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EXPLORING GENETIC DIVERSITY IN ONION GENOTYPES: A DETAILED ASSESSMENT

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ABSTRACT

To determine the genetic diversity of onions, a field experiment was carried out in 2018 during the kharif season at Haveli farm, College of Horticulture, Bagalkot, Karnataka. In order to investigate the genetic divergence, forty onion genotypes were assessed for seventeen traits using a randomized block approach. The genotypes under investigation were shown to be genetically diverse by the D^2 statistic. Seven clusters were formed from the genotypes based on D^2 values. Between clusters II and VII, the inter-cluster D^2 value was highest (D^2 = 101.25), followed by cluster IV and VII (D^2 = 99.62), and lowest (D^2 = 24.03) between clusters II and IV. After cluster Id", cluster III displayed the highest intra-cluster diversity. There were five genotypes in cluster III, seven genotypes in cluster Id!, twenty-four genotypes in cluster I, and a single genotype in each of the clusters II, V, VI, and VII. According to D^2 analysis, the parents with the greatest diversity were B-780, Kadarkoppa Local 4, Kadarkoppa Local 1, and Arka Bheema. To increase onion productivity, these genotypes could be used as parents in a breeding program.

***Key words*:** Onion, genotype, genetic diversity, D^2 analysis, cluster.

Introduction

The Alliaceae family of bulb crops includes onions (*Allium cepa* L, 2n = 2x = 16). The primary origin of onion is in Central Asia, with the Mediterranean region serving as a secondary centre (Lyngkhoi *et al*., 2021). It is a significant vegetable and spice crop that is farmed in temperate, tropical, and subtropical climates worldwide (Dorrigiv *et al*., 2021). This crop is biannual for seed production and annual for bulb production, with a high degree of cross-pollination. Though year-round cultivation occurs, our nation's *Rabi* season sees the most amount of cultivation. It exhibits a wide range of morphological characteristics, including fertility, bulbil (top set) development, flower colour, and bulb and leaf size, colour, and form. There are two types of onions farmed commercially. The common onion (*Allium cepa* L.) is the original type. Its plants are grown by seeds and have large, typically single bulbs. The second type is known as a multiplier onion (*Allium cepa* L. var aggregatum Don.), which yields a large number of tiny bulbs that combine to create an aggregate cluster. The onion is a member of the Allium genus, which is incredibly genetically diverse. The degree of genetic variety influences how successful a crop development effort is. In terms of shape, size, yield, quality, and other attributes, there is the greatest diversity among the various cultivars that are available in India and outside the country. To prevent genetic loss, it is crucial to preserve and collect the genetic diversity of onions. Further to species identification, genotype characterization and assessment are critical tasks. The most dependable and widely used technique among the several discovered or created to investigate the genetic divergence in the genotypes is the Mahalanobis D^2 (Mahalanobis., 1936). The degree of genotypic diversity

is estimated by genetic divergence analysis, which may be useful to plant breeders in choosing heterozygous parents for intentional hybridization. This tool proves to be helpful in selecting parents for a hybridization program. To ascertain the genetically distinct kinds of onion genotypes, the current investigation has been conducted.

Material and Method

In Haveli Farm, College of Horticulture, Bagalkot Kharif 2018-19, the experiment was carried out. Positioned at 160 10' North latitude and 750 42' East longitude, and 542.00 meters above mean sea level, the experimental site is located in the Northern Dry Zone (zone-3) of Karnataka state. Bagalkot benefits from both the North-East and South-West monsoons, falling under zone III of region 2. Forty different onion (*Allium cepa* L.) genotypes constituted the material. Three replications were included in the randomized block design (RBD) used to set up the experiment. 15 centimeter's separated rows, and 10 centimeter's separated plants. In each plot, five plants were chosen at random to record Days to maturity, plant height (cm), leaf diameter (cm), and number of leaves per plant Number of rings per bulb, dry matter content of bulb (%), average bulb weight (g), 10 bulb weight (g), total yield (q/ha), neck thickness (cm), Equatorial bulb diameter (cm), Polar bulb diameter (cm), and TSS (^{0}Brix). The genetic divergence was measured using Mahalanobis D^2 statistics on the data, as recommended by Dangi *et al*., (2018).

Results and Discussion

Significant differences were found for every attribute across all forty genotypes in the analysis of variance, suggesting that there is enough genetic variation among the genotypes. Plant breeders can categorise genotypes into distinct groups according to genetic diversity between them with the aid of D^2 statistics, a concept introduced by Mahalanobis in 1936. In order to evaluate genetic diversity in plant breeding, Rao (1952) recommended using this method. The D^2 value estimates for onions in the current investigation varied from 0 to 101.25. The wide range of D^2 values suggested that the genotypes of onions under investigation exhibited a high degree of diversity. Rivera *et al*., (2016) also got high ranges for D^2 values. Seven clusters were formed from the genotypes under investigation (Table 1). There were twenty-four genotypes in Cluster I, seven in Cluster I, and five in Cluster III. The V, VI, and I clusters were monogenotypic. Comparable research was published in Rashid *et al*., (2012), Gurjar *et al*., (2003), and Mohanty and Prusti (2002). Table 2 displays D^2 values from the divergence analysis, which were used to calculate intra- and inter-cluster D^2 values. Cluster II and IV (D^2 = 24.03) had the smallest inter-cluster distance, followed by cluster V and VII (D^2 = 32.41) and cluster I and II (D^2 = 32.87). The greatest inter-cluster distances (D^2 = 101.25) were seen for genotypes that fell between cluster II and VII, followed by cluster IV and VII (D^2 = 99.62) and cluster I and VI (D^2 = 85.82). This suggests that the genetic composition of the genotypes within this cluster may differ significantly from one another. Cluster I had the lowest intra-cluster distance (D^2 = 24.78). The genotype in cluster III (D^2 = 31.28) showed the greatest intra-cluster distance, followed by cluster IV (D^2 = 29.18). This suggests that the genotype of these clusters has a variably

Table 1: Clustering pattern of 40 onion genotypes based on D^2 values.

Cluster number	No. of genotypes	Genotypes included
I	24	Kadarkoppa Local 2, Kadarkoppa Local 3, Kadarkoppa Local 5, Mudhol Local, Tulasigeri Local, Kanchanganga, Nasik Red, Badnoor Local, Hanamaneri Local, Belavanaki Local, Lokapur Local, Savalagi Local, Bijapur Local, Babaleshwar Local, Belagavi Local, Kalasakoppa Local, Naragund Local, Kerur Local, Bhima Raj, Gote Local, Bijapur Local 2, Arka Niketan, Arka Lalima, Arka Kirthiman
II	1	Kadarkoppa Local 4
III	5	Ron Local, Navalgund Local, Bhima Red, Shivapur Local, Arka Kalyan
IV	7	Sathara Local, Panchganga, Kumate Local, Gadag Local, Bhima Super, Bilagi Local, Singel Red
V	1	Arka Bheem
VI	1	Kadarkoppa Local 1
VII	1	B- 780

Table 2: Average intra cluster and inter cluster D^2 values of seven clusters.

Clusters	I	II	III	IV	V	VI	VII
I	24.78	32.87	36.09	49.47	68.76	33.55	85.82
II		0.00	64.68	24.03	69.35	42.72	101.25
III			31.28	84.51	80.50	44.35	71.71
IV				29.18	53.76	51.27	99.62
V					0.00	49.04	32.41
VI						0.00	45.14
VII							0.00

Table 3: The mean values for growth, yield and quality parameters of seven clusters in 40 onion genotypes.

Clusters	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17
I	5.33	8.64	11.67	29.21	37.25	45.55	0.86	0.51	4.58	4.26	121.04	720.14	76.22	7.70	12.85	16.69	337.15
II	4.20	7.40	12.13	27.10	35.60	44.23	0.85	0.37	4.54	4.21	124.00	633.65	63.20	7.50	12.38	15.10	259.17
III	5.29	8.75	12.31	28.09	36.05	42.95	0.77	0.54	4.52	4.30	113.27	800.14	81.68	8.27	13.06	16.32	381.11
IV	4.71	7.62	11.16	29.61	38.22	45.72	0.81	0.50	4.64	4.28	122.95	527.17	57.67	7.41	12.44	16.18	274.05
V	4.80	8.00	10.40	24.40	32.47	41.80	0.81	0.43	4.80	4.32	114.00	433.65	60.02	8.27	14.83	18.77	326.43
VI	5.27	8.80	11.90	24.80	36.27	45.23	1.06	0.45	4.60	4.34	115.67	619.97	79.41	7.27	11.62	14.50	331.10
VII	5.20	8.53	11.60	25.67	35.07	44.03	0.85	0.38	4.20	3.86	100.00	560.43	67.52	7.93	14.56	15.53	338.87

1. Number of leaves 30 DAT; 2. Number of leaves 50 DAT; 3. Number of leaves 90 DAT; 4. Plant height 30 DAT; 5. Plant height 50 DAT; 6. Plant height 90 DAT; 7. Bulb neck thickness (cm); 8. Leaf diameter (cm); 9. Polar bulb diameter (cm); 10. Equatorial bulb diameter; 11. Days to maturity; 12. 10 bulb weights (g); 13. Bulb weight(g); 14. Number of rings per bulb; 15. TSS of bulb; 16. Dry matter content of bulb; 17. Total yield (q/ha) 50 DAT

structured genetic makeup. The clusters II, V, VI and VII showed zero intra cluster distance due to monogenotypic nature. The cluster means for seventeen characters reveled wide range of variability among the clusters for the characters Number of leaves 30 DAT (4.20 to 5.33), Number of leaves 50 DAT (7.40 to 8.80), Number of leaves 90 DAT (10.40 to 12.31), Plant height 30 DAT (24.40 to 29.61), Plant height 50 DAT (32.47 to 38.22), Plant height 90 DAT (41.80 to 45.72), Bulb neck thickness (cm) (0.77 to 1.06), Leaf diameter (cm) (0.37 to 0.54), Polar bulb diameter (cm) (4.20 to 4.80), Equatorial bulb diameter (3.86 to 4.34), Days to maturity (100 to 124), 10 bulb weight (g) (527.17 to 800.14), Bulb weight (g) (57.67 to 81.68), Number of rings per bulb (7.27 to 8.27), TSS of bulb (11.62 to 14.83), Dry matter content of bulb (14.50 to 18.77) and Total yield (q/ha) (259.17 to 381.11) presented in Table 3. Previous researchers Singh *et al.*, (2013) similarly noted significant variation in yield and the majority of the yield-contributing features between the clusters. Different proportions of each attribute went towards the overall genetic diversity. Table 4 shows the frequency with which each of the seventeen traits occurred in the top rank as well as the corresponding percentage contribution to genetic divergence. Ten bulb weight was observed to be the largest contributor to the diversity with 35.26 per cent by taking 275 times first ranking followed by total yield (18.97 %) by 148 times, T.S.S. of bulb (14.23 %) by 111 times, days to maturity (13.97%) by 109 times, bulb weight (4.23 %) by 33 times, dry matter of bulb (3.97 %) by 31 times, bulb neck thickness (1.92 %) by 15 times, plant height at 90 DAT (1.67 %) by 13 times, plant height at 30 DAT (1.41 %) by 11 times, number of rings per bulb (1.41 %) by 11 times, number of leaves per plant at 50 DAT (0.90 %) by 7 times, polar bulb diameter (0.77 %) by 6 times, leaf diameter (0.64%) by 5 times, number of leaves per plant at 90 DAT (0.51 %) by 4 times and number of leaves per plant at 30 DAT (0.13 %) by 1 time In contrast, the remaining trait *viz.*, Plant height 50 DAT (cm), Equatorial bulb diameter (cm), did not contribute to the total divergence. Bulb weight was similarly found to have the largest contribution (Singh *et al.*, 2013). According to Dhotre *et al.*, (2010), the attribute that contributes the most to genetic diversity is bulb yield.

Table 4: Relative per cent contribution of different characters to the total divergence in 40 onion genotypes.

S. No.	Source	Times ranked	Contribution %
1	Numberof leaves 30 DAT	1	0.13
2	Numberof leaves 50 DAT	7	0.9
3	Numberof leaves 90 DAT	4	0.51
4	Plant height 30 DAT (cm)	11	1.41
5	Plant height 50 DAT (cm)	0	0
6	Plant height 90 DAT (cm)	13	1.67
7	Neck thickness of bulb (cm)	15	1.92
8	Leaf diameter (cm)	5	0.64
9	Polar bulb diameter (cm)	6	0.77
10	Equatorial bulb diameter (cm)	0	0
11	Days to maturity	109	13.97
12	10 bulb weight (g)	275	35.26
13	Bulb weight (g)	33	4.23
14	Number of rings per bulb	11	1.41
15	TSS of bulb	111	14.23
16	Dry matter content (%)	31	3.97
17	Total yield (q/ha)	148	18.97

Conclusion

The most diverse parents for a crossing program could be Kadarkoppa Local 4, Kadarkoppa Local 1, Arka Bheema, and B-780, according to the overall D2 analysis for onions. Selecting accessions from clusters with high inter-cluster distance and high bulb yield as parents in recombination breeding programs is desirable. The most diverse genotypes could be used in breeding programs to widen and improve the genetic base of onions for the

selection of superior lines. Genotypes with multiple superior traits could be used for the simultaneous transfer of multiple genes in crop improvement.

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