Genetic Diversity of Shallot (*Allium cepa* var. *aggregatum*) Segregating Populations from Ethiopia Using Multivariate Analysis

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Abstract

Shallot is an important traditional crop used for seasoning of various national cuisines. However, productivity of shallot is low partly due to lack of improved varieties that are adapted to diverse agro-ecologies of Ethiopia. It has been difficult to improve the genetic base of local shallot germplasm due to its vegetative propagation nature. However, some plants within the germplasm were found bolting and producing seeds providing the opportunity for broader genetic base. Therefore, the present study was initiated to characterize and classify some segregating genotypes so as to use them for future breeding program. The study was undertaken at Debre Zeit Agricultural Research Center. It comprised of sixty genotypes generated through natural out-crossing and three released varieties (Minjar, Huruta and DZSHT-005/-02/90 DZSHT-005/02) used as controls. The experiment was laid-out in augmented design with three blocks. Twenty bulbs of each genotype were planted on a ridge comprising two rows. The three control varieties were also planted in the same way but replicated at in each block. Data on yield and yield components, percent bolting and number of flowerstalks/plant were collected. Analysis of variance, cluster and principal component analyses were also undertaken on data recorded. The results of the study showed that the genotypes significantly differed in yield/plant, number of bolting plants and number of flowerstalks/plant. However, they did not differ in bulb diameter, bulb height and downy mildew severity. Eight genoytypes had better yield/plant than all the three controls. Cluster analysis grouped the genotypes into seven clusters. Clusters I through VII comprised of 1(1.6%), 2(3.2%), 14 (22.2%), 10(15.9%), 5(7.9%), 22(34.9%) and 9(14.3%) genotypes, repectively. The genotypes within Clusters I through VI had atleast 87.5%, 85.2%, 85.0%, 85.8%, 82.9% and 84.1% similarity, respectively. Cluster III had the second highest mean for yield/plant, bulb diameter and number of bulb splits/plant. On the other hand, Cluster VII had the highest mean for yield/plant, bulb height and doweny mildew severity. It had also high inter cluster distances with other clusters. The principal componenet analysis identified seven components, five of which contributed to 83.1% of the variation. Generally, the eight genotyes with better yield were recommended for further variety trials under different environments while maintaining the other genotypes as a source of for variation future for breeding activities.

Keywords: characterization, cluster analysis, germplasm, quantitative traits, principal componenet analysis

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Introduction

Shallot (*Allium cepa L. var. aggregatum*) is a close relative of onion (*Allium cepa L. var. cepa*) and are no longer considered to be different species (Fritsch and Friesen, 2002; Rabinowitch and Kamenetsky, 2002; Brickell *et. al*., 2016). It is one of the most important vegetables used for seasoning local cuisines in Ethiopia. The largest producers of shallots are China and Japan, with more than 500,000 tons of shallot bulbs produced per year, followed by New Zealand, Mexico, Iran, Iraq, Cambodia, and Cameroon (FAOSTAT, 2018). Ethiopia produces about 374.7 thousand tons of onion and shallot on 48.4 thousand hectares of land (CSA, 2011).

Shallot is propagated mainly using vegetative bulbs and hence breeding endeavors of shallot were limited to clonal selection of genotypes or population collected from different parts of the country. Clonal selection often dealt with existing diversity of germplasm pool (Awale *et. al.*, 2011; Ita *et. al.,* 2016), with less possibility of further diversifying the genetic pool. According to Seifu (1981) Ethiopia is considered as the center of diversity for shallot. Getachew and Asfaw (2000) observed wide diversity among Ethiopian shallot accessions in growth habit, leaf width, sheath length, bulb shape, size and color, days to maturity, number of bulb splits and bulb yield/plant. Fasika *et. al.* (2008) also studied forty-nine accessions collected from Shewa, Gojam and Welo areas and reported highly significant phenotypic and genotypic coefficients of variance ranging from 7.6-41.6% and 4.4-27.9%, respectively. The genotypes varied in plant height, number of leaves and bulb splits/plant, bulb diameter, bulb yield, harvest index, total soluble solids, bulb dry weight and pungency. Similarly, Awale *et. al.* (2011) reported high phenotypic and genetic variances among forty-nine accessions collected from Shewa, Harghe and Jimma areas for the above-mentioned traits as well as for days to maturity and sprouting of stored bulbs. Hasanah *et. al.* (2022) reported that eleven shallot varieties originated from North Sumatra, Indonesia had high genetic diversity and categorized them into two main groups with dissimilarity coefficient of 76%. In addition, Noor *et. al*., (2012) confirmed the presence of significant genetic variability for important agronomic and morphological traits in Indonesia.

In Ethiopia, shallot variety improvement program was started in 1986 at Debre Zeit Agricultural Research Center (DZARC) with germplasm collected from major growing regions (Getachew and Asfaw, 2000). Currently, the center holds about 134 shallot accessions. So far, four vegetative propagated and two seed propagated varieties were released. Moreover, two seed propagated varieties from Melkassa Agricultural Research Center (MARC) and one seed propagated variety from Haramaya University were released

for production (MoANR, 2019). Some shallot plants within the germplasm holding of the DZARC were observed bolting, flowering and producing viable seeds providing an opportunity of natural out-crossing among plants and thus widening the germplasm base. Utilization of this opportunity, unequivocally, will have accelerated the development new varieties with better yield and quality.

Accessions collected from different parts of the country were characterized for morphological traits of growing plants as well as bulbs. Similarly, Josipa *et. al*., (2021) reported that morphological characterization revealed phenotypic diversity in vegetative and reproductive traits in shallot genotypes of Croatia. Besides, descriptors of vegetative and bulb morphology were used to discriminate among different shallot genotypes in Croatia (Major *et. al*., 2018). Method of data analysis is also crucial to efficiently utilize morphological data in diversity studies. The biplot analysis provides a useful tool of data analysis and allows visual appraisal of the structure of large data matrices. It specially reveals the principal component analysis, where the biplot can show inter-unit distances and indicates clustering of units as well as display variances and correlations of the variables (Gabriel, 1971). Moreover, Hanci and Gokce (2016) used principal components analysis for data reduction and estimation of genetic diversity of onion breeding materials.

Genetic diversity is a critical component in breeding program of any crop. Selection of genetically diverse parents on the basis of divergence could be more promising to get hybrid varietities, and to create a broad spectrum of variability in segregating generation (Singh *et. al*., 2020). Therefore, the objective of the present study was to characterize and classify some shallot genotypes generated from segregating populations for future breeding activities.

Materials and Methods

Description of the study area

The experiment was undertaken at DZARC, East Shewa zone, Ethiopia. The DZARC is located 47 km southeast of Addis Ababa at 08^{0}44'N latitude and 38^{0}58'E longitude. It has an altitude of 1860 m.a.s.l, annual min. and max. temperature of 8.9°C and 24.3°C, and annual rainfall of 851 mm (DZARC, 2008). The soil of the center is Alfisol soils with pH ranging from slightly acidic (6.1) to moderately neutral (7.9) (EARO, 2003).

Plant material and experimental design

Initially, the genotypes for the experiment were developed by planting the shallot accessions collected from different parts of Ethiopia at Kulumsa Agricultural Research Center (KARC). KARC has higher altitude (2200 m.a.s.l.) and cooler environment than DZARC, and allowed shallots to bolt, flower and out-cross naturally. Seeds of these accessions were collected and sown at DZARC to produce bulbs. The bulbs were selected for bulb size, color, and shape uniformity. The selection process was undertaken for three cycles and uniform bulbs were maintained by vegetative propagation.

The experiment comprised of sixty genotypes that were developed as described above. It was laid out using an augmented design with three blocks. Three improved shallot varieties (Huruta, Minjar and DZSHT-005-02/90) were planted at every block as controls. Twenty uniform bulbs of each genotype were planted on a ridge comprising two rows. All agronomic practices were undertaken as recommended by Getachew *et. al.* (2008).

Data collection

Based on the descriptors for allium developed by International Plant Genetic Resources Institute (IPGRI, 2001), data on yield/ per plant, weight, diameter and height of bulbs, and number of bulb splits/plant were recorded from five randomly selected plants per genotype. Percent bolting was recorded as the proportion of bolted plants with respect to the total number of plants/ per plot and number of flower stalks/plant was a mean of flower stalks/ per bolted/ per plants. Downy mildew severity was recorded on plot bases using 1 to 5 scales.

Data analysis

Analysis of variance was undertaken using the control genotypes and the variance was used to separate means of the genotypes. Cluster analysis was done using the unweighted pair-group method with arithmetic average (UPGMA) employing Minitab statistical software (Minitab® 19.2020). Graphical representation of the cluster analysis (dendrogram) was constructed to elucidate the relation between genotypes. Principal Component Analysis was also undertaken and the subsequent Scree and biplot were generated using the same software.

Results and Discussions

Mean performance of quantitative traits

The genotypes significantly ($P<0.05$) differed in yield/plant, number of bolting plants and number of flowerstalks/plant. However, bulb diameter, bulb height, number of bulb splits/plant and downy mildew severity were not significantly different among the genotypes (Table

1).Yield/ per plant ranged from 26.52 g in DZSHT-017-1/90 to 196.6 g in DZSHT-OP-100-2-3/90. Genotypes DZSHT-OP-005-1-2, DZSHT-OP-009-2/90, DZSHT-OP-100-2-2/90, DZSHT-OP-100-2-3/90, DZSHT-OP-255-2/90, DZSHT-OP-255-2-1/94, DZSHT-OP-255-2-3/90 and DZSHT-OP-41-4A had better bulb yield/plant than all the three controls. Inline with the present study, Awale *et. al.* (2011) and Fasika *et.al.* (2008) reported significant variations in morphological and yield parameters in shallot accessions collected from different parts of Ethiopia.

The bolting percentage of the genotypes ranged from no bolting in DZSHT-155-1B-1 to 100% in DZSHT-OP-005/02. Almost all the test genotypes, except DZHT-OP-051-1/90, had higher percent bolting than the control varieties, which were selected for their low bolting. Likewise, Wassu *et. al.* (2018) and Getachew (2018) reported that shallot genotypes had a potential of attaining 95% and 86-98% bolting, respectively. Similarly, Josipa *et al*. (2021) found that Croatian shallot accessions had bolting percentage ranging from 0 to 100% and classfied tham into four categories as: no (<10%), rare(15-30%), most(40-60%) and obligatory (70-100%) bolters. Moreover, Getachew (2004) reported that complete bolting was attained in some shallot genotypes that received verenalization at 8 or 12^{o}C for 60 days.

Genotype DZSHT-OP-94-3/94 produced the highest (four) flowerstalks/plant than any other genotype. Sixteen (28%) of the test genotypes had about three flowerstalks/plant while bolted plants of the controls Huruta and Minjar had an average of one flowerstalks/plant. The high bolting was associated with low bulb yield/ per plant owing to more photosynthete partitioning to flower stalks than to bulbs (Wallace *et. al,* 1993).

Table 1. Bulb and bolting characterstics of sixty three shallot genotypes generated from open pollinated accssions

Genotype Code	Genotype	Bulb yield/ plant	Bulb diameter (mm)	Bulb height (mm)	No. bulb splits	Bolting (%)	No. flower stalks/ plant	Downy Mildew (1-5 scale)	Genotype Code	Genotype	Bulb yield/ plant	Bulb diameter (mm)	Bulb height (mm)	No. bulb splits	Bolting (%)	No. flower stalks/ plant	Downy Mildew (1-5 scale)
1	DZSHT-OP-005/02	41.93ghi	37.47	60.7	5.53	0.00q	0.00d	1.83	35	DZSHT-OP-155-1B	69.13c-i	48.23	59.8	5.25	43.99f-n	2.38abc	2.38
2	Huruta	38.6hi	36.07	58	4.93	0.97pq	0.67cd	2.17	36	DZSHT-OP-155-1B-1	61.63c-i	37.83	89.8	8.45	100a	2.78abc	3.88
3	Minjar	47.87ghi	39.4	70.7	5.33	4.17opq	1.1bcd	2.67	37	DZSHT-OP-155-1B-2	59.13c-i	52.23	67.8	3.65	76.39a-e	3.58a	3.88
4	DZSHT-OP-255-2/90	87.33b-f	40.3	73.2	5.78	29.09i-o	1.35a-d	1.38	38	DZSHT-OP-155-1B-3	54.33d-i	39.03	75.8	4.25	87.09abc	2.98ab	3.38
5	DZSHT-OP-255-2-3/90	94.73bcd	54.1	65.2	4.58	55.39d-i	1.25a-d	1.88	39	DZSHT-OP-19-3-1/94	63.03c-i	41.63	65.8	4.25	59.69c-h	2.58abc	3.38
6	DZSHT-OP-255-2-1/90	38.93ghi	50.9	69.2	8.38	39.79g-n	2.15a-d	2.88	40	DZSHT-OP-94-3/94	53.23f-i	40.23	69.8	3.45	34.69h-n	3.78a	3.38
7	DZSHT-OP-255-2-1/94	114.73b	50.7	49.2	7.38	62.99c-h	2.25abc	2.88	41	DZSHT-OP-19-3-2/94	48.23f-i	35.63	83.8	3.25	63.99c-h	3.38a	3.38
8	DZSHT-OP-255-2-3	61.73c-i	37.7	79.2	3.18	40.69g-n	1.75aa-d	1.88	42	DZSHT-OP-19-3-3/94	44.13ghi	35.23	61.8	3.85	54.09d-k	3.28ab	1.88
9	DZSHT-OP-41-4A	92.23b-e	54.1	59.2	8.38	52.89d-k	1.05bcd	4.38	43	DZSHT-OP-251-1B-3	36.43hi	37.23	53.8	2.65	79.69a-d	3.38a	2.38
10	DZSHT-OP-41-4A-1	72.23c-h	45.1	75.2	5.38	37.49q-n	0.95bcd	2.38	44	DZSHT-OP-001-3-2/94	43.62qhi	41.83	66.5	3.78	13.66n-q	1.33a-d	0.63
11	DZSHT-OP-41-4A-2	59.23c-i	47.9	81.2	3.18	64.79c-h	1.15a-d	2.88	45	DZSHT-OP-005-1-2	89.82b-e	36.83	46.5	5.58	40.86g-n	1.23a-d	1.63
12	DZSHT-OP-41-4A-3	46.43ghi	38.7	69.2	5.78	25.39j-p	1.55a-d	1.88	46	DZSHT-OP-005-1-1	44.47ghi	40.13	83.5	4.18	45.61e-m	1.53a-d	1.38
13	DZSHT-OP-41-4A-4	53.63e-i	49.9	65.2	3.18	77.79a-e	1.15a-d	3.38	47	DZSHT-OP-005-1-3	40.92ghi	32.03	66.5	3.98	24.86j-q	2.23abc	2.13
14	DZSHT-OP-54-2	52.93f-i	41.7	59.2	4.58	56.99c-i	1.65a-d	1.38	48	DZSHT-OP-005-1B	68.22c-i	32.03	52.5	5.58	31.36i-n	1.43a-d	3.13
15	DZSHT-OP-54-2-2	39.83ghi	38.8	60.2	3.78	43.79f-n	1.95a-d	1.63	49	DZSHT-OP-009-2/90	89.52b-e	40.83	42.5	4.78	74.06a-f	2.83abc	3.13
16	DZSHT-OP-72-2-2/90	71.28c-i	43.2	58.2	3.68	98.44ab	2.7abc	2.38	50	DZSHT-OP-009-2/07	53.6f-i	44.27	55.3	4.93	33.63i-n	2.17abc	2.83
17	DZSHT-OP-79-1A	42.93ghi	43.7	75.2	3.78	16.49l-q	0.85bcd	1.88	51	DZSHT-OP-009-2-2/07	43.12ghi	34.03	52.5	5.18	20.26l-q	2.33abc	1.63
18	DZSHT-OP-79-1A-1	52.13f-i	41.3	85.2	4.38	21.59l-q	0.75bcd	1.88	52	DZSHT-OP-009-2-3	35.42hi	37.03	50.5	3.58	43.76g-n	1.53a-d	3.13
19	DZSHT-OP-79-1A-2	61.83c-i	40.1	79.2	5.18	22.09k-q	0.75bcd	1.88	53	DZSHT-OP-009-2-3/90	38.82ghi	26.43	60.5	3.78	32.46i-n	2.53abc	2.63
20	DZSHT-OP-79-1A-3	53.53f-i	41.7	53.2	4.58	20.59l-q	1.95a-d	1.88	54	DZSHT-OP-009-2-4/07	57.02c-i	39.43	70.5	4.38	0.76pq	1.03bcd	1.63
21	DZSHT-OP-91-3/94	75.73b-g	43.7	85.2	5.98	37.79g-n	1.75a-d	3.38	55	DZSHT-OP-009-02/07	53.6f-i	44.27	55.3	4.93	33.63i-n	2.17abc	2.83
22	DZSHT-OP-91-3-1/94	34.93hi	36.7	55.2	5.78	35.69h-n	2.45abc	1.88	56	DZSHT-OP-017-1/90	26.52i	39.83	62.5	3.18	39.96g-n	2.33abc	3.13
23	DZSHT-OP-91-3-4/94	57.63c-i	40.5	65.2	4.58	62.19c-h	2.35abc	3.38	57	DZSHT-OP-017-1-1/90	51.42f-i	41.43	58.5	4.18	15.56m-q	1.93a-d	3.13
25	DZSHT-OP-54-2-5	48.93f-i	35.23	75.8	3.25	61.39c-h	3.48a	3.38	59	DZSHT-OP-051-1-1/90	55.62d-i	38.03	68.5	4.98	1.06opq	1.43a-d	2.63
26	DZSHT-OP-91-3-5/94	67.13c-i	38.53	69.8	4.25	54.44d-j	2.53abc	2.88	60	DZSHT-OP-051-1-2/90	45.52ghi	50.03	66.5	3.58	26.76i-o	1.63a-d	1.63
27	DZSHT-OP-100-2/90	56.83d-i	36.03	61.8	3.85	69.09b-g	1.68a-d	2.88	61	DZSHT-OP-051-1/90	33.82hi	33.23	44.5	3.38	68.76b-g	2.13a-d	2.13
28	DZSHT-OP-100-2-1/90	73.73b-h	41.83	79.8	4.45	48.39e-l	3.78a	3.38	62	DZSHT-OP-051-1-4/90	28.52hi	40.43	38.5	3.18	65.66c-h	2.13a-d	0.63
29	DZSHT-OP-100-2-2/90	97.73bc	47.43	73.8	6.05	48.19e-l	2.88abc	2.38	63	DZSHT-OP-054-2-3	32.22hi	30.43	46.5	2.78	88.86abc	2.53abc	3.13
30	DZSHT-OP-100-2-3/90	196.63a	35.23	93.8	3.85	35.49h-n	2.28abc	3.88		Mean	56.85	40.14	66.1	4.55	42.82	1.98	2.4
31	DZSHT-OP-12/90	70.03c-i	42.03	85.8	5.25	59.69c-h	2.88abc	2.38		SE	21.1	7.02	1.5	1.9	14.93	1.34	1.21
32	DZSHT-OP-12-1/90	67.93c-i	43.03	69.8	3.65	56.39d-j	3.38a	3.38		CV (%)	23.38	10.75	14.02	25.4	22.88	43.39	31.4
33	DZSHT-OP-121-1-1/90	41.33ghi	48.83	65.8	3.45	75.39a-e	2.78abc	2.38		Significance	*	ns	ns	ns	***	***	ns
34	DZSHT-OP-12-1-2/90	48.73f-	39.83	55.8	3.65	47.59e-m	2.48abc	2.88									

Cluster Analysis

Cluster analysis of the genotypes based on the seven variables grouped the genotypes into seven clusters. Simiarity among the genotypes within and between clusters is depicted by the dendrogram (Fig. 1). Cluster VII had the lowest similarity (18.5%) with other clusters (Fig. 1). Genotypes within Clusters I through VI have at least 87.5%, 85.2%, 85.0%, 85.8%, 82.9% and 84.1% similarity, respectively. Ita *et. al* (2016) and Lina *el. al.*(2019) also reported that Indonesian shallot genotypes were divided into three major groups and differences within a group demonstrated the existance of diversity among genotypes. Cluster I has fourteen genotypes and is characterized by the lowest cluster means for bolting and downy mildew severity and also low means in other parameters (Tables 2 and 3). Clusters II and IV comprised ten and twenty two genotypes, respectively; they have moderate cluster means for all parameters. Cluster III consist of five genotypes and has the highest bulb diameter and number of bulb splits, and the second highest yield per plant. Cluster V has nine genotypes and is characterized by the lowest number of bulb splits and bulb yield/ per plant. On the other hand, Cluster VI consisted of two genotype (DZSHT-OP-72-2-2/90 and DZSHT-OP-009-2/90) and has the highest percent bolting and flowerstalks/ plant but the shortest bulb height. Cluster VII consisted of only one unique genotype (DZSHT-OP-100-2-3/90) that has the highest bulb yield/plant, bulb height and doweny mildew severity but the lowest bulb diameter, number of bulb splits and flowerstalks/plant than those in other clusters.

The three improved varieties (Huruta, Minjar and DZSHT-005/02), used as controls in the study, were assigned to the Cluster I despite the fact that the varieties were adapted to and released for different agro-ecologiacl zones.The high similarity of the varieties could be attributed to similarity in bulb diameter, bulb height, number of bulb splits/plant, low bolting and number of flowerstalks/plant. Inclusion of other morpho-physiological parameters could help further differerntiate the genotypes that could otherwise belong to the same cluster.

Results of cluster distance analysis (Table 4) showed that Cluster V had the highest intra-cluster distance followed by clusters II and IV indicating the presence of high genetic diversity within these clusters. The inter-cluster distance (D^2) ranged from 24.9 to 154.9. Cluster VII had the highest inter cluster distance with all the other six clusters, ranging from 94.9 with Cluster III to 154.9 with Cluster V (Table 4). Crossing genotypes in these clusters with genotype (DZSHT-OP-100-2-3/90) could result in high hetrosis. Moreover, Cluster VI is distant from all clusters, except from cluster III.

Cluster V is highly distant from clusters I, II and III. Cluster III is also distant from clusters IV and I. The result indicated that hybridization between genotypes of these clusters could result in hybrid vigor and better recombinants in the population. The findings are in agreement with Singh *et.al* (2020); Ravindra *et.al* (2018) and Singh *et.al* (2013) who reported that onion genotypes belonging to distant clusters had wide spectrum of variation in segregates. Fitrana and Susandarini (2019) studied twelve shallot cultivars from Indonesia based on sixteen characters. They classified the cultivars in to two clusters based on bulb skin color, bulb skin layering and bulb shape which had higher loading values as indicated by principal componenet analysis. Khandagale and Gawande (2019) also underlined the importance of bulb color for breeding program and as a criterion for classifying genotypes.

Table 2. Distribution of sixty three genotypes into seven clusters based on Euclidean distance

Cluster number	No. of genotypes	Percentage	Name of genotypes
I	14	22.2	DZSHT-OP-005/02, DZSHT-OP-79-1A-2, DZSHT-OP-009-2-4/07, DZSHT-OP-051-1-1/90, DZSHT-OP-41-4A-3, DZSHT-OP-94-3/94, DZSHT-OP-79-1A-1, DZSHT-OP-79-1A-3, DZSHT-OP-001-3-2/94, DZSHT-OP-017-1-1/90, HURUTA, MINJAR, DZSHT-OP-54-2-2, DZSHT-OP-79-1A
II	10	15.8	DZSHT-OP-255-2/90, DZSHT-OP-255-2-3, DZSHT-OP-100-2-1/90, DZSHT-OP-41-4A-1, DZSHT-OP-91-3/94, DZSHT-OP-009-2/07, DZSHT-OP-91-3-5/94, DZSHT-OP-005-1B, DZSHT-OP-155-1B, DZSHT-OP-051-1-2/90
III	5	7.9	DZSHT-OP-255-2-3/90, DZSHT-OP-41-4A, DZSHT-OP-100-2-2/90, DZSHT-OP-005-1-2, DZSHT-OP-255-2-1/94
IV	22	34.9	DZSHT-OP-255-2-1/90, DZSHT-OP-91-3-1/94, DZSHT-OP-12-1-2/90, DZSHT-OP-005-1-3, DZSHT-OP-009-2-2/07, DZSHT-OP-009-2/07, DZSHT-OP-009-2/07, DZSHT-OP-009-2-3/90, DZSHT-OP-41-4A-2, DZSHT-OP-54-2, DZSHT-OP-19-3-1/94, DZSHT-OP-005-1-1, DZSHT-OP-91-3-4/94, DZSHT-OP-12/90, DZSHT-OP-12-1/90, DZSHT-OP-54-2-2, DZSHT-OP-100-2/90, DZSHT-OP-54-2-5, DZSHT-OP-19-3-2/94, DZSHT-OP-009-2-3, DZSHT-OP-19-3-3/94, DZSHT-OP-017-1/90
V	9	14.3	DZSHT-OP-41-4A-4, DZSHT-OP-155-1B-2, DZSHT-OP-121-1-1/90, DZSHT-OP-051-1-4/90, DZSHT-OP-251-1B-3, DZSHT-OP-155-1B-3, DZSHT-OP-051-1/90, DZSHT-OP-155-1B-1, DZSHT-OP-054-2-3
VI	2	3.2	DZSHT-OP-72-2-2/90, DZSHT-OP-009-2/90
VII	1	1.6	DZSHT-OP-100-2-3/90

Table 3. Cluster means of seven traits in sixty three genotypes of shallot

Variable	**Cluster**							
	I	**II**	**III**	**IV**	**V**	**VI**	**VII**	**Grand**
Yield /plant (g)	48.7	68.0	95.8	45.9	40.9	86.1	186.9	56.8
Bulb diameter (mm)	39.1	42.1	47.3	38.3	40.8	42.5	34.2	40.2
Bulb height (mm)	6.9	7.0	6.1	6.6	5.9	4.7	9.0	6.6
No of splits/plant	4.4	4.7	6.3	4.4	4.0	4.4	4.0	4.5
Bolting (%)	13.8	34.8	48.4	45.7	76.9	90.8	25.8	42.7
Flower stalk /plant	1.8	1.9	1.9	2.1	2.2	3.2	1.3	2.0
Downy mildew (1-5 scale)	1.9	2.3	2.4	2.5	2.7	2.5	3.5	2.4

Table 4. Intra (diagonal) inter (off diagonal) cluster Euclidean distances (D^2) among seven clusters in shallot genotypes

Cluster	I	II	III	IV	V	VI	VII
I	**17.7**						
II	28.7	**20.9**					
III	59.0	31.4	**19.2**				
IV	32.0	24.9	50.8	**20.8**			
V	63.6	50.1	62.2	31.7	**21.6**		
VI	85.7	58.9	43.8	60.6	47.4	**13.2**	
VII	138.8	119.5	94.9	142.5	154.9	120.3	**0.00**

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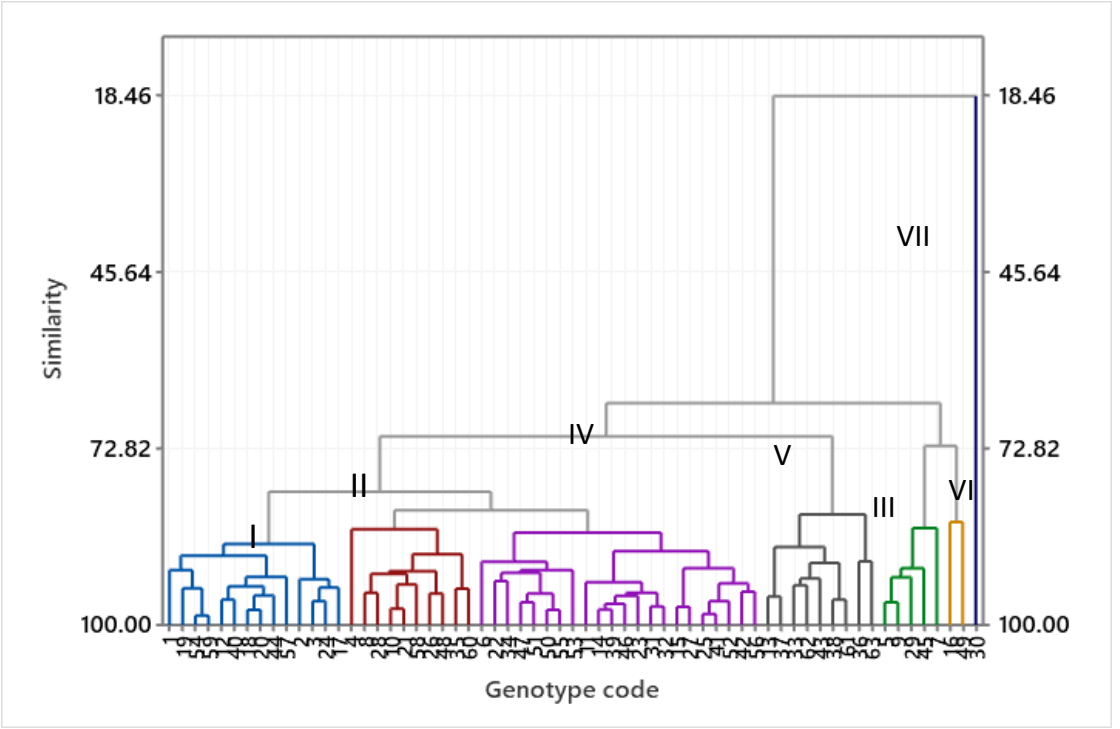

Figure 1. Dendrogram showing hierarchical clustering patterns of sixty three shallot genotypes for seven traits

Principal Component Analysis

The Scree plot showed that the first two components had Eigen values greater than unity, which could explain about 48.4% of the variability, whereas 83.1% of the variability is explained by the first five components (Fig. 2) i.e., the first five principal components are responsible for most of the variability. The coefficients of components indicated that bulb height, percent bolting, and number of flower stakes/plant were the major contributors to PC1; downy mildew severity, bulb diameter, number of splits/ plant and yield/plant to PC2; downy mildew severity and bulb diameter to PC3; number of bulb splits and percent bolting to PC4 and bulb height and yield/plant to PC5. Bulb weight and yield/ per plant had large positive loadings on component 1 whereas downy mildew and percent bolting had large positive loadings on component 2. These results are partly in agreement with the result of Hanci and Gokce (2016) who examined genetic diversity of 87 onion genotypes and reported that 71.8% of the variations were accounted for nine principal components. In addition, Ravindra *et.al.* (2018)

reported five principal components with 78.5% variability in 58 onion accessions.

The bi-plot of components 1 and 2 (Fig. 3) showed that yield/ plant was highly related with number of bulb splits/plant and to a lesser degree to bulb diamter. On the other hand, percent bolting, number of flowerstalks/plant and downy mildew severity were unrelated to yield and yield componenets. Similarly, Singh *et. al.* (2020) observed seven principal components having 83.87% of total variability. Their results showed that bulb weight, marketable bulb percentage, total and marketable bulb yield were negatively correlated with, downy mildew infestation and percent bolters for 34 onion genotypes.

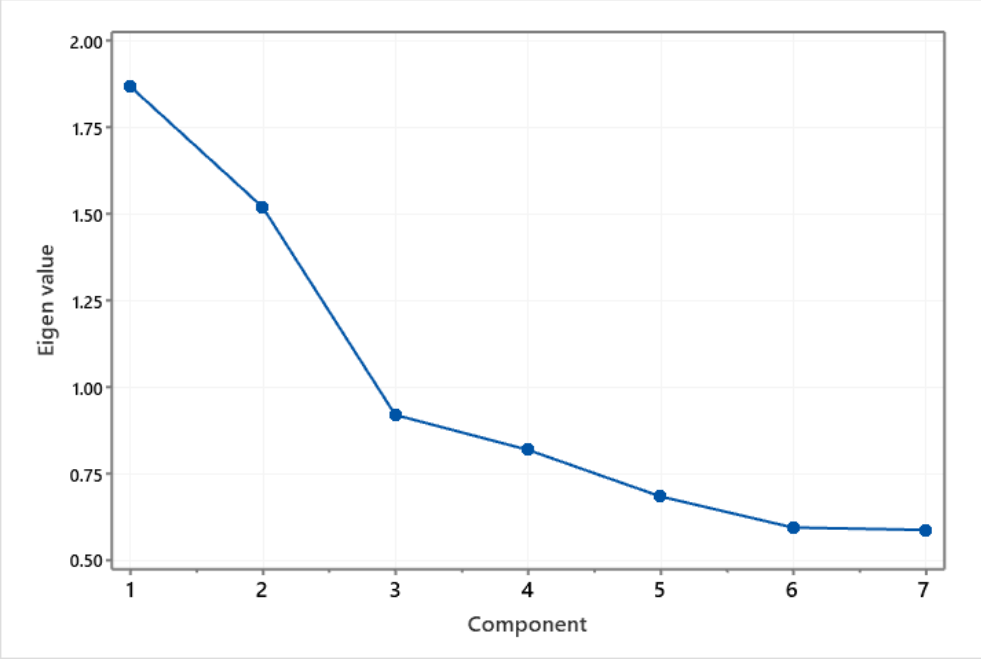

Figure 2. Scree plot of the seven variables

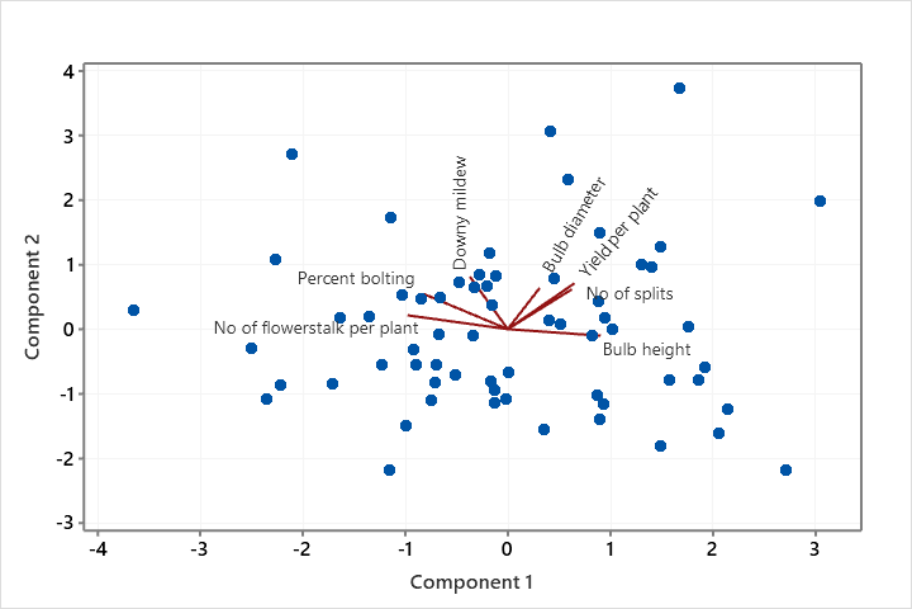

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Figure 3. Bi-plot of principal componenents 1 and 2

Conclusions and Recommendation

Clonal selection of shallots slowed down the rate of variety development, with only a few varieties developed in the past three and half decades. Regeneration of shallots through true seeds provided an opportunity of natural out-crossing among plants and thus widening the genetic base. The present study was thus aimed at characterizing and classifying about sixty of the genotypes derived from segregating populations of shallot including three improved varieties used as controls for use in future shallot breeding activities. The results of the study showed that shallot genotypes significantly differed in yield/plant, percentage of bolting plants and number of flowerstalks/ plant. However, they did not differ in bulb diameter, bulb height and downy mildew severity. Eight genoytypes had better yield/ plant than all the three controls. Cluster analysis grouped the genotypes into seven clusters based on their genetic similarities and differences using the the seven morphological traits. The principal componenet analysis also identified seven components, five of which contributed to 83.1% of the variation. Consequently, eight genotypes with better yield were recommended for further variety development trials under different environments while maintaining the other genotypes as sources genetic materials for future breeding activities.

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