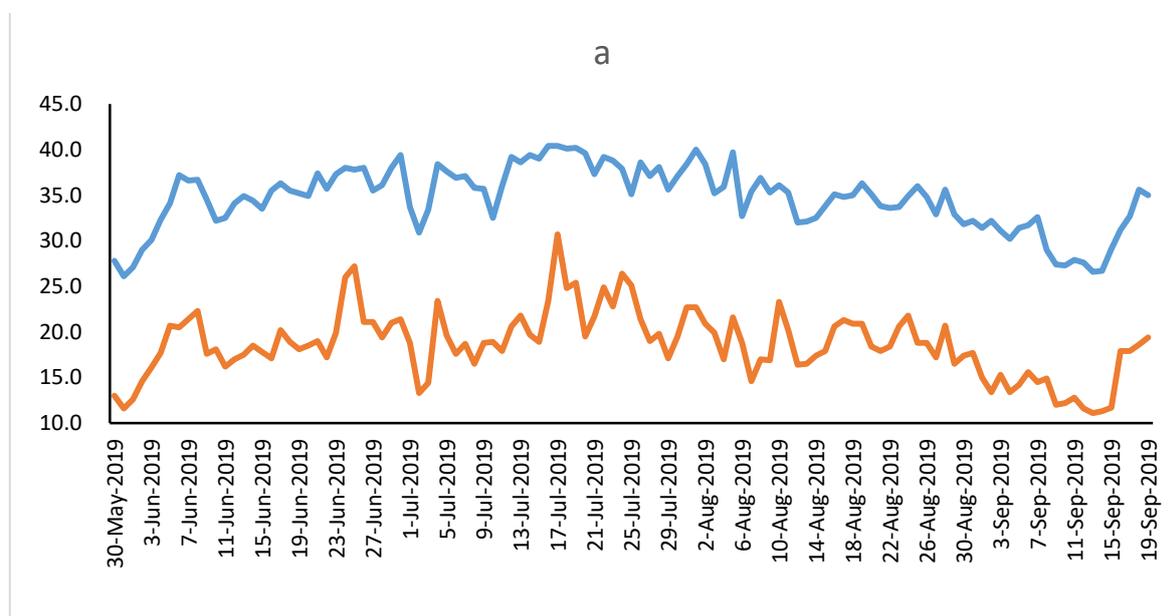
Table 1. Characteristics of the evaluated melon accessions that were used in this study. Accessions with TN code number obtained from gene bank of Seed and Plant Research Improvement Institute of Iran, with FLT code from Falat Iranian Seed Company and the rest collected by research team.

NO	Code or local name	Origin	Horticultural group	No	Code or local name	Origin	Horticultural group
1	Khatouni	Neishabur	Var. <i>Inodorus</i>	31	Till	Khorasan	Var. <i>Cantalupensis</i>
2	TN-93-8246	Abadan	Var. <i>Inodorus</i> (<i>Garmak</i>)	32	Isfahan	Isfahan	Var. <i>Inodorus</i> (<i>Garmak</i>)
3	TN-93-486	Sistan	Var. <i>Cantalupensis</i>	33	TN 92-2025	Khorasan	Var. <i>Inodorus</i> (<i>Garmak</i>)
4	TN-94-21	Fars	Var. <i>Flexuosus</i>	34	TN-93-7224	Kerman	Var. <i>Inodorus</i>
5	TN-94-44	Sistan	Var. <i>Flexuosus</i>	35	TN-92-1026	Bushehr	Var. <i>Inodorus</i>
6	TN-94-28	Khorasan	Var. <i>Flexuosus</i>	36	TN- 82- 126	Fars	Var. <i>Cantalupensis</i>
7	KC-3571	Sistan	Var. <i>Inodorous</i>	37	TN 92-2015	Fars	Var. <i>Inodorus</i> (<i>Garmak</i>)
8	Atashbar	Miyaneh	Var. <i>Cantalupensis</i>	38	Atashbar	Miyaneh	Var. <i>Cantalupensis</i>
9	Ardakan	Yazd	Var. <i>Inodorus</i>	39	Zangabadi	Kerman	Var. <i>Dudaim</i>
10	Bojnurd	North Khorasan	Var. <i>Cantalupensis</i>	40	Izabel	Spain	Var. <i>Cantalupensis</i>
11	Chegherche	Kermanshah	Var. <i>Inodorus</i>	41	Charentais	France	Var. <i>Cantalupensis</i>
12	KC-357033	Khorasan	Var. <i>Inodorus</i>	42	Japan	Japan	Var. <i>Cantalupensis</i>
13	Kangavar	Kermanshah	Var. <i>Dudaim</i>	43	Italy	Italy	Var. <i>Cantalupensis</i>
14	TN-93-5	Karaj	Var. <i>Inodorous</i>	44	FLTM1008	Spain	Var. <i>Cantalupensis</i>
15	Abadan	Khuzestan	Var. <i>Dudaim</i>	45	FLTM 35	Spain	Var. <i>Cantalupensis</i>
16	TN-92-1012	Esfahan, Iran	Var. <i>Inodor</i> <i>us</i> (<i>Garmak</i>)	46	FLT708	Spain	Var. <i>Cantalupensis</i>
17	TN-94-3	Fars	Var. <i>Flexuosus</i>	47	Niagara	Spain	Var. <i>Cantalupensis</i>
18	TN-92-100	Esfahan	Var. <i>Inodorus</i> (<i>Garmak</i>)	48	FLTM655	Spain	Var. <i>Cantalupensis</i>
19	TN-92-82	Ahvaz	Var. <i>Cantalupensis</i>	49	FLTM27	Spain	Var. <i>Cantalupensis</i>
20	Tabas	South Khorasan	Var. <i>Cantalupensis</i>	50	FLTM4605	Spain	Var. <i>Cantalupensis</i>
21	Jarjoo	Gorgan	Var. <i>Cantalupensis</i>	51	FLTM79	Italy	Var. <i>Cantalupensis</i>
22	dastan	Yazd	Var. <i>Cantalupensis</i>	52	FLTM 32	Italy	Var. <i>Cantalupensis</i>
23	TN-93-741	Khorasan	Var. <i>Cantalupensis</i>	53	FLTM9003	Spain	Var. <i>Cantalupensis</i>
24	TN-93-7024	Fars	Var. <i>Inodorus</i>	54	Souski	Semnan	Var. <i>Inodorus</i>

NO	Code or local name	Origin	Horticultural group	No	Code or local name	Origin	Horticultural group
25	Miyaneh	East Azerbaijan	Var. <i>Cantalupensis</i>	55	Jafa	France	Var. <i>Cantalupensis</i>
26	TN-92-1071	Birjand	Var. <i>Cantalupensis</i>	56	TN-93-7520	Bushehr	Var. <i>Inodorus (Garmak)</i>
27	Samsouri	Varamin	Var. <i>Reticulatus</i>	57	Tashkandi	Khorasan	Var. <i>Inodorus</i>
28	TN-92-105	Fars	Var. <i>Cantalupensis</i>	58	Atrak	Gorgan	Var. <i>Inodorus</i>
29	Varamin	Tehran	Var. <i>Cantalupensis</i>	59	Majdi	Khorasan	Var. <i>Cantalupensis</i>
30	Meybod	Yazd	Var. <i>Dudaim</i>	60	Eyvanaki	Semnan	Var. <i>Inodorus</i>

Accession with TN code number was obtained from the gene bank of Seed and Plant Research Improvement Institute of Iran. FLT code obtained from Falat Iranian Seed Company and the research team collected others. The experiment was conducted in summer 2019 in the Research Station of Horticultural Science, University of Tehran. Soil analysis revealed loam texture (pH 8.36 and EC 1.55 ds/m) with 37%, 37%, and 26%

sand, silt, and clay, respectively. Irrigation water characterized with pH of 7.58, EC of 0.55 ds/m, TDS 352 mg/L. The minimum and maximum levels of air temperature, relative air humidity, and an average of soil layers temperature at the surface, 5, 10, 20, 30, 50, 100 cm, and daily duration of the sunshine hour for the growing season are shown in Figure 1a, b, c, and d, respectively.



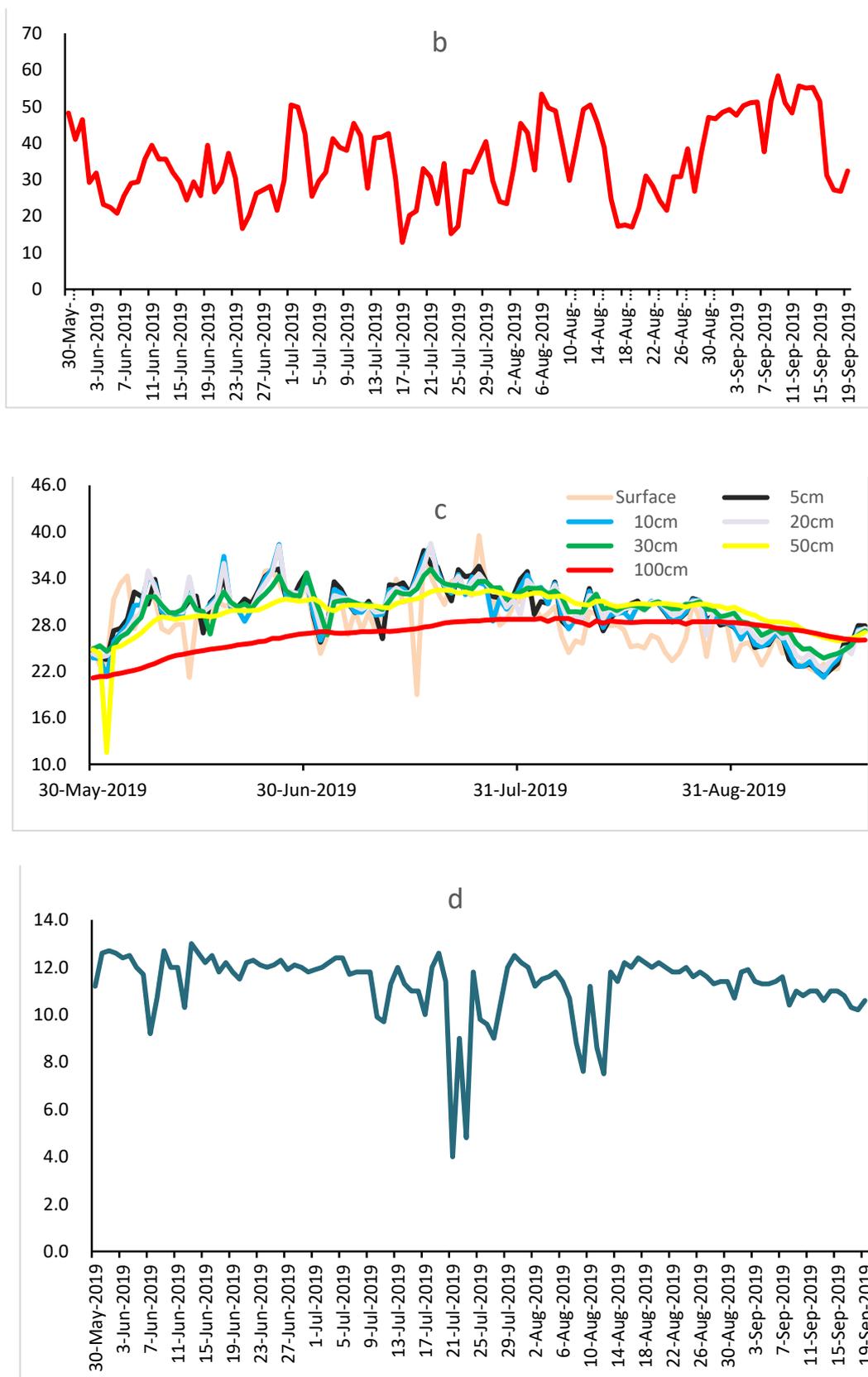


Fig. 1. The minimum and maximum of air temperatures (°C) (a), relative air humidity (%) (b), average of soil layers' temperature (surface, 5, 10, 20, 30, 50, 100 cm) (°C) (c), and daily duration of sunshine (hr) (d).

The average minimum and maximum temperatures were 6 and 32.8 °C, respectively.

Furthermore, the Iranian collected population is illustrated in Figure 2.

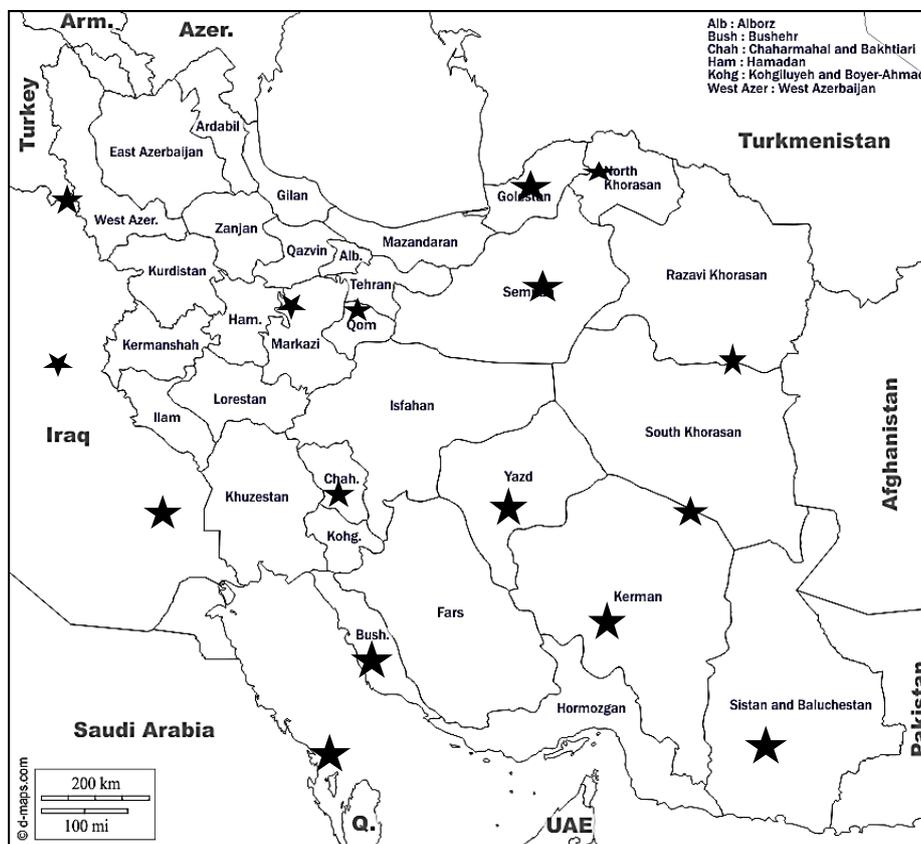


Fig. 2. Collected areas for studied accessions which have been shown on map ("With permission, base map from <https://d-maps.com>").

Study design

The experiment was laid out as Randomized Complete Block Design with three replications, and five plants per replicate. Therefore, there were 15 plants in total for each cultivated accession. The plants were sown in rows that were distanced 1.5 m with 1 m within rows. Measurements of morphological characters were based on three randomly selected plants in each replication. Pesticide and insecticide were applied when needed.

Morphological traits

Traits were recorded based on instructions of melon IPGRI (International Plant Genetic Resources Instit., 2003). Traits included first node female flower appearance, number of female flowers, flowering habits, number of

fruits, average fruit weight, longitudinal diameter of fruits, the transverse diameter of fruits, mesocarp diameter, seed cave diameter, total soluble solid, leaf area, flesh firmness, and fruit yield were investigated. Evaluation of flower traits was performed throughout the growing season, and leaf area was measured using a leaf area meter (Model: DELTA-T DEVICES, Cambridge, UK) in the middle of the growing season. At harvest, the solid soluble content of fruit juice was measured using a refractometer. Flesh firmness was determined using a penetrometer device (Model: TA. XT, PLUS).

Data analysis

Statistical analysis of physiological and morphological data was carried out with SPSS

version 22 software. A principal component method, based on a correlation matrix was used for the factor analysis.

Results

Mean comparison by the least significant difference test method at the 1% probability

level showed that the traits had significant differences among all studied accessions (Table 2). Component analysis is presented in Table 3 and Table 3-1. Results showed that Kangavar from group Dudaim (Cluster3) had the highest fruit number and the lowest fruit mean weight and mesocarp diameter.

Table 2. Analysis of variance for studied traits of 60 melon accessions.

S.O.V	df	First node female	Female number	Fruit number	Fruit mean weight (gr)	Yield (gr)	Fruit longitudinal(cm)	Fruit transverse diameter(cm)
Block	2	2.236	9.465	0.718	890276.675	24063487.009	1.446	2.621
Accession	59	29.701**	180.972**	24.047**	1756536.54**	82613726.311**	376.159**	14.939**
Error	118	1.044	6.530	0.802	363533.648	20308990.093	6.452	1.195

Using the least significant difference test values at $< .05$ and < 0.01 represented as * and ** respectively.

Table 2. 1. Continued

S.O.V	Df	Mesocarp diameter	Seed cave diameter	TSS	Firmness	Leaf area	Flowering habit
Block	2	0.194	0.955	0.315	0.661	28080623.637**	0.006*
Accession	59	1.483**	7.462**	15.656**	20.380**	1024570366.769**	0.431**
Error	118	0.131	0.503	0.368	0.431	8720472.786	0.006

Using the least significant difference test values at $< .05$ and < 0.01 represented as * and ** respectively.

TN92100 (var. *inodorous*- cluster 1), TN93741 (var. *cantalupensis*- cluster1), TN 937024 (var. *inodorous*- cluster2), TN921071 (var. *cantalupensis*- cluster1) and TN 922025 (Var. *Inodorous*-cluster1) had the lowest fruit number. The highest fruit number, seed cave, and leaf area were obtained for Samsouri (var. *reticulatus*- cluster2), also TN921071 (var. *cantalupensis*- cluster 1) had a wide seed cave. Furthermore, the lowest seed cave results, TSS, first node number for female flower appearance, and yield were observed from var. *dudaim* (Zangabadi- cluster3). The highest TSS, number of female flowers, and flesh firmness were obtained in the cantaloupe group (FLTM655-cluster3, TN921071- cluster1, FLTM655- cluster 3, FLTM4605- cluster 4, respectively). Additionally, Charentais (var. *cantalupensis* in cluster1) and FLTM 27(cluster3) showed the lowest firmness and leaf area. At last, the lowest female number was obtained in var. *cantalupensis* (TN93741-cluster1) and var. *inodorous* (TN92100- cluster 1) with the same mean number (5.33). The information about the population of 60 melon accessions can help to select and find a better accession based on the dendrogram classification distance, component analysis for main factors, and means comparison of the traits for specific breeding purposes.

Table 3. Means comparison of fruit attributes of melon accessions and flowering habit.

NO	Code or local name	First node female	Female number	fruit number	fruit mean weight (gr)	yield (gr)	fruit Longitudinal	Fruit Transverse diameter(cm)	Mesocarp diameter	Seed cave diameter	TSS	Firmness	Leaf area	Flowering Habit ^d
1	Khatouni	6.33	12.33	7.11	2128.00	12674.7*	33.33	14.26	3.83	5.37*	11.83*	9.43*	52317.33*	1
2	TN-93-8246	8.67*	18.00	3.67	1510.00	5494.00	16.60	13.50	3.90	6.17	6.33	7.33	63196.67*	1
3	TN-93-486	8.33*	10.33	2.67	751.00	2022.67	14.00*	13.70	2.93*	6.43	10.33	5.17*	39953.33	1
4	TN-94-21	4.67	14.33	2.67	3119.3*	8143.67*	49.00	11.58	2.20*	6.60	6.17*	4.97*	40824.00*	2
5	TN-94-44	6.00	14.00	2.33	3733.3*	8703.33*	68.03	11.43	2.70*	5.97*	5.83*	5.00*	45726.00*	2
6	TN-94-28	5.33	16.67	2.67	3078.67	7955.00*	51.87	11.20	2.67*	7.40	6.00*	4.10*	45716.00*	2
7	KC-3571	5.33	7.67	1.67	1744.33	2832.67	19.20*	15.93*	3.33	8.37	8.67*	7.03	57735.33*	1
8	Atashbar	7.00*	15.67	1.67	1534.67	2459.33	17.83	11.70	3.40	7.83	7.83	6.87	49537.67*	1
9	Ardekani	3.67	10.67	1.33	2092.67	2680.67	19.37	11.87	2.87*	7.67	10.67*	8.40	66323.33*	1
10	Bojnurd	5.67	8.33	1.67	1486.33	2440.00	15.97	14.47	4.13	9.13*	8.17*	8.17	31963.00*	1
11	Chegherche	7.33	7.33	1.67	1213.67	2005.00	16.57*	10.73*	2.27*	7.77	7.17*	6.17	32294.00	1
12	KC-357033	4.67	10.33	1.67	2739.33	4437.00*	24.37	13.33	3.23	8.60	9.33*	8.00	47122.67*	1
13	Kangavar	4.67*	31.3*	14.0*	124.00*	1675.67	9.80*	7.07*	1.03*	6.27	6.33*	5.03*	25362.67*	1
14	TN-93-5	10.67*	6.33	1.33	1298.67	1677.67	16.97	12.13	2.87*	7.83	8.33	7.93	62836.00*	2
15	Abadan	5.33	11.33	7.22	1468.33	9893.88	17.50	15.56*	4.55*	7.47	11.33*	7.10	38340.33*	1
16	TN-92-1012	9.33*	9.67	2.33	911.33	2072.00	12.83	13.00	3.23	6.97	7.50*	5.67*	44108.00	1
17	TN-94-3	6.33	10.33	2.00	3115.7*	6231.33*	52.10	11.33	2.03*	9.07	5.83*	3.07*	38104.00	2
18	TN-92-100	12.33*	5.33	1.00*	2414.33	2414.33*	38.73	13.23	3.33	7.40	5.33*	4.30*	60617.00*	2
19	TN-92-82	4.33*	18.00	2.67*	1605.33	4302.33	15.03	14.67	4.53*	8.80	9.17*	2.80*	27860.33*	1
20	Tabas	6.33	9.33	1.33	2859.6*	3708.67*	29.67	13.57	3.93	8.23	9.17*	7.80	41165.00	1
21	Jarjoo	7.67*	9.67	2.33	2640.67	6135.33*	23.17	11.50	3.30	6.83	7.13*	8.67*	41711.33	1
22	dastan	11.33*	9.33	1.67	1988.33	3181.00	18.13	13.30	3.97	6.57	10.17	8.43	50728.67*	1
23	TN-93-741	13.00*	5.33	1.00*	2599.33	2599.33*	24.57	13.67	2.97	9.73*	7.17*	4.07*	48896.33*	1
24	TN-93-7024	9.33	8.33	1.00	1759.00	1759.00	16.47	12.73	3.77	8.30	7.83*	5.77	49860.33*	1
25	Miyaneh	8.67	9.33	1.67	1957.67	3171.67	18.57*	16.00	3.50	9.13*	8.83*	3.03*	65583.00*	1
26	TN-92-1071	13.33*	6.67	1.00	1632.33	1632.33	15.00*	16.07*	3.17	10.63	8.17*	4.30*	38432.00*	2
27	Samsouri	4.67	14.33	2.33	1732.00	3986.00	17.70	15.57	3.03	10.63*	8.17*	2.93*	75166.67*	1
28	TN-92-105	9.00*	9.67	1.33	2231.00	2932.67	19.80	15.53	3.97	9.67*	10.33	4.67*	52621.33*	1
29	Varamin	4.67	14.67	2.67	1509.67	3996.00	13.87	14.23	2.73*	10.47*	9.67*	3.77*	49300.33*	1
30	Meybod	11.67*	13.0*	4.67	984.00	4699.33	12.10*	10.17*	2.90*	5.23*	9.50*	8.33	73816.67*	1

* The mean difference is significant at the 0.01 level (using the least significant difference test).
a:1&2 related to andromonoecious and monoecious respectively.

Table 3.1 Continued

31	Till	9.67*	12.33	2.67	1186.33	3173.67	13.80	12.20	3.03	6.80	9.50*	2.97*	34245.67	1
32	Isfahan	8.33*	12.33	1.67	1675.33	2643.33	16.93	13.47	2.80*	9.53*	10.00*	5.23*	56924.00*	1
33	TN 92-2025	10.0*	5.67	1.00*	1836.33	1836.33	16.53	12.10	3.03	8.90	7.00*	6.20	54689.67*	2
34	TN937224	8.33	7.67	1.67	2146.33*	3500.67*	19.47	13.90	2.70*	8.10	7.67*	6.93	46326.67*	1
35	TN921026	10.33*	8.67	2.67	2081.00	5362.67	19.80	15.53	3.97	9.67*	10.33	4.03*	30834.00*	2
36	TN 82 126	5.67*	16.33*	5.67	852.67	4766.67	11.43*	9.10*	3.13	5.27*	8.33*	4.70*	41516.67	1
37	TN 922015	9.67*	10.33	1.33	1721.33	2279.67	17.67	13.57	3.90	8.83	5.83*	8.50	30377.67*	1
38	Atashbar Miyaneh	7.67	10.33	3.33	991.00	3256.67	13.37	11.97	3.17	7.03	8.50	4.93	50846.67	1
39	Zangabadi	1.33*	27.00*	8.00*	1139.0*	1117.33*	3.90*	5.03*	1.70*	3.47*	5.00*	3.03*	48924.00*	1
40	Izabel	4.00*	17.33	3.67*	1165.00	4283.33	11.49	12.14	3.03	7.63	10.67	8.27	61409.33*	1
41	Charente	3.33	15.67	3.67	958.33	3475.33	13.97	12.57	3.93	5.30*	10.50	2.57*	38027.67	1
42	Japan	2.67*	16.67	3.33	1334.00	4445.33	13.53	12.63	4.10	5.37*	11.33	8.97*	38571.00	1
43	Italy	4.00	13.67	2.67	2216.33	5899.67*	31.83*	8.17*	2.67*	5.23*	5.67*	8.90*	31199.33*	1
44	FLTM1008	3.00*	25.33*	5.67	1875.00	10574.00	18.25	14.31	3.32	7.04	10.08	6.76	10948.67*	1
45	FLTM 35	2.33*	20.50*	7.67*	1560.67	11563.67	16.96	12.69	3.35	6.10	10.75	8.22	11652.00*	2
46	FLT708	2.33*	25.50*	3.67	1911.33	6871.33	19.42	15.70	3.95	6.42	12.58	11.90*	11897.00*	1
47	Niyagara	3.00*	28.83*	4.67*	1641.33	7538.67	14.21	14.37	2.89*	9.29*	8.74*	7.23	12624.66*	1
48	FLTM655	3.33*	39.33*	8.33	3225.00*	2607.67*	11.21*	10.59*	2.79*	5.51*	14.47*	10.92	8109.00*	1
49	FLTM27	2.00*	32.67*	5.33*	1354.67	7206.33	12.98	13.26	3.34	6.63	9.83*	7.53	7047.33*	2
50	FLTM4605	2.00*	22.83	3.33*	2102.67	6763.33*	21.45	14.35	3.64	7.06	13.05*	12.69*	9168.66*	1
51	FLTM79	2.33*	23.67*	4.33*	1102.67	4763.00	16.19	12.34	3.10	6.70	13.64*	9.40*	9380.33*	1
52	FLTM 32	3.67*	30.83*	7.00	1146.33*	7981.33	16.02	11.98	2.85*	6.41	9.00*	7.49	10896.00*	1
53	FLTM9003	1.67*	26.50*	4.67	3675.00*	17241.67*	26.43*	17.13*	3.99	7.92	13.39*	12.23*	18281.00*	1
54	Souski	3.33*	17.67*	7.67*	2449.07	18955.3*	16.36	11.99	2.44*	6.09	11.07	9.85*	24151.67*	1
55	Jafa	2.67*	15.67*	14.00*	1880.00	25385.3*	23.72*	17.08*	5.24*	7.43	9.97*	10.87*	10572.00*	1
56	TN937521	3.33*	22.00*	8.33*	1788.07	14871.0*	17.25	12.52*	4.28	6.42	12.73*	12.24*	11843.67*	1
57	Tashkandi	6.40*	10.70*	6.80	1388.00	9438.40*	24.54*	10.80*	2.64*	4.77*	12.30	8.40	51218.77*	1
58	Atrak	7.42*	11.82*	4.45	1612.00	7173.40	17.21	14.03	3.04	7.77	7.80*	5.67*	45412.20*	1
59	Majidi	4.33	8.33	3.46	1357.00	4695.22	16.82	12.55	2.78*	6.30	6.75*	6.37	31268.66*	1
60	Eyyanaki	5.84	11.36	3.82	1700.00	6494.00*	20.64	13.38	2.88*	6.75	9.00*	7.68	10752.2*	1

* The mean difference is significant at the 0.01 level (using the least significant difference test).

Correlation assay

Correlations coefficients between the traits are presented in Table 4. Measurement of correlations coefficients of traits indicate the indirect prediction of other related traits. Also, it helps with identifying the most important quantitative features to recognize and describe the population. In the current study, a high correlation with an acceptable significant level was observed. The first node of female flower appearance was positively correlated with leaf area and flowering habit (Table 4).

In contrast, negative correlations between the number of female flowers and fruit number and yield were detected. Female flower numbers correlated with fruit number and fruit yield but interestingly showed a negative

relation with leaf area. In regards to fruit traits, we found positive correlations between fruit mesocarp diameter and seed cave and TSS content. Khatouni, as the most popular melon in Iran with high fruit firmness and total soluble solids content, possesses a large seed cave. Fruit weight showed a positive relation with flowering habit and fruit diameter where TSS correlated with firmness. Accessions with monoicous flowering habits showed a lower TSS level and longer fruit shapes formed from female flowers in lower nodes. Understanding the correlation between various characters will help to distinguish the most important quantitative features for recognizing and general descriptions of the population.

Table 4. The correlation coefficient between studied traits in 60 studied melon accessions.

	First node female flower	Female flower number	Fruit number	Fruit mean weight	Yield	Fruit longitudinal	Fruit transverse diameter	Mesocarp diameter	Seed cavity diameter	TSS	Firmness	Leaf area	Flowering habit
First node female flower	1.000												
Female flower number	-0.701**	1.000											
Fruit number	-0.516**	0.625**	1.000										
Fruit mean weight	-0.037	-0.048	-0.236*	1.000									
Yield	-0.470**	0.488**	0.645**	0.409	1.000								
Fruit longitudinal	0.046	-0.213	-0.209	0.733**	0.152	1.000							
Fruit transverse diameter	0.110	-0.218*	-0.230*	0.210	0.154	0.012	1.000						
Mesocarp diameter	0.000	-0.123	-0.043	0.070	0.230*	-0.105	0.684**	1.000					
Seed cavity diameter	0.365**	-0.385**	-0.499**	0.184	-0.280*	0.026	0.610**	0.169	1.000				
TSS	-0.383**	0.379*	0.293*	-0.010	0.493**	-0.309**	0.359**	0.406**	-0.128	1.000			
Firmness	-0.389**	0.338*	0.322**	0.173	0.552**	-0.086	0.130	0.320**	-0.309**	0.579**	1.000		
Leaf area	0.558**	-0.622**	-0.480**	-0.035	-0.519**	0.088	-0.073	-0.137	0.204	-0.376**	-0.446**	1.000	
Flowering habit	0.217*	-0.129	-0.181	0.312**	-0.038	0.515**	-0.028	-0.175	0.142	-0.309**	-0.257*	0.028	1.000

*, and **: significant at the 5% and 1% levels probability, respectively.

Factor analysis

Factor analysis for the 60 accessions in the current study was performed and results are presented in Table 5. Three main factors with the total variance and the percentage of each factor's traits were identified. The first factor included female flower number, fruit number, yield (g), TSS, firmness of the first female node, and leaf area, which had significant correlation (Table 4). Fruit transverse diameter, mesocarp diameter, and seed cave diameter were identified as the second factor. The third factor consisted of average fruit weight (g), fruit diameter (cm), and flowering habit. The traits including female number, fruit number, yield (g), TSS, leaf area, first node female, and firmness can be used for evaluation and identification of population.

Cluster analysis

The heat map of 60 accessions is presented in Figure 3. The map displays the relationship between melon populations and can be used to identify cluster group errors. The heat map can assist to visualize the possibility (Lee and

Sonnhammer, 2003) and co-expression patterns (Ritschel et al., 2004). The closer distances among different populations are indicated by the orange and red colors. Distant populations are identified in yellow and ranged between -4 to 4. The heat map confirmed the accuracy of the cluster group's results.

According to the dendrogram (Fig. 3), four main groups were identified in which the first group belonged to nine accessions of *Cantalupensis*, 7 accessions of *Inodorus*, and one accession of *Dudaim*. The minimum range of female flower numbers, yield, and firmness belonged to the group 1. In contrast, group 2 had the highest significant rate of fruit diameter, seed cave, fruit transverse diameter, and average weight, whereas mesocarp and leaf area were in the lowest significant rate group. Group 2 consisted of one accession of *Reticulatus*, 4 accessions of *flexuous*, 7 accessions of *Inodorus*, and 9 accessions of *cantaloupensis*. Fruit numbers and TSS not only demonstrated the lowest range, but TSS had the lowest range for group 2.

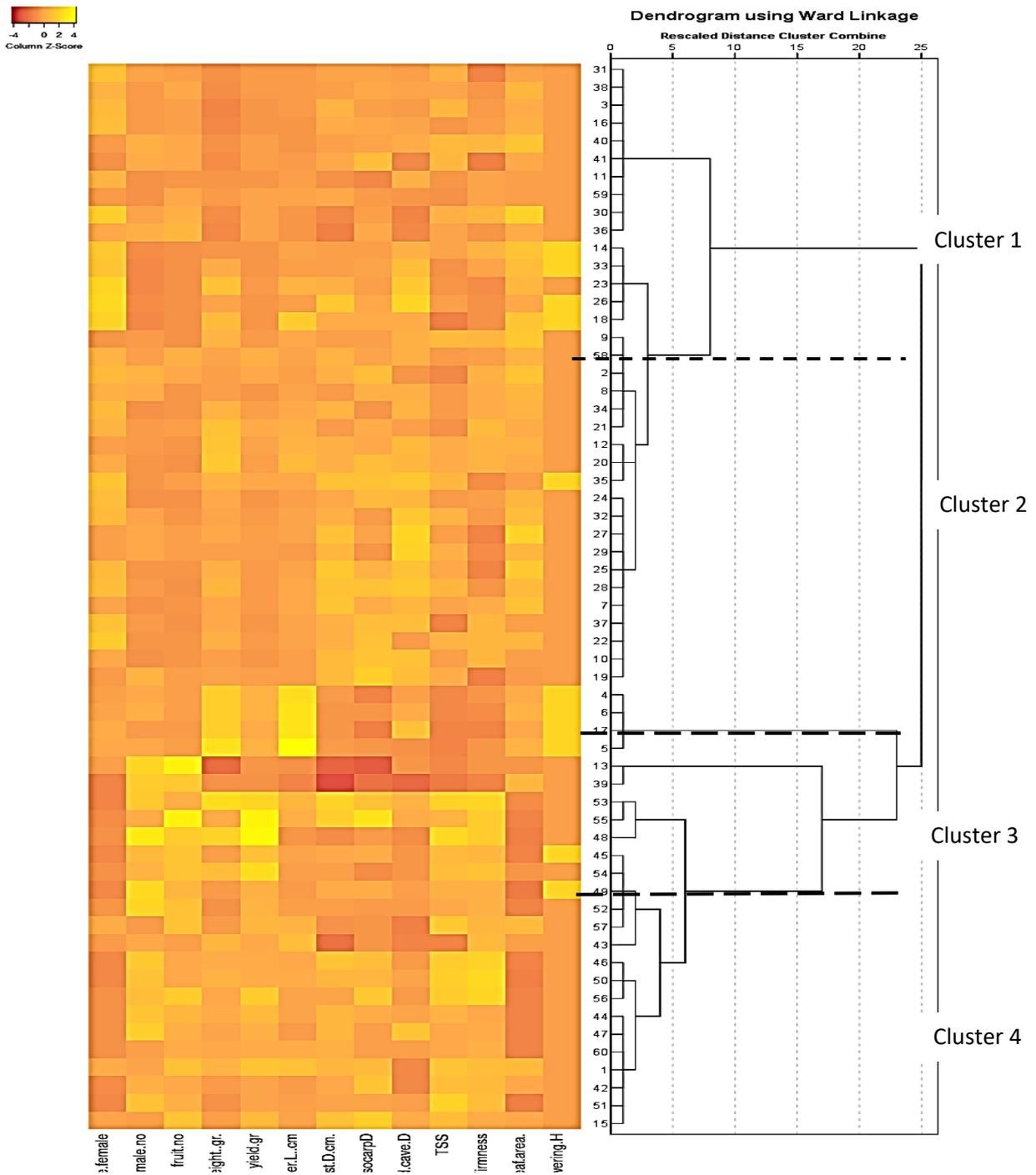


Fig. 3. Heat map of the morphological traits measured for melon accessions. Orange and yellow colors represent reduced and augmented representation levels, respectively. Hierarchical clustering of samples and traits are also shown.

Traits which contributed to the first factor scattered in cluster one and two (Table 5). These traits with high weighted and more coefficient in the component analysis therefore, should be specifically considered. As shown in Figure 2, cluster 3 consisted of 1

accession of Inodorus, 2 accessions of Dudaim, and 5 accessions of cantaloupe. In comparison with other clusters, cluster 3 had maximum rate in female number, yield, and fruit number. The lowest number of first node females, fruit transverse diameter, and fruit

diameter were noticeable. Also, it can be concluded that smaller seed cave size is a character that should be considered for seed breeding programs.

Cluster 4 contained 1 accession of Dudaim, 4 accessions of Inodorous, and 8 accessions of cantaloupe which had the highest rate in mesocarp, leaf area, TSS, and firmness. In

regards to sex expression, all accessions in cluster 4 were andromonoecious. Four accessions which were monoecious (TN-93-5, TN 92100, TN 921071, TN 922025 placed in Cluster1 and FLTM 27, FLTM 35 as forgings hybrids placed in cluster 2 close to accessions from Iran including TN-92 1026, TN-94-21, TN- 94-44, TN-94-28 and TN-94-3).

Table 5. Principal component analysis and variables contribution on each factor of morphological traits in the studied melon accessions. Values in bold show the most relevant characters (>0.5) that contributed to the variation of the components.

Variables	PC1	PC.2	PC.3
First node female	-0.781	0.082	0.049
Female number	0.805	-0.205	-0.130
Fruit number	0.764	-0.226	-0.212
Fruit mean weight	0.117	0.248	0.865
Yield	0.807	0.238	0.283
Fruit diameter(length)	-0.059	-0.075	0.915
Fruit transverse diameter	-0.105	0.915	0.078
Mesocarp	0.093	0.821	-0.102
Seed cave diameter	-0.542	0.519	0.140
TSS	0.575	0.533	-0.265
Firmness	0.664	0.354	-0.035
Leaf area	-0.739	-0.110	-0.010
Flowering habit	-0.185	-0.179	0.669
%variance	32.119	18.902	17.581
Cumulative variance%	32.119	51.02	68.602

Stepwise regression analysis and Pearson correlation

Regression analysis was used to identify the

role of variables on yield as independent variable (Table 6).

Table 6. Stepwise regression analysis for yield as the dependent variable and other characteristics as independent variables for 60 melon studied accessions.

Phase	r	r ²	Adjustment r	Regression parameter	T	Standard Error
1	0.560	0.313	0.309	Intercept	-1.360	0.56
				fruit mean weight	9.012**	
2	0.877	0.769	0.767	Intercept	-13.591**	0.732
				fruit mean weight	19.649**	
				fruit number	18.705**	
3	0.911	0.830	0.827	Intercept	-12.531**	0.926
				fruit mean weight	22.966**	
				fruit number	20.749**	
				fruit diameter(length)	-7.938**	

Phase	r	r ²	Adjustment r	Regression parameter	T	Standard Error
4	0.917	0.841	0.838	Intercept	-10.303**	
				fruit mean weight	21.211**	0.878
				fruit number	20.272**	0.647
				fruit diameter(Length)	-6.067**	-0.259
				TSS	3.526**	0.119
5	0.921	0.848	0.843	Intercept	-4.724**	
				fruit mean weight	21.552**	0.907
				fruit number	17.865**	0.610
				fruit diameter(Length)	-6.625**	-0.285
				TSS	3.188**	0.107
6	0.924	0.854	0.849	Seed cave diameter	-2.669**	-0.091
				Intercept	-5.235**	
				fruit mean weight	21.757**	0.899
				fruit number	18.397**	0.619
				fruit diameter(Length)	-6.970**	-0.296
				TSS	1.554	0.058
				Seed cave diameter	-3.859**	-0.158
Fruit transverse diameter	2.831**	0.117				
7	0.923	0.852	0.848	Intercept	-5.078**	
				fruit mean weight	23.021**	0.917
				fruit number	18.779**	0.627
				fruit diameter(Length)	-8.308**	-0.323
				Seed cave diameter	-4.749**	-0.182
				Fruit transverse diameter	4.005**	0.146

*, and **: significant at the 5% and 1%.

The traits were entered into regression step by step. The results showed that fruit mean weight, fruit number, fruit diameter (length), seed cave diameter, and fruit transverse diameter were included in the regression model, but other traits were removed from the models since they had no significant effect on yield. In step 2, fruit number was added to the model. Fruit diameter (length), TSS, seed cave diameter, and fruit transverse diameter were added in steps 3, 4, 5, and 6, respectively. The phase 6 had great impact on yield (85.4%). TSS variable removed from model 7. Based on results in current study, yield improvement of melon fruit can be achieved by indirect selection through fruit mean weight, fruit number, fruit diameter (length), seed cave diameter, and fruit transverse diameter. The final regression analysis model (which represents standardized regression or path

analysis) is presented as:

$$Y = 6.46 X_1 + 1403.72 X_2 - 196.06 X_3 - 658.75 X_4 + 247.73 X_5 - 6116.18$$

$$R^2 = 0.8613 \quad (1)$$

$$\text{Adj R-sq} = 0.8513$$

In Equation (1), Y is yield, X_1 is fruit mean weight, X_2 is fruit number, X_3 is Fruit diameter (length), X_4 is seed cave diameter, X_5 is fruit transverse diameter, are coefficients of determination and Adj R-sq is adjusted coefficient of determination.

To achieve a clear relationships of various component characters in yield, Pearson correlation was used for a better explanation of direct and indirect effects of studied features (Table 7).

Table 7. Direct and indirect effects of characteristics based on Pearson correlation of studied traits parameters of 60 melon accessions.

Pearson Correlation	Yield	First node female flower	Female flower number	Fruit number	Fruit mean weight	Fruit diameter (length)	Fruit transverse diameter	Mesocarp diameter	Seed cave diameter	TSS	Firmness	Leaf area	Flowering habit
Yield	1.000												
First node female flower	-0.376**	1.000											
Female flower number	0.409**	-0.661**	1.000										
fruit number	0.516**	-0.485**	0.633**	1.000									
Fruit mean weight	0.560**	-0.004	-0.074	-0.247**	1.000								
Fruit diameter(length)	0.105	0.043	-0.206**	-0.237**	0.630**	1.000							
Fruit transverse diameter	0.117	0.103	-0.195*	-0.268**	0.277**	0.037	1.000						
Mesocarp diameter	0.148*	0.018	-0.113	-0.105	0.118	-0.094	0.627**	1.000					
Seed cave diameter	-0.179**	0.334**	-0.363**	-0.434**	0.220**	0.036	0.574**	0.194	1.000				
TSS	0.364**	-0.360**	0.358**	0.210*	0.036	-0.300**	0.316**	0.353**	-0.118	1.000			
Firmness	0.420**	-0.369**	0.317**	0.270**	0.162*	-0.088	0.128*	0.286**	-0.278**	0.554**	1.000		
Leaf area	-0.440**	0.529**	-0.592**	-0.491**	-0.039	0.085	-0.066	-0.142*	0.191**	-0.365**	-0.433**	1.000	
Flowering H	-0.022	0.252**	-0.204*	-0.178	0.284**	0.546**	-0.020	-0.152*	0.154*	-0.325**	-0.270**	0.079	1.000

*, and **, significant at the 5% and 1%.

Under these circumstances, yield had significant positive correlation between firmness, TSS, mesocarp diameter, fruit mean weight, fruit number and female flower number. Leaf area, seed cavity diameter, first node female flower had negative correlation with yield. Fruit number showed positive significant direct effect and seed cavity diameter had negative indirect effect on yield.

Discussion

In this evaluation a positive correlation was observed between fruit mesocarp diameter with seed cavity and TSS content, however, Naserabadi et al. (2012) based on morphological variation of different Iranian melon accessions reported significant negative relation in fruit length and seed cavity. Genetic diversity and interrelationship among Indian and exotic melons based on fruit morphology, quality components showed that there were significant differences in fruit weight, fruits per vine, yield per plant, flesh thickness, fruit shape index, and total soluble solids (Singh et al., 2020). This result is in line with our observation. Interestingly negative correlation between leaf area and yield was observed. As Castellanos and her research team (2011) declared, the vegetative growth rate decreased and reached to the plateau level when the maximum yield was achieved. Also Aslani et al. (2020) reported negative correlation between the leaf area index and the net assimilation rate, no significant difference in the net assimilation rate between different sink/source ratios which declare that the excess leaf area index does not contribute to increase in the assimilate production and total yield. However, Cargnelutti et al. (2020) reported that cultivars with a greater number of leaves and a larger leaf area are associated with higher yield.

In a study on population structure, morphological and genetic diversity within and among melon landraces in Iran, it was shown that all of the Iranian Inodorus

genotypes exhibit different shapes of fruits, lowest values of TSS and flesh thickness (Maleki et al., 2018). In contrast, 4 Iranian inodorous varieties of cluster 4 (Khatouni, Eyvanaki, TN-93-7520 and Tashkandi) showed highest TSS and firmness and Samsouri from Reticulatus genotypes showed the lowest firmness, which are in accordance with Hatami et al. (2016) results.

In another study among melon landraces (*Cucumis melo* L.) from Greece and other melon germplasm of diverse origins, all Flexuosus accessions were monoecious, and inodorus group and cantalupensis accessions were andromonoecious (Staub et al., 2004). In our germplasm, 4 accessions of cluster 1, 2 accessions of cluster 2 and 5 accessions of cluster 3 were monoecious that belonged to Flexuosus and also Cantalupensis groups. The importance of sex flower expression of being monoecious can be pointed out that emasculation is not needed in the breeding program. It is evident from previous studies that differentiation between group Inodorous and Cantaloupe is impossible due to their genetic similarities. Findings obtained from current study are highly in concert with the findings of previous studies (Bagherian et al., 2013; Feyzian E. et al., 2007; Lopez-Sese et al., 2003; Monforte et al., 2003). In contrary to our findings, Yildiz et al. (2011) and Sensoy et al. (2007) observed a difference between the accessions of the Inodorus and Cantalupensis groups. Comparing cluster 2 and cluster 3 showed that Dudaim was separated from Flexuosus which is based on the report of Soltani et al. (2010). Munger (1991) reported that the Reticulatus group is generally dissimilar to the Cantalupensis group in having a netted area. Based on UPGMA cluster analysis of Maleki et al. (2018), 'Talebi' genotype is classified as Reticulatus group. Further, Ritschel et al. (2004) based on the Robinson and Decker-Walters offered that Reticulatus group should be part of the Cantalupensis group which have

been also seen in the classification of our clusters. Yield and quality in melon crops are important parameters for selection. A direct positive correlation between marketable yield, length and diameter of fruit size, pericarp thickness, total number of fruit per plant, and number of marketable fruit per plant has been reported (Boitshepo et al., 2020). Another study on correlation and path coefficient analysis in muskmelon reported positive associations of vine length with number of branches per vine, number of fruit per vine, fruit cavity length, and fruit yield and pulp thickness with fruit diameter, fruit cavity width, and rind thickness (Reddy et al. 2017).

Conclusion

Cucumis melo L. has rich germplasm and wide genetic diversity. The morphological diversification of accessions in female flower number, fruit number, first female node, TSS and firmness, confirms the importance of these features for hybridization program and breeding. Fruit attributes have the most important role in distinguishing genetic relationship and high yield value. Yield is a complex trait which is affected directly and indirectly by other traits. In this study high yield was correlated to fruit mean weight, fruit number and fruit transverse diameter while fruit longitudinal diameter and seed cave diameter had indirect effect. Monoecious flowering habits expressed in some Inodorous, Cantaloupensis and Flexuous groups, originated from Iran could be proper accessions for sex expression studies and as main trait for melon crop breeding programs. Through heat map analysis, there were no differences among Inodorous, Cantaloupensis and Dudaim groups. Reticulates and Flexuous groups showed genetic similarities and tended to be one group with inodorous and Cantaloupensis but they were separated from Dudaim groups.

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