DIVERGENCE STUDIES IN GLADIOLUS (*GLADIOLUS HYBRIDUS* L.) GERMPLASM

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Abstract: An investigation was carried out to identify the extent of genetic divergence that exist for the flower yield and yield contributing characters of fifteen genotypes of gladiolus. Multivariate analysis was performed on field data using Mahalanobis's D^2-statistics, Tochers method of clustering and combined analysis of variance. Analysis of variance revealed considerable differences among the genotypes for all the morphological traits studied. All the 15 genotypes of gladiolus (*Gladiolus hybridus* L.) were grouped into three clusters on the basis of the morphological diversity. Maximum intra-cluster distance was observed in cluster III (4.544) was recorded between cluster III and I. whereas the minimum average inter cluster D^2 value (3.699) was recorded between clusters III and II. The analysis of divergence indicated significant differences among parental lines for all the agro-morphological characters. On the basis of results obtained in the present investigation, it was concluded that the allelic diversity can be used for future breeding program. The traits under study are also major flower and corm yield contributing traits and are largely associated with each other. Therefore, these traits should be taken into consideration either simultaneously or alone for selecting a high yielding gladiolus genotype.

Keywords: Gladiolus, investigation, germplasm, Iridaceae

INTRODUCTION

Gladiolus (*Gladiolus hybridus* L.), a member of family Iridaceae. It occupies 4th place in international cut flower trade after Rose, Carnation and Chrysanthemum (Farhat, 2004). It is one of the leading cutflower crops grown in our countries, known for its majestic spikes which contain attractive, elegant and delicate florets. With over 260 accepted species, Gladiolus is the second largest genus of Iridaceae family after Iris L. itself (Goldblatt and Manning, 2008). A huge quantum of diversity exists in this crop with respect to shape, growth habit, flowering behaviour, vase life, etc. Inspite of such variability, very few are having desirable characters in terms of yield and quality. Knowledge of divergence studies helps the plant breeder to ascertain the real components of yield and provide an effective basis of selection. The characters contributing significantly to desirable traits can be significantly identified, and can be used as alternate selection criteria in crop improvement programmes. Through collection and selection program, a number of strains have been introduced and acclimatized in various parts of the world, but evaluation studies of yield and its contributing quantitative and qualitative traits are scarce. The multivariate analysis has been established by several investigators for measuring the degree of divergence and for ascertaining the relative contribution of different characters to the total divergence (Singh *et. al*.,2002). Such a study also permits to select the genetically divergent parents to obtain the desirable recombinants in the segregating generations. Moreover, precise information about the extent of genetic divergence and characters used for discrimination among the population is crucial in any crop improvement program (Ashana and Pandey, 1980; Pandey, 2009). Therefore, the present investigation was designed to provide information on genetic divergence of 15 garlic genotypes collected from different sources. The diverse parents belonging to different distant clusters would provide an opportunity for bringing together gene constellations of diverse nature promising hybrid derivatives result probably due to complementary interaction of divergent in parent (Murthy, 1965) and Anand and Murthy, 1968.

MATERIAL AND METHOD

Plant materials

A total of 15 cultivars of gladiolus collected from different parts of the country were used in the present study (Table 1). The experimental field is situated at 29º 01 latitude in the North and 77 º43 longitudes in the Eastern elevation of about 219.75 meters above sea level. The experimental trials were laid out in randomized block design with three replications. Each genotype was assigned to six rows per plot with a distance of 30 cm line to line and 25 cm plant to plant. Data were recorded on five vegetative characters, namely, plant height (PH), number of leaves/plant (NLPP), length of the longest leaf (LLL), width of longest leaf (WLL) and number of suckers/plant (NSPC), nine flowering characters namely, length of spike (LS), length of rachis (LR), spike diameter (SD), spikes per corm (SPC), number of florets per spike (NFPS), flower diameter (FD), visibility of first spike in days (VSD), opening of first flower in days (OFFD), longevity of spike in days(LSD) and four corm chracters i.e. diameter of corm (DC), weight of corm (WC), number of corms/plant (NCPP), cormels per plant (CPP) respectively. The five randomly selected plants in each genotypes of all replication were utilized for taking the observation at appropriate stage. The mean values of the genotypes in each replication for quantitative characters were used for statistical analysis (Table 2). The data were processed with the help of the software programme SPAR-1 (Doshi and Gupta, 1991) utilizing various standard statistical procedures. The data recorded on nine different quantitative traits was subjected to the D^2 statistic of Mahalanobis (Rao, 1952) and average intra- and -inter cluster distances were calculated (Table. 2).

RESULT AND DISCUSSION

The analysis of variance revealed a significant difference among the 15 genotypes for all the 16 characters indicating the existence of high genetic diversity. Cluster formation based on Tocher analysis of field data of morphological traits generated three clusters (Table-2). Maximum inter cluster D^2 value (4.544) was recorded between cluster III and I. whereas the minimum average inter cluster D^2 value (3.699) was recorded between clusters III and II. The intra cluster divergence were found to range between 3.022 for cluster III, 3.987 for cluster I and 4.217 for cluster II. Singh et al. (2012) formed 10 clusters in 32 genotypes of garlic on the basis of 14 morphological characters.

Combined analysis of variance indicated that the magnitude of mean sum of square for maximum weight of corm followed by length of rachis and length of spike and these traits are also known as qualitative traits of gladiolus (Table 3).

The distribution of genotypes belonging to same geographical region in different cluster and grouping of genotypes collected from different location in one cluster is common. This grouping pattern of genoptypes suggested no parallelism between genetic divergence and geographical distribution of genotypes. Sheikh and Khandy, (2008) Swaroop (2010), Singh and Duvey (2011) and Singh *et al.* (2012) also reported that genotypes diversity was independent of geographically region. Murthy and Arunachalam (1966) stated that genetic drift and selection in different environment could cause greater diversity environment could cause greater diversity than geographic distance. Similarly maximum intra- cluster (D^2= 4.217) was observed in cluster II (representing 3 genoypes of the 15 genotypes), (Table.4), followed by, cluster I (D^2 = 3.987) and minimum intra-cluster distance (D^2=3.022) was found in cluster III. Singh et al.,(2012) who had also observed the similar findings.

Cluster means are concerned different clusters have higher mean values for different traits, indicating that few of cluster contained genotypes with most of the desirable characters. It was observed that cluster I included the genotypes with highest length of spike, higher corm weigh, maximum diameter of corm, maximum number of cormlets (Table.5). Similar observations had been earlier reported by Swaroop and Janakiram (2010) in gladiolus. The characters showed in terms superior characters i.e qualitative charectars deserve to be considered as potent parents for further utilization in garlic breeding programme. Therefore, based on D^2 analysis, it has been understood that characters need to be given more weightage, while selecting parents for improvement programme.

Cluster analysis based on Euclidean coefficient values obtained from morphological data showed that four genotypes namely Punjab Glace , Pacific , Orange Ginger , Aldebaran , Arka Kesher found to be present separately from other 15 genotypes that were found to be largely aggregated. These genotypes could be a good alternative for fruitful gladiolus breeding program.

Table 1. List of genotypes with their origin

1	Punjab Pink	PAU, Ludhiana, Punjab
2	Punjab Glace	PAU, Ludhiana, Punjab
3	Pacific	NBRI, Lucknow, Uttar Pradesh
4	Orange Ginger	NBRI, Lucknow, Uttar Pradesh
5	Prabha	NBRI, Lucknow, Uttar Pradesh
6	Sylvia	NBRI, Lucknow, Uttar Pradesh
7	Aldebaran	NBRI, Lucknow, Uttar Pradesh
8	Pricilla	IARI, New Delhi
9	Navalux	IARI, New Delhi
10	Gold Field	IARI, New Delhi
11	Ocilla	IARI, New Delhi
12	Kum-Kum	IIHR, Bangalore, Karnataka
13	Arka Kesher	IIHR, Bangalore, Karnataka
14	Arka Gold	IIHR, Bangalore, Karnataka
15	American Beauty	Meerut, Uttar Pradesh

Table 2. Average intra and inter cluster (D^2 value) distance in gladiolus cultivars

Cluster	I	II	III
I	3.987	4.485	4.544
II		4.217	3.669
III			3.022

Table 3. Combined analysis of variance of 16 morpho-agronomic traits

Source	d.f	PH (cm)	NLPP	LL(cm)	LW (cm)	NSPC	LS (cm)	LR (cm)	SPC	DS (cm)	NFPS
REP	2	0.35	0.01	3.27	0.04	0.00	9.09	17.02	0.00	0.00	2.11
TRET	14	98.28**	0.28**	91.68**	1.27**	1.15**	303.59**	314.59 **	0.15**	0.04**	21.81**
EROR	28	6.72	0.09	4.90	0.02	0.01	9.06	4.16	0.00	0.00	0.46

Source	d.f	FD (cm)	VSD	OFFD	LSD	DC (mm)	WC (gm)	NCPP	CPP
REP	2	0.01	2.00	20.30	0.84	0.12	7.95	0.00	0.03
TRET	14	1.96**	187.78**	264.05**	37.07**	2.23**	2421.36**	0.31**	10.60**
EROR	28	0.24	17.14	27.46	2.56	0.10	13.70	0.01	0.51

Table 4. Distribution of 15 genotypes of Indian gladiolus

Clusters number	No. of genotypes	Genotypes
I	5	Punjab Glace , Pacific , Orange Ginger , Aldebaran , Arka Kesher
II	3	Punjab Pink, Prabha , Sylvia
III	7	Pricilla , Navalux , Gold Field , Ocilla , Kum-Kum, Arka Gold, American Beauty

Table 5. Clusters mean values of different traits

Character / Cluster	PH (cm)	NLPP	LL(cm)	LW (cm)	NSPC	LS (cm)	LR (cm)	SPC	DSPC (cm)	NFPS	FD (cm)	VSD	OFFD	LSD	DC (mm)	WC (gm)	NCPP	CPP
1	-0.80	-0.95	--0.94	-0.76	0.32	--0.77	-0.72	--0.33	-0.68	0.84	-0.57	-0.56	-0.52	0.86	0.39	0.26	0.14	0.59
2	1.50	0.81	1.57	0.09	-0.89	0.08	--0.43	-0.65	-0.41	-0.24	-0.35	0.00	-0.13	-0.18	0.14	0.16	0.07	0.12
3	-0.07	0.33	0.00	0.51	0.15	0.52	0.70	0.51	0.66	0.70	0.56	0.40	0.43	-0.53	-0.34	-0.25	-0. 13	-0.47

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