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RESEARCH PAPER

Estimation of genetic diversity in onion genotypes

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Abstract: Onion being important vegetable crop of our country gaining more importance due to its high export potential and internal consumption. Due to its cross pollinated nature we can observe lot of variation in the genetic component of onion crop. Analysis of genetic diversity helps to choose the better genotype for specific purpose and we can improve that character through breeding programme. In this regard an experiment was conducted to study the Genetic diversity of onion genotypes at the site of All India Co–ordinated Network Research Project on Onion and Garlic (AICRP) the Main Agricultural Research Station UAS, Dharwad. The results revealed that fifty six genotypes were distributed in six clusters, there a moderate to high diversity noticed in these genotypes. The genotypes GKD-3, Bhima Shakti, Bhima Dark Red, GKD-42, Arka Kalyan, Bhima Super, RGP-1, GKD -75 these genotypes present in the cluster II, III, IV, V, and VI and lines L-883, Pune Red, L-863, DOGR-344, L-355, Bhima Kiran, PRO-7, RGP-2, RGP-3, present in the cluster I exhibited moderate diversity and having good storage and resistance to disease and pest.

Key words: Cluster, Disease, Diversity, Genotype, Onion, Pest

Introduction

Onion is one of the important export earning vegetable crop, which earns nearly 4000 crores foreign exchange annually. It has been cultivated for more than 5000 years in the world. Onion (*Allium cepa* L.) is monocotyledonous vegetable crop of the family *Alliaceace* sub-family *Allioideae* and order Asparagales having chromosome number 2n = 2x =16. In India no kitchen is free from onions, it means in each and every home Indians use onion in one or other form everyday hence, it is regarded as **"Queen of Kitchen".** It is also called by different names *Pyaz, Ullagaddi, Eerulli, Neerulli* in vernacular languages. The evidence of onion was seen in Chinese gardens, Egyptian pyramids and inner wall of their paintings and also mentioned in Bible.

Onion contains an enzyme known as *Allinase* responsible for catalyzing chemical reactions that produce the volatile chemicals which gives good flavor and odor. The pungency is due to volatile oil "*Allylpropyl disulphide* ($C_6H_{12}S_2$), the colour of outer skin is due to quercetin, anti fungal factor is due to phenolic compound known as catechol and tear inducing action is due to lachrymator factor *i.e.,* 1-Propenyl sulfonic acid.

The estimation of genetic diversity helps in identifying the genotypes for the hybridization programme. The selection of diverse parents for crossing is the first thing to obtain a character of interest in any crop. Some time genotypes with moderate diversity were also chosen to identify the best combinations (Vinutha, 2000). Genetic diversity signifies the differences in gene frequencies. Mahalanobis generalized distance is the most widely used technique in plant breeding to know the distance between the genotypes. This statistical tool has been used extensively by the breeders to resolve genetic divergence at their varietal and species levels in classifying crop plants. Lokhande *et al.* (1987) and Dhotre *et al.* (2010)

Material and methods

An experiment on "Diversity studies in onion genotypes"(*Allium cepa* L.) was undertaken during 2017 December at the site of All India Network Research Project on Onion and Garlic, Department of Horticulture, Main Agriculture Research Station UAS, Dharwad. Using randomized complete block design with three replications, spacing followed was 15 cm × 10 cm and total area of experiment was 900 m^2 The experimental material was collected from DOGR and the all the package of practices were carried out as per the recommendation give by DOGR.

Forty five days old seedlings were transplanted in the main field on 5-12-2017, harvested during March 2018. The data recorded for individual character from the selected plants were averaged and mean values obtained from this were subjected to simple RCBD analysis then final analysis was done using INDOSTAT.

Results and discussion

Successful breeding programme can be achieved through the adoption of proper methods. Analysis of the genetic diversity present in the parents which is foremost important. The significance of genetic diversity in the hybridization programme has long been customary by the breeders. The genetic diversity was studied to know the extent of genetic divergence among 56 onion genotypes for various characters. The diversity was determined by using Mahalanobis D^2 statistics. It also helped to know the relative distances between these genotypes for the characters under study. The results are based on the D^2 values and indicated that there was adequate diversity among the genotypes. Analysis of genetic divergence has been used to quantify the genetic distance between the genotypes and to identify the promising ones to initiate crossing programme to generate hybrids with desirable character.

Composition of clusters

56 genotypes distributed in six clusters based on D^2 values. Cluster I includes the maximum number of genotypes *i.e.,* forty-eight, cluster IV has two genotypes, cluster VI has three genotypes cluster II, III and V are solitary clusters because these clusters have only one genotype in it (Table 1).

Inter and intra- cluster distances

Fifty-six genotypes differed significantly for inter-cluster and intra-cluster values and formed six clusters. The average values ranged from 0 to 630.05. The highest intra-cluster distance was noticed in cluster VI (630.05) and the lowest was observed in clusters II, III, and V (0) respectively. The maximum inter-cluster values (4600.71) were noticed between the cluster III and VI, where minimum inter-cluster distance was obtained between the cluster II and III (195.06) (Table 2).

Cluster means for various important in onion genotypes

Cluster means analysis of 56 onion genotypes for important characters were worked out and presented in the Table 3. Cluster means for different parameters under study indicated that, considerable genetic divergence was present in the groups,

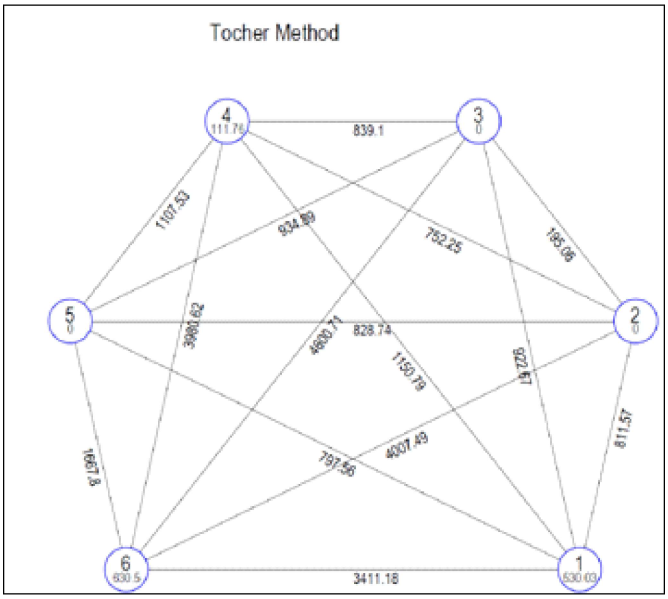

Fig. 1. Average intra (With in) and inter-cluster (between) D^2 values of onion genotypes

Table1. Composition of clusters

Clusters	Number of genotypes	Genotypes
I	48	L-355, Bhima Kiran, PYO-102, DOGR-361, GAWO-2, Bhima Red, RGP-4,Oriental hybrid, GKD-3, DOGR-344, RGP-2, Indam-4-F1, Bhima Sweta, Pune Red, DOGR Hyb-8, PRO-7, IHR-AKS-30, IHR-AKS-35, DOGR Hyb-6, Jindhal Pune Fursangi, DOGR-1605, L-883, JWO-11, DOGR-KHM-4 Bhima Shubra, PKV White, Jindal Riva , Rampur local , Col-819, PCH-3, RGP-3, Bhima Safed, BSS-262, DOGR Hyb-5, RO-645, W-344, DOGR-1606, DOGR-White -Hyb-2, JRO-07-17, L-857, RO-654, Sel-153-1, L-359, PCH-5, DOGR White hybrid -1
II	1	GKD-3
III	1	Bhima Shakti
IV	2	Bhima Dark Red , GKD-42
V	1	Bhima Super
VI	3	Arka Kalyan, RGP3,GKD-75

Table 2. Average intra (With in) and intercluster (between) D^2 values of onion genotypes

Cluster	I	II	III	IV	V	VI
I	530.03	811.57	922.67	1150.79	797.56	3411.18
II		0	195.06	752.25	828.74	4007.49
III			0	839.1	934.89	4600.71
IV				111.76	1107.53	3960.62
V					0	1667.8
VI						630.05

Diagonal values indicates intra-cluster distance and above diagonal values indicates inter-cluster values

Table 3. Cluster means for important characters *kharif*

Cluster	Number of genotypes	PH (cm)	NOL	NT (cm)	ED (cm)	PD (cm)	ABW (g)	TSS (Brix)	MY t/ha	TY t/ha	TWL (%)	DTH
I	48	50.25	5.87	0.78	5.18	4.74	46.22	13.14	34.98	38.71	53.15	108.26
II	1	57.50	5.67	0.95	5.63	3.43	51.15	13.22	31.00	36.57	14.07	106.67
III	1	60.98	7.17	0.97	6.17	5.90	52.80	12.60	34.40	39.25	12.57	106.67
IV	2	37.66	5.47	0.70	5.40	5.00	47.63	13.05	37.40	39.50	25.71	108.83
V	1	54.61	5.52	0.97	6.11	5.40	79.39	11.42	50.44	54.90	1.00	112.67
VI	3	56.05	6.49	0.60	5.38	4.42	48.08	13.18	51.03	56.19	2.00	114.78

Note: Plant height (cm), Number of leaves, Neck thickness (cm), Equatorial diameter(cm), Polar diameter(cm), Average bulb weight (g), Total soluble solids(ºbrix), Marketable yield (t/ha), Total yield (t/ha) , Total weight loss (%), Days taken for harvest (DTH) hence significant differences was observed among different parameters.

Mean values for growth parameters *viz.,* plant height (60.98 cm), leaf number (7.17) and neck thickness (0.97 cm) were noticed highest in genotype present in the cluster III and lowest plant height (37.66 cm), leaf number (5.47) and neck thickness (0.70 cm) was noticed in the genotype of the cluster IV respectively. The genotypes of cluster III also exhibited the highest equatorial bulb diameter (6.17 cm), polar bulb diameter (5.90 cm) and it was significantly lowest in the genotype present in cluster II (3.43 cm). Highest mean values for bulb weight (79.39), marketable yield 50.44, and total yield 54.90 were found in cluster V and the lowest values for these parameters were recorded in the cluster I & III bulb weight (46.22) marketable yield (31.00) and total yield (36.57). Mean values for total soluble solids were noticed highest in cluster II *i.e.,* 13.22 and it was recorded lowest in the cluster V *i.e.,* 11.42 respectively. For storage Cluster III registered lowest total weight loss (12.57), rot loss (5.67) and sprout loss (7.00) and highest mean values were obtained for total weight loss (53.15), rot loss (19.53) and sprout loss (19.20) in the cluster I. Mean values for days taken to harvest was lowest in the genotypes of the cluster II and III (106.67).

GKD-3, Bhima Shakti, Bhima Dark Red, GKD-42, Arka Kalyan, Bhima Super, RGP-3, GKD -75 these genotypes present in the cluster II, III, IV, V, and VI showed variation for growth, yield and storage characters. Utilizing these genotypes in the hybridization program can improve the growth, yield and quality of onion.

The character which appeared first in the rank and its contribution towards total divergence was presented in Table 4.

Among different parameters studied total weight loss was ranked first which contributed (44.48%) followed by total sprouts number (22.60%). Average bulb weight (15.39 %), marketable yield (8.51%), days taken for harvest (3.83 %), plant height (3.44 %), equatorial bulb diameter (0.78 %), the polar bulb diameter (0.58 %), total yield contributed (0.19 %) total soluble solids, total rot loss by number and purple blotch contributed (0.06%) to total divergence. On contrary to this there was no contribution from the traits like thrips incidence, neck thickness, and the number of leaves to the total divergence in onion genotypes. Highest cumulative contribution was noticed for total yield (99.80%) and it was lowest in total sprout number (67.08%).

Onion (*Allium cepa* L.) is one of the leading commercial export-oriented crops of India which contribute 70 per cent to production. Because of its highly cross pollinated nature it behaves differently. Genetic diversity studies helps the breeder to understand the crop behavior and proper knowledge of diversity present in the particular germplasm resources helps in selecting better lines to initiate any breeding programme. This is possible by clustering the germplasm trails based on D^2 values, as it represents the index of genetic diversity among genotypes and clusters. Based on the D^2 values, 56 genotypes were grouped into six clusters. There were 48 genotypes in the cluster I and two genotypes present in cluster IV. In the cluster, VI had three genotypes, while clusters II, III, and V were solitary ones.

The formation of a solitary cluster may be due to the total isolation, preventing the gene flow or intensive natural or human selection for diverse adaptive complexes. The intra-cluster distance varies from 0 in clusters II, III, and IV and the maximum distance was noticed in cluster VI (630.05). This indicates the presence of divergent genotypes within different clusters. Patil (1997)

The inter-cluster D^2 values also ranged widely with a minimum value of 195.06 between clusters II and III and maximum inter-cluster distance was noticed in between cluster III and VI 4600.67 indicating high diversity among the genotypes. Cluster IV with two genotypes (Bhima Dark Red, GKD-42), cluster VI with three genotypes (Arka Kalyan RGP-3 GKD -75) cluster II, III V has single genotypes in them these were the most divergent groups. It is desirable to select accessions from clusters showing high inter-cluster distance. All most all the clusters showing high to a moderate value of diversity. Among the different characters studied, the most important character contributing to the divergence was total weight loss followed by total sprouts. Similar results were noticed by Vinutha (2000), Panthee *et al.* (2006) and Yadav

Table 4. Per cent contribution of 56 genotypes to total divergence during *kharif*

Character	% Contribution	% Cumulative contribution to total divergence
Total weight loss (%)	44.48 %	-
Total sprouts number	22.6 %	67.08
Average bulb weight (g)	15.39 %	82.47
Marketable yield (t/ha)	8.51 %	90.98
Days taken for harvest	3.83 %	94.81
Plant height (cm)	3.44%	98.25
Equatorial bulb diameter (cm)	0.78%	99.03
Polar bulb diameter (cm)	0.58%	99.61
Total yield (t/ha)	0.19 %	99.80
Total soluble solids(°brix)Total rot Number Purple blotch	0.06 %	99.86
Number of leaves Neck thicknessThrips incidence	0.00	-

Per cent contribution of different characters for total divergence *et al.* (2018) in garlic. Mohanty, (2001) also reported the highest contribution from bulb weight. Whereas, Patil (1997) reported that ten bulb weight, marketable bulb per cent and loss due to sprouting were the characters that exhibited maximum contribution towards the diversity in onion. Ningadalli (2006) reported that bulb yield, bulb weight, number of leaves, and storage loss were the maximum contributing characters towards genetic diversity. Dhotre *et al.* (2010) reported that fresh bulb weight, equatorial bulb diameter, bulb splitting, bulb yield total loss as the maximum contributing characters towards genetic diversity these types of results were also observed in our study.

Conclusion

Fifty six genotypes were evaluated to study the genetic diversity using Mahalanobsis D^2 statistics and it was found that GKD-3, Bhima Shakti, Bhima Dark Red, GKD-42, Arka Kalyan, Bhima Super, RGP-1, GKD -75 genotypes present in the cluster II, III, IV, V, and VI and lines L-883, Pune Red, L-863, DOGR-344, L-355, Bhima Kiran, PRO-7, RGP-2, RGP-3, present in the cluster I exhibited moderate diversity. Hence, these can be utilized as lines in hybridization programme for improving growth, yield and storage characters

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