

**MORPHOLOGIC AND CYTOPLASMIC ASSESSMENTS OF BULB ONION
(*Allium cepa* L.) LANDRACES**

Esra CEBECI^{1*}, Huseyin PADEM², Ali Fuat GOKCE³

¹Bati Akdeniz Agricultural Research Institute, 07800, Antalya-Turkey

²Isparta University of Applied Sciences, Department of Horticulture, 32260, Isparta- Turkey

³Omer Halisdemir University, Faculty of Agricultural Sciences and Technologies, 51240,
Nigde-Turkey

Cebeci E., H. Padem, A. F. Gokce (2021). *Morphologic and cytoplasmic assessments of bulb onion (*Allium cepa* L.) landraces*. - Genetika, Vol 53, No.1,167 -180.

Today climate change threatens to reduce crop yield and harming the food security. Local landraces have adaptation skills to shifting climatic conditions. Using of this local source in plant breeding programs becoming an alternative strategy. In this study, 97 landraces were collected to initiate the bulb onion breeding program eligible for the current trends. Collected materials were morphologically characterized using 21 descriptors, derived from UPOV (International Union for the Protection of New Varieties of Plants). Clustering which was conducted by the NTSYS (Numerical Taxonomy and Multivariate Analysis System) program using UPGMA (Unweighted Pair Group Method of Arithmetic Averages) method, showed that the genetic similarity rate of the landraces was calculated between 0.06-0.96. Hybrid onion breeding program depends on the cytoplasmic-genic male sterility (CMS) system. Thus, the PCR-markers were applied to identify the cytoplasm types of the landraces. Among landraces N-cytoplasm was found in 78 accessions and S-cytoplasm was found in 19 accessions. At the end of the study, a qualified gene pool has been established consisted of characterized onion genotypes which will might be used in further breeding studies.

Keywords: characterization, CMS, diversity, NTSYS, onion breeding,

Corresponding author: Esra Cebeci, Bati Akdeniz Agricultural Research Institute, 07800, Antalya-Turkey, email; esrac3@hotmail.com, Phone: +90 532 5833701

INTRODUCTION

The genus *Allium* is contained several edible vegetable crops with the great economic importance like onion (*Allium cepa* L.), garlic (*Allium sativum* L.) and leek (*Allium porrum* L.). Compared to the leek and garlic, onion is the most widely cultivated species of this genus. Onion can be consumed dry or green. Dry onions are produced in varied colours and shapes in different cultures. A region of principal diversity for onion was reported as Turkey and the Irano-Turanian floristic area (HANELT, 1990). It has been maintained by using open pollinated populations (OP) since the ancient periods. Generally, growers selected the populations considering the market demand and this behaviour led to the exceptional genetic variations among the onions (BREWSTER, 2008).

Onion flower is composed of hundreds of small flowers thus; emasculation of male organs is not practical in cross-breeding efforts. Benefiting from cytoplasmic-genic male sterility (CMS) in onion breeding was first reported by JONES and CLARKE (1943) and later by BERNINGER (1965). Determination of CMS lines with classical methods is required 4-8 years (HAVEY, 1995; HAVEY, 2000; SHIGYO and KIK, 2008). The identification of male sterile and maintainer lines significantly facilitated via the use of molecular markers. While some markers are distinguishing only Normal (N) and Sterile (S) cytoplasm (HAVEY, 1995; SATO, 1998; VON KOHN *et al.*, 2013) the other markers could distinguish all the three cytoplasm (S, N and T) from each other (ENGELKE *et al.*, 2003; KIM *et al.*, 2009). In T cytoplasm, male sterility can change depend on the temperature fluctuations. Therefore onion breeders mostly prefer to use the S cytoplasm due to stability (HAVEY, 2000).

Local landraces which may be useful under effects of global climate change are the valuable genetic resources for sustainable horticultural facilities. Their diversity can be exploited in breeding programs for the production of new commercial cultivars with targeted traits (PETROPOULOS *et al.*, 2019). Using both morphological and molecular markers together have great potential to explore this genetic diversity. Before start any breeding program, establishment of crop germplasm is a prerequisite for the long-term achievements (GLASZMANN *et al.*, 2010).

The aim of this study was to establish a gene pool to initiate the onion breeding program which was eligible for the current trends. For this reason, at least 30 bulbs of each 97 landraces were collected and characterized. The PCR-based markers developed by SATO (1998) and ENGELKE *et al.*, (2003) were applied to identify the cytoplasm types. At the end, a qualified gene pool which consisted of local genotypes has been established and presented to the use of breeders.

MATERIAL AND METHOD

Plant material

Plant materials were collected by the researchers with the helping of agricultural district offices. Thirty bulbs for each landrace were collected from 33 different cultivation areas (Table 1). Beside 96 local genotypes, a bulb sample from a commercial OP variety ("Janset" belongs to Kafkas Seed Co.) was used as a plant material.

Table 1. Accession number, location name and geographical origin of the onion landraces

N	Acc.	Location	Geographical Origin	No	Acc.	Location	Geographical Origin
1	Y100S	Bolu	40°44'8.99"	N 50	Y149S	Tokat	40°18'50.00"
2	Y101S	Bolu	40°44'8.99"	N 51	Y150S	Tokat	40°18'50.00"
3	Y102S	Bolu	40°44'8.99"	N 52	Y151S	Tokat	40°18'50.00"
4	Y103S	Bolu	40°44'8.99"	N 53	Y152S	Tokat	40°18'50.00"
5	Y104S	Bolu	40°44'8.99"	N 54	Y153S	Tokat	40°18'50.00"
6	Y105S	Burdur	37°43'13.00"	N 55	Y154S	Tokat	40°18'50.00"
7	Y106S	Burdur	37°43'13.00"	N 56	Y155S	Tokat	40°18'50.00"
8	Y107S	Burdur	37°43'13.00"	N 57	Y156S	Ankara	39°55'11.53"
9	Y108S	Burdur	37°43'13.00"	N 58	Y157S	Ankara	39°55'11.53"
10	Y109S	Burdur	37°43'13.00"	N 59	Y158S	Ankara	39°55'11.53"
11	Y110S	Burdur	37°43'13.00"	N 60	Y159S	Ankara	39°55'11.53"
12	Y111S	Bursa	40°11'44.12"	N 61	Y160S	Ankara	39°55'11.53"
13	Y112S	Corum	40°32'56.00"	N 62	Y161S	Ankara	39°55'11.53"
14	Y113S	Corum	40°32'56.00"	N 63	Y162S	Zonguldak	41°26'59.99"
15	Y114S	Diyarbakır	37°54'49.07"	N 64	Y163S	Zonguldak	41°26'59.99"
16	Y115S	Diyarbakır	37°54'49.07"	N 65	Y164S	Karaman	37°10'52.00"
17	Y116S	Diyarbakır	37°54'49.07"	N 66	Y165S	Karaman	37°10'52.00"
18	Y117S	Diyarbakır	37°54'49.07"	N 67	Y166S	Kırıkkale	39°50'59.99"
19	Y118S	Adıyaman	37°45'51.88"	N 68	Y167S	Kırıkkale	39°50'59.99"
20	Y119S	Adıyaman	37°45'51.88"	N 69	Y168S	Sırnak	37°30'50.15"
21	Y120S	Adıyaman	37°45'51.88"	N 70	Y169S	Bartın	41°38'8.99"
22	Y121S	Adıyaman	37°45'51.88"	N 71	Y170S	Adana	37°00'6.01"
23	Y122S	Adıyaman	37°45'51.88"	N 72	Y171S	Adana	37°00'6.01"
24	Y123S	Adıyaman	37°45'51.88"	N 73	Y172S	Adana	37°00'6.01"
25	Y124S	Elazığ	38°40'27.52"	N 74	Y173S	Edirne	41°40'37.88"
26	Y125S	Gaziantep	37°03'33.98"	N 75	Y174S	Edirne	41°40'37.88"
27	Y126S	Gaziantep	37°03'33.98"	N 76	Y175S	Afyon	38°45'24.01"
28	Y127S	Gaziantep	37°03'33.98"	N 77	Y176S	Afyon	38°45'24.01"
29	Y128S	Gaziantep	37°03'33.98"	N 78	Y177S	Afyon	38°45'24.01"
30	Y129S	Istanbul	41°00'44.06"	N 79	Y178S	Bitlis	38°24'4.14"
31	Y130S	Istanbul	41°00'44.06"	N 80	Y179S	ACHRE*	40°39'18.04"
32	Y131S	Istanbul	41°00'44.06"	N 81	Y180S	ACHRE	40°39'18.04"
33	Y132S	Istanbul	41°00'44.06"	N 82	Y181S	ACHRE	40°39'18.04"
34	Y133S	Istanbul	41°00'44.06"	N 83	Y183S	ACHRE	40°39'18.04"
35	Y134S	Kastamonu	41°22'40.98"	N 84	Y184S	Ankara	39°55'11.53"
36	Y135S	Kastamonu	41°22'40.98"	N 85	Y185S	Balıkesir	39°38'57.01"
37	Y136S	Kastamonu	41°22'40.98"	N 86	Y186S	Balıkesir	39°38'57.01"
38	Y137S	Kırklareli	41°44'6.29"	N 87	Y187S	Janset	39°38'57.01"
39	Y138S	Kırklareli	41°44'6.29"	N 88	Y188S	Ankara	39°55'11.53"
40	Y139S	Kırşehir	39°08'44.99"	N 89	Y189S	Konya	37°52'16.86"
41	Y140S	Kırşehir	39°08'44.99"	N 90	Y190S	Konya	37°52'16.86"
42	Y141S	Kırşehir	39°08'44.99"	N 91	Y191S	Hatay	36°25'29.39"
43	Y142S	Konya	37°52'16.86"	N 92	Y192S	Hatay	36°25'29.39"
44	Y143S	Kutahya	39°25'27.01"	N 93	Y193S	Hatay	36°25'29.39"

45	Y144S	Manisa	38°36'43.27"	N	94	Y194S	Hatay	36°25'29.39"	N
46	Y145S	K.maras	37°35'4.92"	N	95	Y195S	Hatay	36°25'29.39"	N
47	Y146S	Mardin	37°18'47.12"	N	96	Y196S	ACHRE	40°39'18.04"	N
48	Y147S	Mardin	37°18'47.12"	N	97	Y197S	Balikesir	39°38'57.01"	N
49	Y148S	Tekirdag	40°58'40.84"	N					

*Ataturk Central Horticultural Research Institute- Yalova/Turkey

Morphological observations

Collected bulbs were morphologically characterized according to 15 descriptors (Table 2) derived from the International Union for the Protection of New Varieties of Plants (UPOV) and stored until the planting season. Bulbs were planted in February 2013 to the open field at a spacing of 15x10 cm. Plants of each genotype were morphologically characterized according to 6 descriptors presented in Table 2. After characterization, each population was isolated separately and left for selfing. Selfed seeds were harvested in July 2013.

Table 2. Descriptors used for characterization and evaluation of onion landraces.

Code	Character	Description
T1	Bulb shape	1=Elliptic, 3=medium ovate, 5=broad elliptic, 7=circular, 9= broad ovate, 11=broad obovate, 13=rhombic, 15=transverse medium elliptic, 17=transverse narrow elliptic
T2	Bulb diameter	Measured
T3	Bulb weight	Measured
T4	Bulb height	Measured
T5	Bulb height/Bulb diameter	Measured
T6	Width of neck	Measured
T7	Bulb shape (in longitudinal section)	1=depressed, 3= flat, 5=slightly raised, 7=rounded, 9=slightly sloping, 11=strongly sloping
T8	Bulb shape of root end	1=depressed, 3=flat, 5=round, 7=weakly tapered, 9=strongly tapered
T9	Coloration of epidermis rings	1=absent, 3=greenish, 5=reddish
T10	Thickness of dry skin	Measured
T11	Colour of dry skin	1=brown, 3=white, 5=red
T12	Thickness of epidermis rings	Measured
T13	Number of growing point	Counted
T14	Dry matter content	Measured
T15	Base colour of bulb flesh	1= light, 2= medium, 3= dark
T16	Foliage waxiness	1= Glossy, 3= semi-glossy, 5= none
T17	Intensity of green colour	1=dark, 3=medium, 5=light, 7=very light
T18	Leaf length (cm)	Measured
T19	Leaf diameter (cm)	Measured
T20	Pseudo stem length (mm)	Measured
T21	Pseudo stem diameter (mm)	Measured

DNA extraction and PCR amplification

Plant samples were taken from the seedlings at 3-4 true leaves stage in 2014 March. For this, 15 plants were randomly selected from each genotype and samples were taken as a bulk. Total mitochondrial DNA was extracted from fresh leaf tissue using Qiagen DNeasy plant mini kit. Primers (Table 3) were used as suggested from SATO (1998) and ENGELKE *et al.* (2003).

PCR was performed using 50 ng of total DNA in a final volume of 20 µl, containing 0.25 µM of each primer, 150 µM of each dNTP. The reaction mixture was incubated in a thermo-cycler for 2 min at 94° C, followed by 40 cycles: 30 s at 94°C, 1 min for annealing, 2 min at 72°C and a final extension for 5 min at 72°C.

PCR products were separated by flatbed electrophoresis using 1.5% agarose gels in 1 x TAE buffer (ENGELKE *et al.*, 2003) and bands were visualized with Kodak Gel Logic 200 Imaging System (Kodak Co., USA). For molecular analysis data, each genotype was identified for each primer based on the presence (1) and absence (0) of bands.

Table 3. Used primers in the study

Primers	Forward Primers (5'-3')	Reverse Primers (3'-5')	Expected Band Size
<i>orfA-501</i>	ATGGCTCGCCTTGAAAGAGAGC	TACCGAGCGGAACTTTCTCTG	473 (Engelke et. al.,2003).
<i>S-cob</i>	GTCCAGTTCCTATAGAACCTATCACT	CTTTTCTATGGTGACAACCTCCTCTT	414 (Sato, 1998).
<i>N-cob</i>	TCTAGATGTCGCATCAGTGGAATCC	CTTTTCTATGGTGACAACCTCCTCTT	180 (Sato, 1998).

Statistical Analysis

Morphological data based genetic similarity dendrogram was examined by the UPGMA (Unweighted pair-group method, arithmetic average) method using the NTSYS software (Numerical Taxonomy and Multivariate Analysis System) pc 2.2 version (ROHLF, 1998). In addition to this, minimum, maximum, mean and standard deviation values of some descriptors (Table 5) and pivot charts (Figure 1) were created in Microsoft Office Excel program (version 2016) for the clarification of the results.

RESULTS AND DISCUSSION

A high morphological diversity among the onion landraces was observed regarding with quantitative and qualitative descriptors used in this study. Some morphological characters of some accessions were presented in Table 4. In terms of bulb shape genotypes described as circular (27), broad obovate (20), rhombic (13), broad elliptic (9), elliptic (8), transverse medium elliptic (6), transverse narrow elliptic (4), medium ovate (3) and broad ovate (3). Regarding the bulb colour of dry skin genotypes grouped as brown (78), white (16) and red (3).

Table 4. Some morphological characters of some accessions (The other data and remaining accessions did not present here to keep the article shorter)

Acces.	T1	T7	T8	T9	T11	T15	T16	T17	Acces.	T1	T7	T8	T9	T11	T15	T16	T17
Y100S	1	2	5	3	1	3	1	5	Y130S	11	3	7	3	1	3	1	1
Y101S	8	3	2	1	1	1	3	5	Y131S	11	3	9	3	1	3	1	1
Y102S	4	3	3	1	1	1	3	3	Y132S	7	5	7	3	1	3	3	1
Y103S	4	3	3	1	1	1	3	5	Y133S	11	9	7	3	1	3	1	1
Y104S	3	3	4	3	1	3	3	5	Y134S	7	9	3	3	1	3	1	1
Y105S	7	2	4	1	3	5	3	3	Y135S	13	7	5	1	1	1	5	3
Y106S	3	5	4	1	3	5	3	3	Y136S	7	7	5	1	1	1	5	3
Y107S	7	4	4	11	3	1	3	5	Y137S	11	9	5	1	1	1	3	3
Y108S	8	2	3	3	3	3	3	3	Y138S	11	5	7	1	1	3	5	5
Y109S	4	2	4	9	3	7	3	3	Y139S	13	5	7	1	1	3	3	3
Y110S	6	2	4	3	1	1	1	1	Y140S	13	5	3	3	1	3	1	1
Y111S	6	2	4	3	1	3	1	1	Y141S	11	7	5	3	1	3	7	3
Y112S	4	3	4	1	1	1	3	5	Y142S	7	5	3	1	1	1	7	3
Y113S	4	4	3	1	1	1	3	5	Y143S	13	7	5	1	1	1	5	5
Y114S	3	4	4	1	1	5	3	3	Y144S	7	5	3	3	1	3	7	5
Y115S	7	3	3	5	5	7	3	3	Y145S	13	9	7	1	5	1	1	1
Y116S	9	1	1	3	1	3	3	5	Y146S	7	7	5	1	1	1	1	1
Y117S	7	3	4	5	5	1	3	3	Y147S	7	5	5	3	1	3	5	5
Y118S	7	2	4	1	1	1	3	5	Y148S	11	5	5	3	1	3	1	1
Y119S	1	5	5	5	5	7	3	1	Y149S	15	3	9	3	1	3	5	5
Y120S	3	3	4	1	1	3	3	5	Y150S	17	3	1	3	1	3	5	3
Y121S	6	2	4	3	1	3	3	3	Y151S	7	3	3	3	1	3	3	3
Y122S	7	3	4	1	1	5	3	5	Y152S	13	5	7	1	1	1	5	7
Y123S	4	3	3	5	5	7	3	3	Y153S	7	5	5	1	1	3	5	1
Y124S	8	2	2	3	1	3	3	1	Y154S	7	7	5	1	1	1	5	1
Y125S	5	3	2	1	1	1	3	1	Y155S	17	5	5	1	1	1	3	5
Y126S	4	3	3	1	1	1	1	3	Y156S	7	3	1	3	1	3	3	3
Y127S	6	4	3	1	1	1	3	5	Y157S	5	5	5	1	1	1	1	1
Y128S	6	2	4	1	1	1	3	1	Y158S	11	7	7	5	5	7	5	5
Y129S	6	2	4	3	1	3	1	1	Y159S	7	3	7	7	5	9	5	5

Abbreviations as in Table 2.

When the waxiness of leaves was considered genotypes defined as glossy (18), semi-glossy (75) and none-glossy (4) (Table 4). ALIMOUSAVI *et al.* (2007) reported that Iranian onion genotypes with glossy leaf were resistant to thrips. According to DAMON *et al.* (2014), semi-

glossy inbred lines were defined to resistant to thrips. Determined genotypes as glossy and semi-glossy in the current study could be used in the further breeding studies to enhance to resistance to some pests. According to intensity of leaves green colour genotypes described as, dark (33), medium (31), light (32) and very light (1) (Table 4). Although intensive cultivation of commercial varieties have led to disappearance of some plant genetic resources (CERICOLA *et al.*, 2013), MUÑOZ-FALCÓN *et al.* (2008) reported that the remaining local genotypes could contribute to enhancing the gene pools.

The pivot table consisted of minimum, maximum, mean and standard deviation values of genotypes using the data of 13 quantitative descriptors were presented in Table 5. Number of growing points of the landraces was ranked between 1-6 and mean was determined as 2.3. Single (31) and two (28) centred genotypes formed as 60.8% of all accessions. As well as onion-processing industries, fresh market also requires single-centred cultivars. However, this trait can be improved through the selection studies as showed in previous studies (WALL *et al.*, 1996; KHOSA *et al.*, 2016). Bulb weight, height and diameter values were found between 14 - 270 g, 3.5 - 16.3 cm and 3.3 - 10.3 cm respectively. Furthermore, mean values of bulb weight, height and diameter were determined as 91.5 g, 6.07 cm and 5.81 cm respectively (Table 4). Major yield determinants of onion are bulb diameter, weight and shape (MCCOLLUM, 1971), and bulb quality is controlled by many factors including number of growing points.

Table 5. Minimum, Maximum, Mean and Standard Deviation values of some descriptors of onion accessions

Descriptor	Minimum	Maximum	Mean	Standard Deviation
Bulb diameter (cm)	3,3	10,3	5,81	0,060
Bulb weight (g)	14	270	91,59	0,944
Bulb height (cm)	3,56	16,3	6,07	0,063
Bulb height/Bulb diameter	0,4	3,7	1,05	0,011
Width of neck (mm)	3	12,78	8,26	0,085
Thickness of dry skin (mm)	0,01	0,12	0,03	0,0001
Thickness of epidermis rings (mm)	1,1	6,6	3,19	0,033
Number of growing point	1	6	2,36	0,024
Dry matter content	6,5	17,5	11,90	0,123
Leaf length (cm)	34,2	73,7	52,41	0,540
Leaf diameter (cm)	0,4	2,85	1,41	0,015
Pseudo stem length (mm)	4,6	77,5	14,36	0,148
Pseudo stem diameter (mm)	10,4	24,48	18,19	0,188

HOSAMANI *et al.* (2010) studied genetic variability of 21 onion genotypes and they stated that average bulb weight of genotypes between 26.67 to 84.00 g. In a previous study, CRAMER (2001) tried to define bulb weights between 249 - 507 g among 23 OP varieties. It was

understood that bulb weight, height and diameter values directly affect the total yield and could change according to consumer and market demands.

Dry matter content of genotypes was detected between 6.5% - 17.5%. The quality of onion cultivars is determined by bulb colour, firmness, number of growing points, neck thickness and dry matter content (BREWSTER, 2008). It was reported that dry matter and pungency are positively correlated to each other but development of less pungent onions with longer storage life (high dry matter content) is still challenging (GALMARINI *et al.* 2001). After observations of significant phenotypic correlations MALLOR *et al.* (2011) reported that larger size and lower soluble solids content cause to milder onion. In the current study, whereas the genotype Y183S has the highest bulb weight (270 g), its dry matter (7.70%) amount was one of the lowest.

In this study pivot charts were also created using excel program and presented in Figure 1 for the better understanding of the results. They showed the some quantitative characters obtained from morphological measurements and their distribution among the landraces mentioned above.

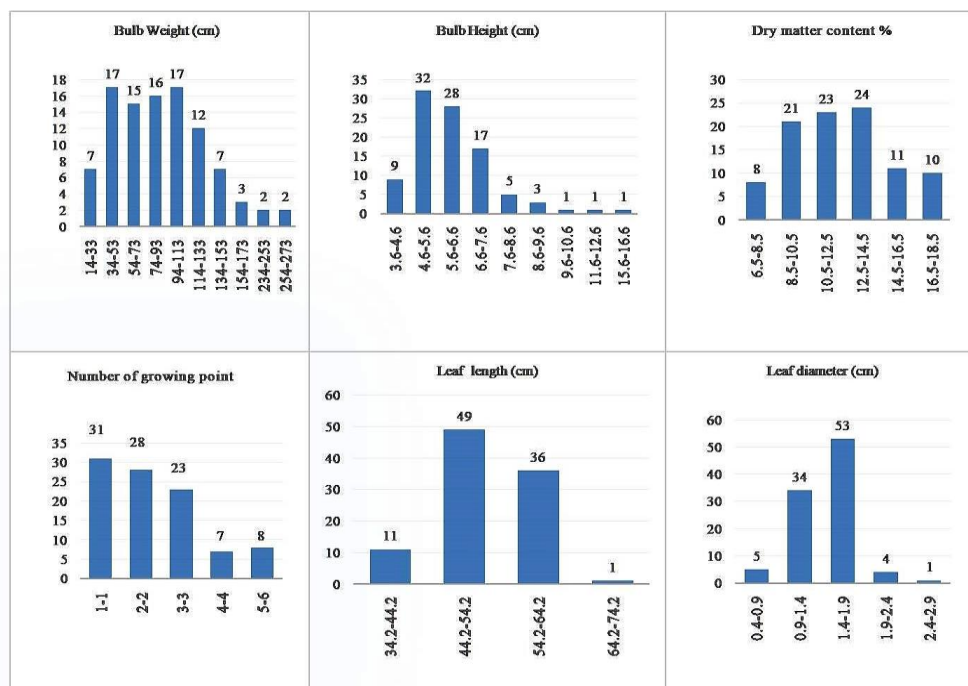


Figure 1. Charts were showed the some quantitative characters obtained from morphological measurements and their distribution among the landraces (horizontal axis: obtained data from the study, vertical axis: number of landraces having these data)

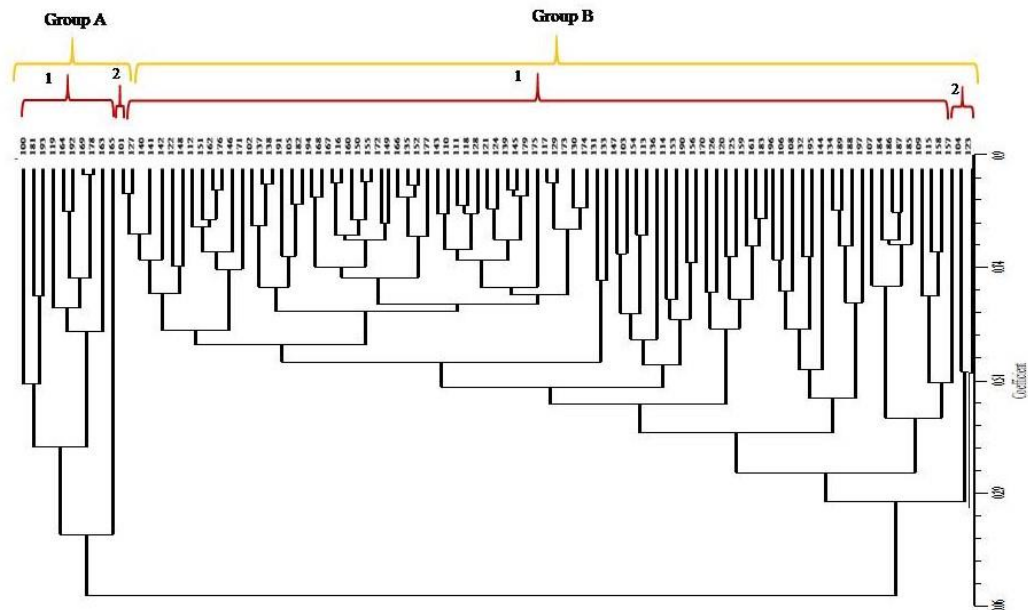


Figure 2. UPGMA dendrogram showing similarity of local onion landraces

The UPGMA dendrogram that was presented in Figure 2 was showed local onion landraces were separated into two major groups (Group A and B) and each of them separated into two sub-groups. Similarity rate of the landraces was calculated between 0.06-0.96 and similarity percentage of the major groups was %29. While the closest genotypes were Y169S and Y178S, the most distant genotypes were Y100S and Y123S. Group A was divided into 2 subgroups with the similarity of 15%. The most distant genotype of this group was Y165S. Group B was also divided into 2 subgroups with the similarity of 26%. Y123S and Y104S were the most distant genotypes of this group (Figure 2).

In this study, used 97 genotypes were also classified according to their cytoplasm types. Agarose gel image of PCR products obtained using 50 ng of DNA with 5' *cob* (SATO, 1998) and *OrfA501* (ENGELKE *et al.*, 2003) primers presented in Figure 3. The 414 bp band in control 1750A shows S cytoplasm, and the 180 bp band in control 1750B shows N cytoplasm and according to the 100 bp DNA measurement marker, 473 bp band represents S or T cytoplasm, the absence of 473 bp band represents N cytoplasm. In addition, the last part of the last comb shows used negative control. Among genotypes, it was found that, 19 of them possessed both S- and N-cytoplasm because of bulk DNA sampling and 78 of them possessed only N-cytoplasm (Table 6). Although the protocol is complied accurately and repeated twice, in this research, *OrfA501*-marker couldn't distinguish S and T cytoplasm from the N. There were some bands

formed but they were not enough for the scientific evaluation. Contrary to our study, for the identification of cytoplasm types of Korean onions, KIM *et al.* (2007) used PCR markers developed by ENGELKE *et al.* (2003) instead of markers developed by HAVEY (1995) and SATO (1998) which were presented unexpected DNA fragments in their study.

Table 6. Cytoplasm types of onion landraces

Genotypes	Primers			Genotypes	Primers			Genotypes	Primers		
	180 S/N	414 S	473 S/T		180 S/N	414 S	473 S/T		180 S/N	414 S	473 S/T
Yalova-100S	1	0	0	Yalova-133S	1	0	0	Yalova-166S	1	0	0
Yalova-101S	1	0	0	Yalova-134S	1	0	0	Yalova-167S	1	0	0
Yalova-102S	1	1	1	Yalova-135S	1	0	0	Yalova-168S	1	0	0
Yalova-103S	1	0	0	Yalova-136S	1	0	0	Yalova-169S	1	0	0
Yalova-104S	1	0	0	Yalova-137S	1	1	0	Yalova-170S	1	0	0
Yalova-105S	1	0	0	Yalova-138S	1	0	0	Yalova-171S	1	0	0
Yalova-106S	1	0	0	Yalova-139S	1	0	0	Yalova-172S	1	0	0
Yalova-107S	1	0	0	Yalova-140S	1	0	0	Yalova-173S	1	0	0
Yalova-108S	1	0	0	Yalova-141S	1	0	0	Yalova-174S	1	0	0
Yalova-109S	1	1	0	Yalova-142S	1	0	0	Yalova-175S	1	0	0
Yalova-110S	1	1	0	Yalova-143S	1	1	0	Yalova-176S	1	0	0
Yalova-111S	1	0	0	Yalova-144S	1	0	0	Yalova-177S	1	0	0
Yalova-112S	1	0	0	Yalova-145S	1	0	0	Yalova-178S	1	1	0
Yalova-113S	1	1	0	Yalova-146S	1	0	0	Yalova-179S	1	0	0
Yalova-114S	1	0	0	Yalova-147S	1	0	0	Yalova-180S	1	0	0
Yalova-115S	1	0	0	Yalova-148S	1	0	0	Yalova-181S	1	1	0
Yalova-116S	1	0	0	Yalova-149S	1	0	0	Yalova-182S	1	0	0
Yalova-117S	1	0	0	Yalova-150S	1	0	0	Yalova-183S	1	1	0
Yalova-118S	1	0	0	Yalova-151S	1	0	0	Yalova-184S	1	0	0
Yalova-119S	1	0	0	Yalova-152S	1	1	0	Yalova-185S	1	1	1
Yalova-120S	1	0	0	Yalova-153S	1	0	0	Yalova-186S	1	0	0
Yalova-121S	1	0	0	Yalova-154S	1	0	0	Yalova-187S	1	0	0
Yalova-122S	1	1	0	Yalova-155S	1	0	0	Yalova-188S	1	0	0
Yalova-123S	1	0	1	Yalova-156S	1	0	0	Yalova-189S	1	0	0
Yalova-124S	1	0	0	Yalova-157S	1	1	0	Yalova-190S	1	0	0
Yalova-125S	1	0	0	Yalova-158S	1	0	0	Yalova-191S	1	0	0
Yalova-126S	1	1	0	Yalova-159S	1	1	0	Yalova-192S	1	0	0
Yalova-127S	1	1	0	Yalova-160S	1	1	0	Yalova-193S	1	0	0
Yalova-128S	1	0	1	Yalova-161S	1	1	0	Yalova-194S	1	0	0
Yalova-129S	1	0	0	Yalova-162S	1	1	0	Yalova-195S	1	0	0
Yalova-130S	1	0	0	Yalova-163S	1	0	0	Yalova-196S	1	1	0
Yalova-131S	1	0	0	Yalova-164S	1	0	0	Yalova-197S	1	0	0
Yalova-132S	1	0	0	Yalova-165S	1	0	0				

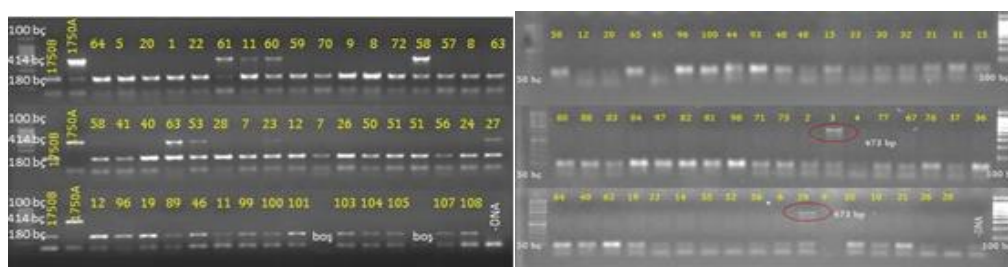


Figure 3. Amplifications of the 5'cob (Sato, 1998) and OrfA primers (ENGELKE *et al.* 2003)

Hybrid varieties of bulb onion show higher heterosis but growers extensively prefer OP varieties (NUNES *et al.*, 2014) regarding to price-performance ratio. Improvements on yield have been achieved through heterosis breeding since the discovery of CMS (KHOSA *et al.*, 2016). Because of their high yielding capacity and the homogeneity, hybrid varieties should be made easily accessible. When morphologic and molecular results of the current research were considered, collected onion landraces are quite rich in diversity of which is thought to be sufficient for the new variety breeding studies suitable for various market demands.

CONCLUSION

As one of the origin centre of bulb onion Turkey was expected to have great diversity. Varied climate conditions of the country made year-round onion production possible. Thus there are lots of different onion genotypes which adapted to different climatic conditions and they have been selected and maintained by the farmers until today. With this study, these landraces were collected and morphologically characterized. Cytoplasm types of the genotypes were also determined with molecular markers. Thus, qualified gene pool which consisted of 97 genotypes was established for the further hybrid onion breeding studies. After this, nucleus types of these genotypes could be detected with the future projects using molecular markers and for the development of fully homozygous onion lines, doubled haploid technology could be useful due to the high inbreeding depression and biennial nature of onion.

ACKNOWLEDGEMENTS

This study was supported by the General Directorate of Agricultural Research and Policies of Turkish Ministry of Agriculture and Forestry. Project Number: TAGEM/BBAD/12/A09/P07/01/02.

Received, April 20th, 2020.

Accepted November 12nd, 2020

REFERENCES

- ALIMOUSAVI, S.A., M.R., HASSANDOKHT, S., MOHARRAMIPOR (2007): Evaluation of Iranian onion germplasms for resistance to Thrips. *International journal of Agriculture and Biology*, 9, 455-8.
- BERNINGER, E. (1965): Contribution a l'etude de la sterite male de l'oignon (*Allium cepa* L.). *Annual Amelior Plantes*, 15:183-189.

- BREWSTER, J.L. (2008): Onions and other vegetable Alliums. CABI publishing, pp: 44-50.
- CERÍCOLA, F., E., PORTÍS, L., TOPPINO, L., BARCHI, N., ACCIARRI, T., CIRIACI, T., SALA, G.L., ROTINO, S., LANTERI (2013): The population structure and diversity of eggplant from Asia and the Mediterranean basin. *PLoS ONE* 8(9):DOI:10.1371/journal.pone.0073702.
- CRAMER, C.S. (2001): Comparison of Open-Pollinated and Hybrid Onion Varieties for New Mexico. *HortTechnology*, 11.1, 119-123.
- DAMON, S.J., R.L., GROVES, M.J., HAVEY (2014): Variation for Epicuticular Waxes on Onion Foliage and Impacts on Numbers of Onion Thrips. *Journal of the American Society for Horticultural Science*. Vol.134, No.34.
- ENGELKE, T., D., TEREFE, T., TATLIOGLU (2003): A PCR based marker system monitoring CMS-S, CMS-T and CMS-N cytoplasm in the onion. *TAG*, 107: 162-167.
- GALMARINÍ, C. R., I. L., GOLDMAN, M. J., HAVEY (2001): Genetic analysis of correlated solids, flavour, and health enhancing traits in onion (*Allium cepa* L.). *Mol. Genet. Genomics* 265, 543—551.
- GLASZMANN, J.C., B., KILIAN, H.D., UPADHYAYA, R.K., VARSHNEY (2010): Accessing genetic diversity for crop improvement. *Curr. Opin. Plant Biol.* 13, 1—7.
- HANELT, P. (1990): Onions and Allied Crops, Chapter 1: Taxonomy, Evolution and History (eds., Rabinowitch, H.D., Brewster, J.L.) pp: 1-27, CRC Press, Inc., Boca Raton, Florida.
- HAVEY, M.J. (1993): Onion Breeding. In: G. Kalloo and B. Berg (Eds.). *Genetic improvement of vegetable crops*, pp.35-49. Pergamon press, Oxford.
- HAVEY, M.J. (1995): Cytoplasmic determination using the PCR to aid the extraction of maintainer lines from open pollinated population of onion. *TAG*, 90: 263-268.
- HAVEY, M.J. (2000): Diversity among male sterility inducing and male fertile cytoplasm of onion. *TAG*, 101: 778-782.
- HOSAMANI, R.M., B.C., PATIL, P.S., AJJAPPALAVARA (2010): Genetic variability and character association studies in onion (*Allium cepa* L.). *Karnataka Journal of Agricultural Sciences*, 23(2).
- JONES, H., A., CLARKE (1943): Inheritance of male sterility in the onion and the production of hybrid seed. *Proc. Amer. Soc. Hort. Sci.*, 43: 189-194.
- KHOSA, J.S., J., MCCALLUM, A.S., DHATT, R.C., MACKNIGHT (2016): Enhancing onion breeding using molecular tools. *Plant Breeding*, 135(1): 9-20.
- KIM, C.W., E.T., LEE, H.J., PARK, Y.S., JANG, I.H., CHOI, J.K., BANG, S.J., AHN, G.C., CHUNG (2007): Evaluation of Cytoplasm types by PCR-marker in Male-Sterility of Onion (*Allium cepa* L.). *Korean J. Breed. Sci.*, 39(2) : 201~205
- KIM, S., E.D.Y., LEE, T., CHO, H., HAN, B., BANG, S., PATIL, Y.K., AHN, M., YOON (2009): Identification of a novel chimeric gene, orf725, and its use in development of a molecular marker for distinguishing three cytoplasm types in onion. *TAG*, 118: 433- 441.
- MALLOR, C., M., BALCELLS, F., MALLOR, E., SALES (2011): Genetic variation for bulb size, soluble solids content and pungency in the Spanish sweet onion variety Fuentes de Ebro. Response to selection for low pungency. *Plant Breeding*, 130(1): 55-59.
- MCCOLLUM, G.D. (1971): Heritability of onion bulb shape and size: estimates from half-sib families. *J. Heredity*, 62: 101—104.
- MUÑOZ-FALCÓN, J.E., J., PROHENS, S., VILANOVA, F., NUEZ (2008): Characterization, diversity, and relationships of the Spanish striped (Listada) eggplants: a model for the enhancement and protection of local heirlooms. *Euphytica*, 164(2):405-419.
- NUNES, R.L.C., A.B.D., OLIVEIRA, A.S., DUTRA (2014): Agronomic performance of onion hybrids in Bara_una, in the semi-arid region of Brazil. *Rev. Cienc. Agron.*, 45: 606—611.
- PATHAK, C.S. (2000): Hybrid Seed Production in Onion, *Journal of New Seeds*, 1: 3, 89-108.

- PETROPOULOS, S.A., I.C., FERREIRA, F.R., L., BARROS, eds. (2019). *Rediscovering Local Landraces: Shaping Horticulture for the Future*. Lausanne: Frontiers Media.
- ROHLF, F.J. (1998): NTSYS-PC: Numerical taxonomy and multivariate analysis system. Release 2.20j. Exeter Software, Setauket, N.Y.
- SATO, Y. (1998): PCR amplification of CMS-specific mitochondrial nucleotide sequences to identify cytoplasmic genotypes of onion (*Allium cepa* L.). *TAG*, 96: 367-370.
- SHIGYO, M., C., KIK (2008): Onion. In: J. Prohens, and J. F. Nuez (eds), *Vegetables II*, 121-159. Springer, New York.
- WALL, M.M., A., MOHAMMAD, J.N., CORGAN (1996): Heritability estimates and response to selection for the pungency and single center traits in onion. *Euphytica*, 87: 133-139.
- VON KOHN, C., A., KIELKOWSKA, M.J., HAVEY (2013): Sequencing and annotation of the chloroplast DNAs and identification of polymorphisms distinguishing normal male-fertile and male-sterile cytoplasm of onion. *Genome*, 56: 737—742.

MORFOLOŠKA I CITOPLAZMATIČNA OCENA POPULACIJA CRNOG LUKA
(*Allium cepa* L.)

Esra CEBECI^{1*}, Huseyin PADEM², Ali Fuat GOKCE³

¹Bati Akdeniz poljoprivredni istraživački institut, Antalija, Turska

²Isparta Univerzitet za primenjene nauks, Departman za hortikulturu, Isparta, Turska

³Omer Halisdemir Univerzitet, Fakultet za poljoprivredne nauke i tehnologiju, Nigde, Turska

Izvod

Klimatske promene danas prete da smanje prinos useva i obezbeđenost hranom. Lokalne populacije imaju sposobnost prilagođavanja na promenljive klimatske uslove. Korišćenje ovih lokalnih izvora u programima oplemenjivanja biljaka postaje alternativna strategija. U ovoj studiji prikupljeno je 97 populacija kako bi se započeo program oplemenjivanja crnog luka koji ispunjava trenutne trendove. Prikupljeni materijali morfološki su okarakterisani pomoću 21 deskriptora izvedenog iz UPOV-a. Grupisanje je urađeno pomoću programa NTSIS primenom UPGMA metode, pokazalo je da je stopa genetičke sličnosti lokalnih populacija između 0,06-0,96. Program oplemenjivanja hibridnog luka zavisi od citoplazmatsko-genetskog sistema muške sterilnosti (CMS). Dakle, PCR-markeri su primenjeni za identifikaciju vrsta citoplazme populacija. Među lokalnim populacijama N-citoplazma je pronađena kod 78 uzoraka, a S-citoplazma je pronađena kod 19 uzoraka. Na kraju studije formiran je genski fond koji se sastojao od okarakterisanih genotipova crnog luka koji će se koristiti u daljim proučavanjima u oplemenjivanju.

Primljeno 20. IV.2020.

Odobreno 12. XI. 2020.