Review Article

Ekin
Journal of Crop Breeding and Genetics

3(1):12-18, 2017

www.ekinjournal.com

Ekin International biannual peer-reviewed journal

Characterization of Some Agronomic Traits and β-Carotene Contents of Orange Fleshed Altinbas Melon Dihaploid Lines

Munevver GOCMEN[1] Ersin AYDIN[2] İsmail SIMSEK[1] Nebahat SARI[2]

İlknur SOLMAZ[2] Ayhan GOKSEVEN[2]

[1] Antalya Tarim, Antalya, Turkey
[2] Çukurova University Faculty of Agriculture, Department of Horticulture, Adana, Turkey

* Corresponding author e-mail: nesari@cu.edu.tr

Citation:
Gocmen M., Aydin E., Simsek I., Sari N., Solmaz I., Gokseven A., 2017. Characterization of Some Agronomic Traits and β-Carotene Contents of Orange Fleshed Altinbas Melon Dihaploid Lines. Ekin J. 3(1):12-18.

Received: 01.11.2016 ***Accepted: 15.12.2016*** ***Published Online: 29.01.2017*** ***Printed: 31.01.2017***

ABSTRACT

The objective of this presented study was to characterize orange fleshed Altinbas melon dihaploid lines that we developed in a breeding program. The study was conducted in greenhouse condition in Antalya, Turkey. The DH lines were developed by irradiated pollen technique and morphologically characterized according to modified UPOV descriptor list for 63 characters. Sixteen quantitative characters (3 seedling, 2 plant, 3 leaf, 8 fruit) were also measured. Cluster analysis was performed for both qualitative and quantitiative data. According the research results, orange fleshed melon pure lines showed different level of variation in case of morphological characterization as well as fruit traits and β-carotene contents.

Keywords: Melon, dihaploidization, β-carotene, UPOV.

Introduction

Melon (*Cucumis melo* L.; 2n =2x =24) is member of Cucurbitaceae family with high economic value cultivated extensively in tropical and subtropical regions in the world. It is thought to have originated in East Africa and the centre of diversification is in Asia from the Mediterranean Sea to Eastern Asia (Pitrat 2008).

Besides located in the secondary genetic diversity centre (Pitrat *et al*., 1999), Turkey is the second largest melon producer country after China with 1.7 million tons of production on 102000 ha area (Anonymous 2014). It has been reported that Turkey is rich in melon genetic resources and they are morphologically diverse especially for fruit characters (Sari and Solmaz 2007; Sensoy *et al*., 2007; Solmaz *et al*., 2010; Mancak *et al*., 2014). Melon cultivation is intensively carried out particularly in Central Anatolia; Aegean, Southeastern Anatolia and the Mediterranean regions (Yilmaz 2009). In Turkey, winter melons which belongs to *inodorus* group, are commonly produced in Aegean, Central Anatolia and the Mediterranean regions in open field conditions and it is reported that many genotypes grown localy (Solmaz *et al*., 2010). Among these, Altinbas is one of the the most important winter melons. These melons have a yellow rind with black points and stains. Their fruits vary in size (1.5-3 kg). They have white-green, odourless, sweet and firm fruits with long shelf life.

In recent years, melon breeding programs are focused on improving fruit internal quality traits such as high sugar concentration, beta-carotene concentration and nutritional value. Melon includes Vitamin C, A, B9 and potassium. These four components are very important for human health. β-carotene (provitamin A) is the major carotenoid in orange fleshed melons

and important antioxidant agent that strengthen the human immune system. In addition, it reduces the occurrence of cancer, prevents cardio vascular system disorders, cataracts and night blindness (Hodges and Lester 2011). Esteras *et al.,* (2015) reported that beta-carotene is the most abundant carotenoid and the orange color of the fruit flesh from most cantalupensis correlated with the highest levels of beta-carotene.

The aim of this study was to characterize morphologically 30 Altinbas (*Cucumis melo* var. *inodorus*) melon lines developed by dihaploidization technique according to the modified UPOV descriptor list for 63 features and determine their performance for some quantitative traits.

Material and Methods

Thirty orange fleshed Altinbas melon lines and one green fleshed commercial variety (Edali F_1, Verim Ziraat) were used in this study. These DH melon lines (1-3, 3-6-A, 3-21, 4-91, 4-94, 5-2-2, 5-51-2, 5-54, 5-84, 7-25, 7-40, 9-12, 9-13, 9-24, 9-25-2, 9-36-3, 9-38, 9-48, 9-49-3, 9-61, 9-66-2, 10-5-5, 10-45-3, 12-40, 13-38, 13- 58-2, 19-38, 19-45, L and 1) were developed by dihaploidization technique in a project supported by Ministry of Science, Industry and Technology (SANTEZ programme) and carried out by Antalya Tarim Inc. and Çukurova University during 2010 and 2012. The experiment was conducted in glass greenhouse at Experimental Station of Antalya Tarim Inc. β-carotene content of melons was analyzed in West Mediterranean Agricultural Research Institute (BATEM) of the Ministry of Food Agriculture and Livestock.

The seeds of thirty melon lines and control variety (Edali F1) were sown in plastic multipots in the Nursery of Antalya Tarim Inc. on 20 January 2012. Seedling characterizations and measurements of cotyledon length (CL, cm) cotyledon width (CW, cm) and hypocotyl length (HL, mm) were done 3 weeks after sowing in 15 seedlings at the first true leaf stage on 8th February 2012. These measurements were carried out with a ruler or a digital compass (Mitutoyo CD-15D). Fifteen seedlings of each line at 2-3 true leaf stage were transplanted at spacing of 25 cm within rows and 150 cm between rows on 27th February 2012 in glasshouse. Plants were grown hydroponically in perlite medium. Pruning, irrigation, fertilization and pesticide application were conducted regularly during vegetation period.

Number of nodes on the main stem were counted and leaf blade length (cm), leaf blade width (cm) and petiole length (cm) were measured with a ruler in 10 plants of each line on 25th April 2012. Morphological characterizations were done for 63 characters using a modified UPOV (The International Union for the Protection of New Varieties of Plants) descriptor list at cotyledon, flowering and mature fruit stages. Mature fruits were harvested on 10th, 11th, 13th and 15th June 2012 and four fruits from each line were analyzed. After taking the fruit weight (g); fruit length (cm), fruit diameter (cm), diameter of seed cavity (cm), length of seed cavity (cm), thickness of flesh (cm) were measured with ruler, total soluble solids (%) were analyzed using a hand held refractometer (ATAGO). The β-carotene content of melons (ppm) were determined by spectrophotometric method according to Sasuni and Adebiyi (2009).

For analyzing qualitative and quantitative data, cluster analysis was performed by the unweighted pairgroup method using arithmetic average (UPGMA) method with NTSYS-PC Prograram (Rohlf, 1998).

Results

Thirty orange fleshed melon lines and 1 green fleshed commercial variety (Edali F1) were characterized for morphological characteristics using 63 traits according to UPOV descriptor list. The distribution of the genotypes according to observed characters were given in %.

According to the observations in seedlings, hypocotyl length was observed as medium in 30 lines (96.8%) and long in 1 line (3.2%). Great diversity was found among the accessions regarding cotyledon size, 1 (3.2%) line had very small, 3 (9.7%) lines had small, 21 (67.7%) lines had medium, 4 (12.9%) lines had large and 2 (6.5%) lines had very large cotyledons. The green color of the cotyledons were all (100%) dark.

The number of nodes on the main stem was medium in 23 (74.2%) lines and high in 8 (25.8%) lines. The length of internodes and leaf blade size were observed as medium in all (100%) lines. Green color of leaf blade was dark in most (93.5%) of the lines and medium in the rest (6.5%). Development of the leaf blade lobes was weak in 12 (38.7%) lines, medium in 14 (45.2%) lines and strong in 5 (16.1%) lines. High level of diversity was observed regarding length of the terminal lobes, dentation of margin, undulation of margin and blistering of leaf blade. Attitude of the petiole was semi-errect in 26 (83.9%) lines and horizontal in 5 (16.1%) lines. Regarding petiole length, all (100%) lines had been observed as medium. Considering the sex expression all (100%) lines were found to be andromonoecious.

The ground color of the fruit before maturity was mainly green (90.3%) while grey-green (6.5%) and

white (3.2%) colors were also observed. Intensity of ground color of fruit before maturity was light in 21 (67.7%) lines, medium in 7 (22.6%) lines and dark in 3 (9.7%) lines.

Fruit length and fruit diameter were also quite variable among the lines. Fruit length of the DH lines was observed as short in 4 (12.9%) lines, medium in 21 (67.7%) lines, long in 4 (12.9%) lines and very long in 2 (6.5%) lines. The medium fruit diameter was dominant reaching 71% of all lines, followed by the wide (16.1%) and narrow (12.9%).

Fruit shape showed high diversity among the lines. It was found round in 45.2%, ovate in 9.7%, like-egg in 9.7%, elliptical in 12.9% and flattened-ovate in 22.6% of the lines respectively. Ground color of fruit skin at maturity was white in 3.2% , yellow in 61.3%, yellow-green in 12.9% and green in 22.6% of the lines. Intensity of ground color of skin at maturity was light in 41.9% medium in 32.3% and dark in 25.8% of the lines. Secondary color of skin was present in 21 (67.7%) and absent in 10 (32.3%) lines. The distribution of secondary color of skin was dominantly (95.2%) in dots and in patches. The intensity of the dots and patches were quite variable among the lines. The fruit peduncle length was observed as medium in 30 (96.8%) and short in 1 (3.2%) line. The thickness of fruit peduncle was medium for all (100%) of the lines. Abscission of peduncle was absent in 24 (77.4%) and present in 7 (22.6%) lines. In terms of shape of base and shape of apex of fruits considerable variation was observed. Size of pistil scar was observed as small in 2 (6.5%) lines, medium in 20 (64.5%) lines and large in 9 (29%) lines. Grooves of fruit were absent in 23 and present in 8 of the investigated lines. The width of fruit grooves was narrow in 3 (37.5%) and medium in 5 (62.5%) lines. The depth of the grooves was observed as shallow in 3 (37.5%) and medium in 5 (62.5%) lines. Color of the grooves was green for all (100%) lines. Creasing of surface varied from absent or very week to strong among the lines. Cork formation was present in 8 (25.8%) and absent in 23 (74.2%) of the lines. Thickness of the cork layer, pattern and density of cork formation, showed different level of diversity. Maximum width of outer layer of fruit flesh was thin in 2 (6.5%), medium in 21 (67.7%) and thick in 8 (25.8%) lines. In melon breeding programmes, maximum width of flesh thickness is a desired trait. It was observed to be medium in most of (83.9%) the lines. Regarding main color of flesh orange color was dominant (87.1%), while 3 (9.7%) lines had green and the control variety (Edali F1) had cream flesh. Intensity of main color of flesh was light in 5 (16.1%) lines, medium in 15 (48.4%) lines and dark in 11 (35.5%) lines. In terms of fruit flesh texture in all genotypes (100%) were assessed as grainy. Fruit cavity was full in 17 (54.8%) and medium in 14 (45.2%) lines. Placenta color was observed as highly variable among the lines. Two lines (6.5%) had transparent, 1 (3.2%) line had white, 8 (25.8%) lines had salmon and 20 (64.5%) lines had orange placenta. Considering the number of carpels 10 (32.3%) lines had 3, 20 (64.5%) lines had 4 and 1 (3.2%) line had 5 carpels. Fruit taste was sweet for all lines (100%) and most lines (71%) contained external aroma.

Seed size was medium in 28 (90.3%) lines and large in 3 (9.7%) lines. The shape of hilum end was sharply pointed in all lines. Shape of cross-section of the seed was elliptical in most (96.8%) lines. The seed color was creamy yellow in all lines and the number of seeds were found medium in 21 (71%) and high in 9 (29%) lines.

Means, minimum and maximum values of the seedling, plant, leaf and fruit measurements of 30 DH lines and 1 control variety (Edali F1) are presented in Table 1. Considering hypocotyl length, maximum value (40.64 mm) obtained from Edali F1 while minimum value (17.54 mm) measured in line 3-21. Longest (2.38 cm) cotyledons were determined in line 13-38 and shortest (1.87 cm) in line 9-61. Cotyledon width ranged between 1.32 cm (9-61) and 2.38 cm (Edali F1). Number of internodes on main stem varied between 26 (5-84) and 33 (9-48). Maximum length of internodes on main stem was found 11.42 cm in line 12-40 and the minimum length (7.71 cm) was measured in line 19-45. The longest (16.79 cm) leaf blade was obtained from line 12-40 and the shortest (9.92 cm) from line 9-61. Both for the maximum leaf blade width (19.75 cm) and petiole length (16.75 cm) line 4-94 had the highest values. Control variety Edali F1 was superior than all other lines in terms of fruit weight (3840.42 g), fruit height (22.23 cm), fruit diameter (18.07 cm), length of seed cavity (15.40 cm) and fruit flesh thickness (6.19 cm). Total soluble solid content (SSC) ranged between 6.71% (1-3) and 11.67% (9-49-3). The highest value for the β-carotene content was 38.20 ppm and obtained from 10-45-3, and lowest was 0.47 ppm in green-fleshed Edali F1.

The dendrogram generated by cluster analysis of 63 qualitative characters is presented in Figure 1.

The DH lines were divided into four main clusters. The first cluster (I) included nine lines (7-25, 9-61, 10-45-3, 10-5-5, 7-40, 9-66-2, 9-38, 9-25-2 and 4-91). While line 7-25 was the most distant, line

10-45-3 and 10-5-5 was the most similar lines within this cluster. The second main cluster (II) consisted of 13 lines and Edali F1. Within this cluster green-fleshed Edali F1 formed one individual sub-cluster. Lines 13-38 and 13-58-2 grouped together and showed close relations than any sub-group in the main cluster. The third cluster (III) composed of 7 lines (3-6-A, 9-49-3, 9-13, 9-48, 9-12, 9-24, 9-36-3, 5-84). The fourth cluster (IV) contained only line 1-3 which was the most distant line from other lines.

Based on quantitative data the clustering dendrogram was created and presented in figure 2. The dendrogram was divided into 5 main clusters. While the first cluster (I) consisted of two lines (green-fleshed Edali F1 and line A), the second cluster contained 5 lines (L, 13-38, 19-38, 7-25, 5-84). The third cluster (III) consisted of only 19-45 line. The fourth cluster (IV) included 14 lines, and two main sub-clusters were identified within this cluster. While the first sub-cluster contained lines 9-13, 4-91 and 3-6-A, all other lines in cluster IV were grouped in the second sub-cluster. The fifth cluster (V) was composed of 10 lines and divided into two sub-clusters. Line 9-49-3 was separeted from the other lines and formed the first sub-cluster. The second sub-cluster were divided into new sub-clusters which showed close relations.

Discussion

Thirty Altinbaş DH lines were characterized for morphological traits and high level of diversity was found except green color of the cotyledons, the length of internodes, leaf blade size, petiole length, sex expression, the thickness of fruit peduncle, color of the grooves, fruit texture, fruit taste, shape of hilum end and seed color. Sixteen quantitative characters (3 seedling, 2 plant, 3 leaf, 8 fruit) were also measured and remarkable variation was found among the lines. Our results are compatible with previous studies regarding morphological characterization of melon (Solmaz *et al*., 2004; Sari and Solmaz 2007; Sensoy *et al*., 2007; Lotti *et al*., 2008; Escribano and Lazáro 2009). In a study reported by Szamosi *et al*., (2010), 58 *Cucumis melo* accessions were studied to compare the morphological characteristics of Hungarian and Turkish germplasm. Their results indicated that both Hungarian and Turkish germplasm resources present wide range of diversity for morphological traits for all the traits tested except intensity of green color of cotyledon and color of petals.

Solmaz *et al*., (2010) collected 78 melon accessions from Eastern and Central Anatolia regions of Turkey and characterized them for morphological traits according to the UPOV melon descriptor list. They also measured twenty quantitative characters (3 seedling, 3 plant, 3 leaf, 2 flower, 9 fruit). Results revealed that the Turkish melon accessions have quite diversity for all the traits examined except intensity of green color of cotyledon, attidude of petiole and color of petals. In our study we have obtained more common characters, it was expected because we had characterized DH lines (pure lines) of which all belong to Altinbas (*Cucumis melo* var. *inodorus*) group of melons. The study reported by Killi (2010) also confirmed our results. In this research morphological characterization of 27 Kirkagac and Yuva melon pure melon lines developed by dihaploidization technique were performed for 68 features according to the modified UPOV descriptor. According to the research findings, melon lines showed different level of variation except attidude of petiole, sex expresssion, color of petal, ovary pubescence, intensity of ground color before maturity, fruit diameter, abscission of peduncle, ease of abscission of peduncle, grooves, cork formation, fruit flesh color, fruit taste, color of flesh of outer layer, shape at hilum end and seed shape accessions. It is also stated by Mancak *et al*., (2014), that Kirkagac accessions shared more common characteristics (8 characters) with one another than they did with other accessions.

It can be concluded that different level of variation was obtained among DH Altinbas melon lines in terms of morphological characters. This finding was also supported by the cluster analysis and measurements of quantitative caharacters.

Finally this valuable germplasm must be conserved and used for the future breeding studies of orange fleshed Altinbas melon cultivars.

Acknowledgments

This research was supported by Ministry of Science, Industry and Technology of Turkey (00655-STZ-2010/2). The authors are grateful to Prof. Dr. Sedat Serce and Res. Asist. Berken Cimen for their kind help in statistical analysis.

Table 1. Means, maximum and minimum values of melon lines obtained by 16 quantitative measurements.

Parameters	Mean	Maximum Value	Line	Minimum value	Line
Hypocotyl length (mm)	26.31	40.64	Edali F1	17.54	1-3
Cotyledon length (cm)	3.11	4.13	13-38	1.87	9-61
Cotyledon width (cm)	1.86	2.38	Edali F1	1.32	9-61
Number of internodes on main stem	28.84	33	9-48	26	5-84
Length of internodes (cm)	9.16	11.42	12-40	7.71	19-45
Length of leaf (cm)	13.09	16.79	12-40	9.92	9-61
Width of leaf (cm)	16.84	19.75	4-94	14.35	9-61
Length of petiole (cm)	13.39	16.75	4-94	10.08	9-24
Fruit weight (g)	1168.36	3840.42	Edali F1	354.17	19-45
Length of fruit (cm)	13.38	22.23	Edali F1	9.52	3-6-A
Diameter of fruit (cm)	12.51	18.07	Edali F1	9	19-45
Length of seed cavity (cm)	8.32	15.40	Edali F1	5.67	3-6-A
Diameter of seed cavity (cm)	6.15	8.36	5-84	4.29	19-45
Thickness of flesh (cm)	3.23	6.19	Edali F1	2.48	3-6-A
Total soluble solids (%)	8.92	11.67	9-49-3	6.71	1-3
β-carotene (ppm)	18.65	38.20	10-45-3	0.47	Edali F1

Figure 1. Dendrogram of melon lines obtained from cluster analysis of 63 qualitative agromorphological traits

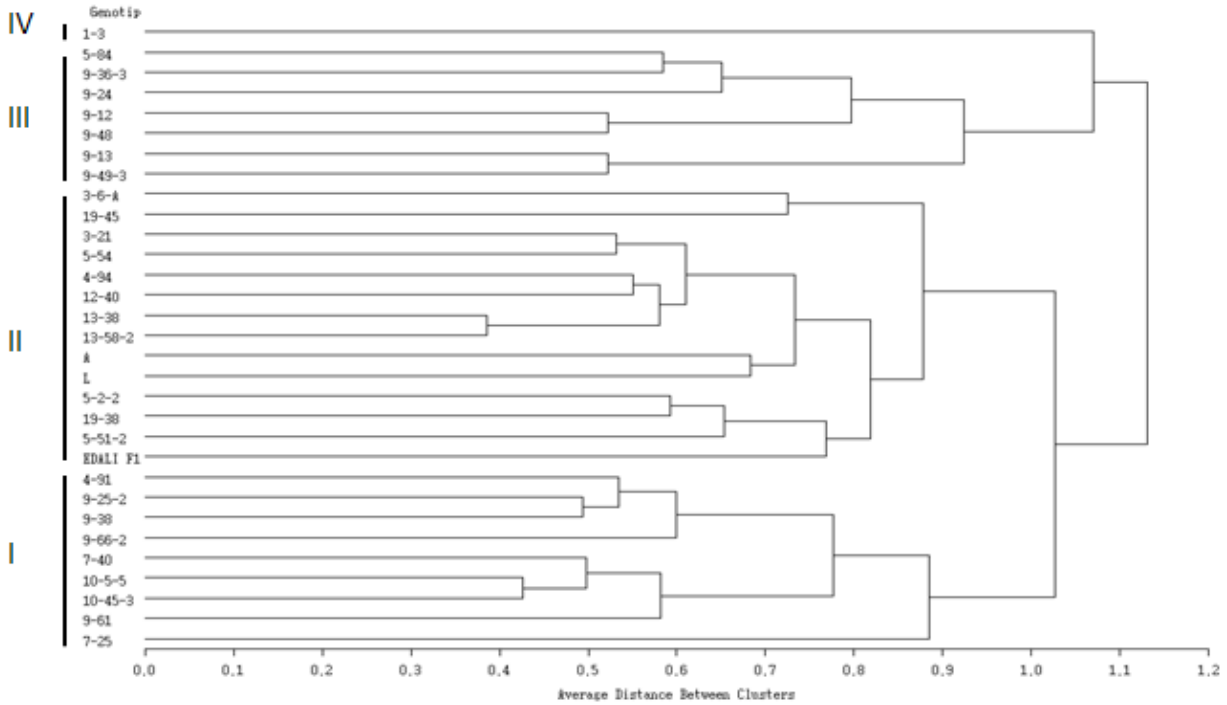
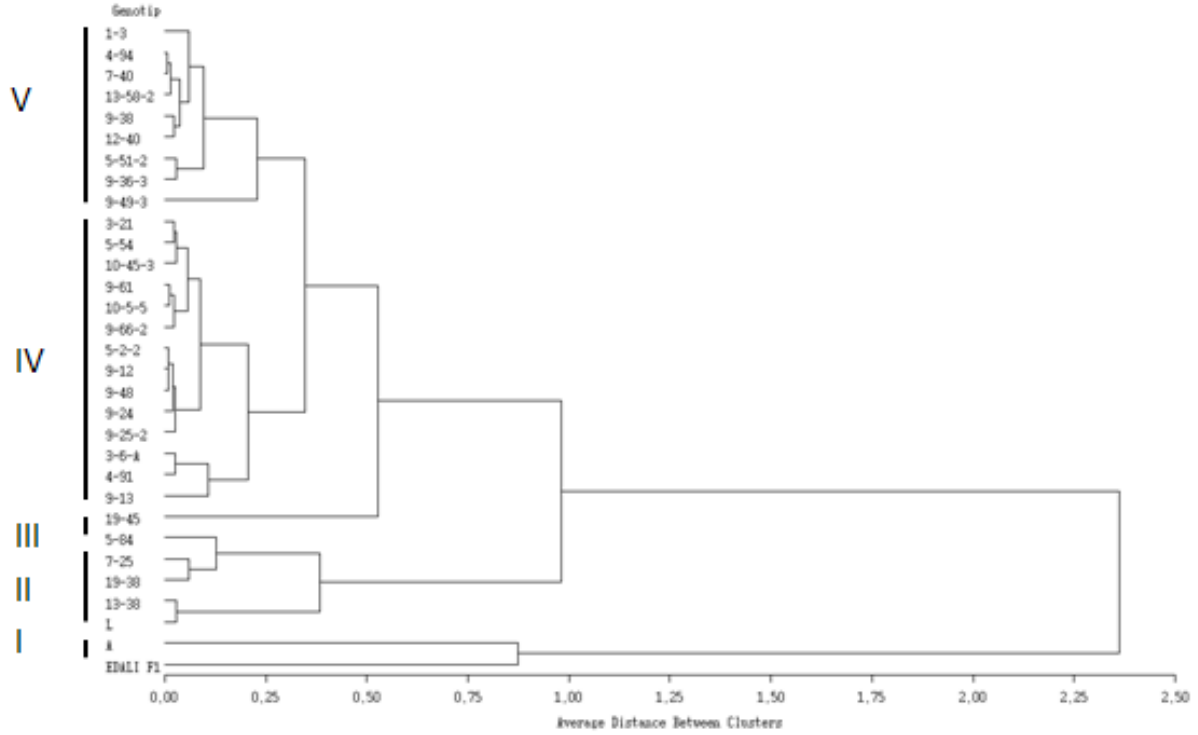


Figure 2. Dendrogram of melon lines obtained from cluster analysis of 16 quantative agromorphological traits



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