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Study of genetic divergence in kharif onion cultivars

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Abstract

Twenty-two diverse onion genotypes were evaluated to study the genetic divergence in *kharif* onion during *Kharif* season at C-block farm, BCKV, Kalyani, Nadia, West Bengal. All the genotypes were clustered into three groups based on Mahalanobis D^2 statistic. Cluster I comprised of accessions with highest yield, yield related traits and TSS. Cluster II was composed of accessions having highest Total sugar, dry matter, pyruvic acid and phenol content. Cluster III was the largest cluster comprising of accessions having highest polar diameter, neck thickness, days to maturity, bolters and ascorbic acid content. Both total yield and marketable yield together explained almost 85 percent contribution of diversity, whereas the contribution of other traits were only 15 percent.

Keywords: *kharif* onion, divergence, cluster

1. Introduction

Onion (*Allium cepa* L.) is most widely cultivated popular vegetable species. It is used for culinary purpose also it has several non-culinary uses like it is used as moth repellent because of its pungent juice, it is used to polish glass and copperware, onion concentrated water can be spray on plants to increased plants pest resistance. India ranks first in term of area and second in production after China with an output of 23.61 million tonnes from an area of 1.2 million ha (NHB, 2019). The significance of *Kharif* onion in checking the sky rocketing prices during October-March and problem of bolting cum rotting in storage are well understood. *Kharif* onion has a major role in enhancing the area and production of the country. Genetic divergence is the variation in heritable characteristics present in a population which serves as one of the most important factors for improvement in any crop species.

2. Material and Methods

The present experiment was carried out with twenty-two *Kharif* onion cultivars during *Kharif* season at C-block farm, BCKV, Kalyani, Nadia, West Bengal during 2016-17. The experiment was laid in Randomized Block Design (RBD) with three replications. Observations regarding growth parameters were taken from randomly selected ten plants per replication at 90 days after transplanting. In similar manner bulb characters and yield were recorded after harvest. Replication wise mean values of each of the 22 genotypes were computed for respective characters and subjected to statistical analysis. The GENRUS statistical tool was carried out for analysing genetic diversity.

3. Result and Discussion

On the basis of Mahalanobis D^2 statistic, the total yield (52.33%) contributed maximum towards divergence followed by marketable yield (32.78%). Both total yield and marketable yield together explained almost 85% contribution of diversity, whereas the contribution of other traits were only 15% (pyruvic acid 6%, phenol 5%, vitamin C 1.34%, average bulb weight 1%, TSS 0.6%, total sugar 0.6% bolters 0.3%). Therefore, above all the traits marketable yield and total yield were considered most important which could explain the phenomenon of divergence. Mohapatra *et al.* (2017) [3] reported marketable yield and gross yield were major contributor towards the genetic divergence in onion (Table 1).

Table 1: Contribution of each character to Divergence

Serial no.	Character	% Contribution
1	Bolters (%)	0.3333
2	Average bulb weight(g)	1.0000
3	Total soluble solids(°brix)	0.6667
4	Total sugar (%)	0.6667
5	Dry matter (%)	0.000
6	Vitamin-C(mg/g)	1.3333
7	Pyruvic acid(µmole/g)	6.0000
8	Phenol(mg/g)	5.0000
9	Marketable yield(q/ha)	32.6667
10	Total yield(q/ha)	52.3333
	Total	100

Cluster means for different characters showed considerable differences between the clusters for all the characters (Table 2). The genotypes of cluster I recorded the superior performance for plant height (56.61cm), number of leaves (8.77), equatorial diameter (49.23mm), average bulb weight (62.23g), minimum double bulb (5.74%), TSS (15.70^0 brix), marketable yield (210.16q/ha) and total yield (219.81q/ha) whereas the genotypes of cluster – II had higher total sugar (2.11%), dry matter (12.75g), pyruvic acid (2.44%), phenol (6.71mg), and desirable minimum values for days to maturity (130.66),neck thickness(8.25mm) and bolters (12.54%). Similarly, the genotypes of clusters-III showed maximum values for polar diameter (47.37mm).

Table 2: Cluster Means

Characters	Cluster I	Cluster II	Cluster III
Plant height(cm)	56.61	52.66	53.60
Number of leaves	8.77	8.25	8.47
Neck thickness(mm)	6.97	6.34	7.60
Polar diameter(mm)	46.07	42.35	47.37
Equatorial diameter(mm)	49.32	41.37	46.39
Double bulb (%)	5.74	6.71	7.20
Bolters (%)	14.42	12.54	13.18
Average bulb weight(g)	62.23	35.62	51.34
Days to maturity	131.33	130.66	133
Total soluble solids(°brix)	15.70	15.18	15.41
Total sugar (%)	1.94	2.11	2.09
Dry matter (%)	12.65	12.79	12.44
Vitamin-C(mg/g)	6.98	6.25	7.10
Pyruvic acid(µmole/g)	2.41	2.44	1.94
Phenol(mg/g)	4.20	6.71	4.88
Marketable yield(q/ha)	210.16	121.19	184.96
Total yield(q/ha)	219.81	133.08	198.55

All the genotypes were grouped into 3 clusters showed the substantial amount of genetic diversity present among the experiment materials. The maximum number of genotypes (12) was included in cluster III followed by cluster I (6) whereas, minimum number of genotypes was recorded in cluster II (4) (Table 3).

Table 3: Clustering of the Genotypes

Cluster	Varieties
Cluster I (6)	Bhima Super, Agrifound Dark Red, BSS 258, Kohinoor-9, Indam Gulab and Bhima Sweta
Cluster II (4)	Arka Bindu, Arka Kalyan, Bhima Red and Bhima Dark Red
ClusterIII (12)	Bhima Shubhra, Arka Kirtiman, Arka Pragati, Arka Lalima, Bhima Raj, Lucifer, Yellow Grano, Baswant-780, Indam Hybrid-4, Arka Niketan, Arka Bheem and Indam Marshall

The highest inter-cluster distance was recorded between clusters I and II (77.038) followed by clusters II and III (63.996), while minimum in cluster I and III (44.26) (Table 4).

Table 4: Inter and Intra Cluster Distances

	Cluster-I	Cluster-II	Cluster-III
Cluster-I	35.838	77.038	44.244
Cluster-II		38.227	63.996
Cluster-III			46.713

The highest distance between cluster I and III indicates that genotypes under that clusters might have originated from different breeding programmes bearing maximum heterogeneity within the population (Kaushik *et al*., 2016) [2]. Therefore, crossing between two genotypes selected from each cluster will produce more heterotic response and produce wide variability with desirable segregants due recombination diverse gene complex. Kale *et al.* (2014) [1] concluded similar inference while studying genetic divergence among group of onion genotypes. The genotype from different origin was accommodated in the same cluster indicating their close affinity due to similar gene complexes. The results suggested that the genotypes with in a cluster might have some degree of ancestral relationship. As a result, the genotype within the same cluster originated from nearest geographical region with more or less similar kind of gene complexes. Singh and Dubey (2011) [4] reported that the distribution of genotypes from different eco-geographical regions into clusters was random indicating geographical distribution.

4. Conclusion

Divergence analysis indicated high magnitude of variability present in the population and the genotypes were grouped into 3 different clusters. The genotypes of cluster I recorded the superior performance for plant height number of leaves equatorial diameter average bulb weight, TSS, marketable yield, total yield and desirable minimum double bulb whereas the genotypes of cluster – II had higher total sugar, dry matter, pyruvic acid, phenol and desirable minimum values for days to maturity, neck thickness and bolters and the genotypes of clusters-III showed maximum values only for polar diameter. Highest inter-cluster distance estimated between clusters I and II suggested genotypes under these clusters have been originated from different geographical origin and crossing between these groups will produce more heterotic response and desirable segregants due genetic recombination of diverse gene complexes.

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