Eco. Env. & Cons. 28 (May Suppl. Issue) : 2022; pp. (S419-S425)
Copyright@ EM International
ISSN 0971–765X

DOI No.: http://doi.org/10.53550/EEC.2022.v28i03s.060

Genetic divergence in gladiolus (*Gladiolus hybridus* Hort.) genotypes

Sripada Swetha[1]*, Balaji S.Kulkarni[2], Mukund Shiragur[3], M.S. Kulkarni[4], Mahantesha B.N.Naik[5], Ravindra Mulge[6] and Laxminarayan Hegde[7]

[1]Kittur Rani Channamma College of Horticulture, Arabhavi, Karnataka, India
[2]Department of Floriculture & Landscape Architecture, University of Horticultural Sciences, Bagalkot
[3]Department of Floriculture & Landscape Architecture, KRC College of Horticulture, Arabhavi, Karnataka, India
[4]University of Horticultural Sciences, Bagalkot, Karnataka, India
[5]Department of Biotechnology & Crop Improvement, KRC College of Horticulture, Arabhavi, Karnataka, India
[6]College of Horticulture, Halladkeri Farm, Bidar, Karnataka, India
[7]College of Horticulture Engineering and Food technology, Devihosur, Karnataka, India

(Received 9 August, 2021; Accepted 22 January, 2022)

ABSTRACT

Genetic diversity is the first and important parameter in crop improvement programme. In the present investigation forty gladiolus genotypes were assessed to know the nature and magnitude of genetic divergence using Mahalanobis D^2 statistics. The population was grouped into four clusters. The average weight of cormels, daughter corm diameter, average weight of daughter corm, days to corm sprouting, floret diameter and number of cormels per plant components were found main parameters contributing towards divergence and played dominant role in the improvement of gladiolus quality. Based on Mahalanobis D^2 analysis, forty gladiolus genotypes were grouped into four clusters with maximum of 36 genotypes in Cluster I. Remaining three clusters II, III and IV are solitary indicating their independent identity and importance due to various unique characters possessed by them. The highest inter cluster D^2 value was recorded between clusters III (Copperking) and IV (Arka Kesar). Cluster I showed maximum intra cluster diversity. Therefore selection for divergent parents based on these traits is recommended for getting desirable hybrids or segregates in Gladiolus.

Key words : *Genetic divergence, Gladiolus, Mahalanobis D^2 analysis, Cluster distance*

Introduction

Gladiolus is very popular cut flower, commonly known as 'Sword Lily'. It is a tender herbaceous perennial belonging to the family Iridaceae and originated in South Africa. The basic chromosome number is n=15. Most member of genus are heteroploids having the chromosomes ranging from 2n=30 to 120 (diploid, triploid, tetraploid, pentaploid, hexaploid, octaploid and hyperaneauploid). It was introduced into cultivation towards the end of the sixteenth century. It contains 250 species which have immense

---

([1]Ph.D. Scholar, [2]Professor & Head, [3]Assistant Professor, [4]Dean (PG Studies), [5]Assistant Professor, [6]Dean , [7]Dean (i/C)) economical, ornamental, display and cultural importance. Out of 250 species, 12 have contributed for development of present day gladioli. In India many beautiful cultivars (>10,000 varieties) have been developed with very attractive spikes with various colours and these cultivars are cultivated for cut flower as well as garden display purposes which also have tremendous export potential.

For any flower crop including gladiolus, novel flower colour, shapes, sizes, yield and vase life will help in increasing the demand in domestic as well as export market. Considering the importance of the crop and potentiality, there is an urgent need for its improvement. Genetic diversity is an important factor for heritable improvement in any crop. The knowledge with regards to nature and degree of divergence in existing germplasm is extremely valuable in identifying suitable parental combinations to create heterotic progenies with high degree of genetic variability for their effective utilization in breeding programmes. The present study estimates the relative extent of genetic variability through genetic divergence in twenty two diverse genotypes of gladiolus.

Materials and Methods

The experimental material consisting of 40 genotypes of gladiolus with the name, origin and collection of place of the cultivars is given in Table 1. The experiment consisted of estimations of genetic variability for qualitative and quantitative characters in *Gladiolus* germplasm during two successive years 2015-2016 and 2016-2017. The experiment was laid out in Randomized Block Design (RBD) with two replications and each genotype had 15 plants or corms per replication by keeping row to row distance of 30 cm and plant to plant distance of 20 cm. Each replication had two rows of 15 corms out of which five plants were selected randomly and observations were recorded. Twenty six observations were recorded on agronomic and flower attributes.

Mahalanobis (1936) D^2 statistics was used for assessing the genetic divergence forty genotypes for different agronomic and flower traits.

$D^2 = \Sigma\Sigma lij$ sai saj

Where,

D^2 = Square of generalized distance

lij = Reciprocal of the common dispersal index

si = Mi1 - Mi2

sj = Mj1 - Mj2

M= General mean

The related contribution of individual characters to divergence was assessed by ranking of components of D^2 over all combinations. Following Tocher's method as described by Rao (1952), the genotypes were grouped into clusters. The criterion of grouping was that any two genotypes belonging to the same cluster should have a smaller D^2 value than those between genotypes belonging to different clusters. Inter and intra-cluster distances were were calculated by formula given by Singh and Chowdhary (1979).

Results and Discussion

The analysis of variance revealed that the genotypes varied significantly for all the twenty six morphological characters under the present investigation. After computing D^2 value for all the possible pairs forty genotypes were grouped into four clusters using Toucher's method (Rao, 1952) which indicated large genetic diversity. The distribution pattern of genotypes into various clusters pooled over both seasons was shown in Table 4.

Contribution of each character towards genetic divergence was estimated from the number of times that character appeared in first rank (Table 2). It was observed that average weight of cormels contributed maximum (24.62%) towards genetic divergence followed by daughter corm diameter (14.62%), average weight of daughter corm (11.54%), days to corm sprouting (10.38%), floret diameter (9.36), number of cormels per plant (8.85%), rachis length (5.13%). This clearly indicated that progenies expected from crossing diverse parents would reveal greater diversity for crop improvement. Similar observations have been recorded by Nimbalkar *et al*. (2002) for average weight of cormels, Agasimani and Patil (2015), Patra and Mohanty (2015b) for diameter and weight of daughter corm, Kanawjia and Saravanan (2016) for floret diameter in gladiolus.

In D^2 analysis, the genotypes were grouped into 4 clusters and among them cluster I was largest with 36 genotypes. Rest of the clusters II, III and IV were of solitary clusters which having genotypes of Anjali, Copper King and Arka Kesar respectively. Archana *et al*. (2013) and Agasimani and Patil (2015) reported that the formation of solitary clusters may be due to total isolation preventing the gene flow or intensive natural or human selection for diverse

Table 1. Details of gladiolus genotypes used in the experiment

S. No	Genotype	Origin	Source
1.	Summer Sunshine	Holland	Jammu & Kashmir
2.	Delhi Local	India	Jammu & Kashmir
3.	Green Bay	USA	Jammu & Kashmir
4.	Copper King	USA	Jammu & Kashmir
5.	Dhanvantari	-	IARI, New Delhi
6.	JesterYellow	Holland	Jammu & Kashmir
7.	LocalYellow	India	Bengaluru
8.	Arka Amar	IIHR	IIHR, Banglore
9.	Arka Naveen	IIHR	IIHR, Banglore
10.	Arka Arti	IIHR	IIHR, Banglore
11.	Darshan	India	IIHR, Banglore
12.	Jyostna	-	IARI, New Delhi
13.	Suchitra	-	IARI, New Delhi
14.	Magma	-	Navsari, Gujrat
15.	Urmil	-	IARI, New Delhi
16.	White Prosperity	USA	Jammu & Kashmir
17.	Pusa Kiran	IARI	IARI, New Delhi
18.	Sindur	-	IIHR, Banglore
19.	Arka Thilak	IIHR	IIHR, Banglore
20.	Punjab Dawn	India	Navsari, Gujrat
21.	African star	-	IARI, New Delhi
22.	Local pink	-	Bengaluru
23.	Pusa Vidushi	IARI	IARI, New Delhi
24.	Legent	-	IARI, New Delhi
25.	Chandini	-	IARI, New Delhi
26.	Mohini	NBRI	IARI, New Delhi
27.	Hunting Song	-	IARI, New Delhi
28.	Golddust	-	IARI, New Delhi
29.	Surya Kiran	-	IARI, New Delhi
30.	Sunayana	-	Navsari, Gujrat
31.	Gunjan	-	PAU, Ludhiana
32.	Novalux	-	PAU, Ludhiana
33.	Punjab glance	India	IARI, New Delhi
34.	Anjali	IARI	Navsari, Gujrat
35.	Shagun	-	IARI, New Delhi
36.	Priscilla	-	IIHR, Banglore
37.	Arka Sagar	IIHR	IIHR, Banglore
38.	Arka Kesar	IIHR	IIHR, Banglore
39.	Arka Gold	IIHR	Jammu & Kashmir
40.	Candyman	USA	Jammu & Kashmir

adaptive complexes. These genotypes may be very unique and useful in breeding point of view. Similar results were obtained out by Nimbalkar *et al*. (2006), Sheikh and Ahmad (2006) and Archana and Patil (2013) in gladiolus.

The main aim of forming the clusters and finding the intra and inter cluster distances was to provide the base for selecting diverse parents for the further crop improvement programmes. The grouping pattern of the genotypes suggested no parallelism between genetic divergence and geographical distribution of genotypes. These results are in conformity with the findings of Sharma *et al*. (2017), Nimbalkar *et al*. (2006), Pal *et al*. (2006) and Sheikh and Ahmad (2006) in gladiolus. Kumar *et al*. (2014) also reported that 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 which indicated that genotype diversity was independent of geographical region.

In D^2 analysis, the genotypes were grouped into 4 clusters and among them cluster I was largest with 36 genotypes. Rest of the clusters II, III and IV were of solitary clusters which having genotypes of Anjali, Copper King and Arka Kesar respectively. Archana *et al*. (2013) and Agasimani and Patil (2015) reported that the formation of solitary clusters may be due to total isolation preventing the gene flow or intensive natural or human selection for diverse adaptive complexes. These genotypes may be very unique and useful in breeding point of view. Similar results were obtained out by Nimbalkar *et al*. (2006), Sheikh and Ahmad (2006) and Archana and Patil (2013) in gladiolus.

All the forty genotypes were grouped into four clusters and had high range of D^2 values suggesting high variability and diversity among the genotypes. The intra cluster distance ranged from zero in cluster II, III and IV to 219.88 in cluster I which showed a considerable degree of diversity. Here cluster II, III and IV are solitary clusters. So intra cluster distance of these clusters was zero. Similar results were also reported by Rashmi *et al*. (2016) wherein they grouped 20 gladiolus genotypes into five clusters and recorded the intra cluster values ranging from 0 to 93.99. While, Archana and Patil (2016) grouped 30 gladiolus genotypes into eight clusters and intra cluster values ranged from 0 to 3.89. Solitary clusters were also obtained by Archana *et al*. (2013) and Patra and Mohanty (2015b) in gladiolus.

The inter-cluster distance was greater than intra-cluster distance as indicated in Table 3 revealing considerable amount of genetic diversity among the genotypes studied. Similar results were also reported by Archana and Patil (2016) and Agasimani and Patil (2015) in gladiolus. The intra-cluster values were lesser than inter cluster values which indicate the homogenous and heterogeneous nature of the genotypes within and between the clusters. The inter cluster distance (D^2) is the main criterion for selection of genotype. The genotypes belong to the cluster with maximum inter cluster distance are genetically more divergent and hybridization between

Table 2. Relative per cent contribution of different characters to the total divergence in gladiolus

Sl. No.	Character	Number of times ranked first	Per cent contribution towards divergence
1	Days to corm sprouting	81	10.38
2	Plant height (cm)	24	3.08
3	Number of shoots per plant	-	-
4	Number of leaves per plant	-	-
5	Leaf length (cm)	-	-
6	Leaf width (cm)	1	0.13
7	Leaf area/plant (cm^2)	-	-
8	Leaf area index	-	-
9	Stem girth (cm)	7	0.90
10	Days to spike emergence	1	0.13
11	Spike emergence to first floret opening	-	-
12	Days to 50 % flowering	1	0.13
13	Flowering duration	-	-
14	No. of spikes /plant	4	0.51
15	Spike length (cm)	2	0.26
16	Spike weight (g)	23	2.95
17	Rachis length (cm)	40	5.13
18	No. of florets/ spike	1	0.13
19	Floret diameter (cm)	73	9.36
20	Vase life	31	3.97
21	Weight of corm before planting (g)	10	1.28
22	No. of daughter corms/plant	16	2.05
23	Daughter corm diameter (cm)	114	14.62
24	Average weight of daughter corm (g)	90	11.54
25	No.of cormels /plant	69	8.85
26	Average weight of cormels (g)	192	24.62
	Total	**780**	**100.00**

genotypes of divergent cluster is likely to produce wide variability with desirable sergeants (Arunachalam, 1981). Therefore, it is suggested that based upon large cluster distances to attempt crossing of genotypes from all the clusters, may lead to broad spectrum of favorable genetic variability for spike yield improvement.

Table 3. Average intra and inter-cluster D^2 values for four clusters in gladiolus genotypes

Clusters	I	II	III	IV
I	219.88	488.22	414.94	670.14
II		0.00	1081.62	448.81
III			0.00	1168.82
IV				0.00

The inter-cluster average D^2 value was maximum (1168.82) between cluster III and IV followed by between cluster II and cluster III (1081.62). The genotypes of cluster I and III (414.94) exhibited lowest inter-cluster distance indicating the resemblance among the genotypes of this group for all the growth and flowering traits studied. Similar results were also obtained by Swaroop and Janakiram (2010) in gladiolus.

Divergence analysis exhibited maximum inter cluster distance between cluster III and IV. The maximum intra cluster distance was also recorded by cluster I. The above findings exhibited the existence of considerable amount of genetic diversity among the genotypes between different clusters and even within the clusters indicated that genetic base of these genotypes is broadened. Based on inter-cluster distant crosses and selection from more diverse parent expected to get better genotype, these clusters constituent genotype could be used in yield improvement. The highest inter-cluster distance between cluster III and IV could be expected to exert high heterosis effect in the hybrids when crossed and consequently might generate desirable segregants. Hence crosses may be made between genotypes of cluster III with genotype IV in order to obtain better segregants. The results are in conformation with the findings of Archana and Patil (2016), Patra and Mohanty (2015b), Agasimani and Patil (2015) and Deshraj and Misra (2000) in gladiolus.

Cluster means are concerned different characters have higher mean values for different traits, indicating that few of cluster contained genotypes with most of the desirable characters. The formation of distinct solitary clusters may be due to the fact that they have recorded too high and too low cluster mean values (Table 5). Cluster II had high cluster mean values for plant height, leaf area/plant, days to spike emergence, days to 50 % flowering. Cluster III recorded high mean values for spike yield and corm yield, and low values for days to corm sprouting. Whereas, cluster IV had high mean values for spike length, spike weight, rachis length, number of florets per spike, vase life, weight of corm before planting, daughter corm diameter, average weight of daughter corm, number of cormels per plant. Since these traits had contributed highest towards genetic divergence such clusters may have been formed. Similar results were obtained by Archana *et al*. (2013) in gladiolus.

In present study, genotypes from cluster III and IV can be chosen for hybridization programme as cluster III (Copper King) recorded the high cluster mean values for four important characters (early emergence of flower spike, number of spikes /plant, floret diameter, number of daughter corms per plant, average weight of cormels) followed by cluster IV (Arka Kesar) which showed highest cluster

Table 4. Clustering pattern of forty genotypes of gladiolus based on D^2 values

Cluster number	Number of Genotypes	Genotypes included
I	37	Suchitra, Sunayana, Urmil, African star, Sindur, Surya Kiran, Mohini, Pusa Kiran, Hunting Song, LocalYellow, Legent, Golddust, Punjab glance, Chandini, Candyman, White Prosperity, Shagun, Priscilla,Green Bay, Arka Naveen, Gunjan, Dhanvantari, Arka Sagar, Punjab Dawn, JesterYellow, Pusa Vidushi, Jyostna, Novalux, Darshan, Arka Thilak, Local pink, Arka Gold, Arka Amar, Arka Arti, Summer Shine, Delhi Local, Magma
II	1	Anjali
III	1	Copper King
IV	1	Arka Kesar

Table 5. Mean values of cluster for different characters in gladiolus (Pooled, 2015-16 & 2016-17)

SI. No.	Character	Clusters			
		I	II	III	IV
1	Days to corm sprouting	11.23	22.79	8.50	13.44
2	Plant height (cm)	62.62	71.02	58.08	70.45
3	Number of shoots per plant	1.71	1.24	1.80	1.50
4	Number of leaves per plant	11.9	10.33	14.00	10.88
5	Leaf length (cm)	59.76	64.5	54.72	70.13
6	Leaf width (cm)	2.92	3.68	3.05	3.28
7	Leaf area/plant (cm^2)	151.02	202.13	142.06	193.4
8	Leaf area index	0.25	0.34	0.24	0.32
9	Stem girth (cm)	10.14	10.99	11.04	13.49
10	Days to spike emergence	71.38	81.05	68.30	75.87
11	Spike emergence to first floret opening	10.20	9.33	10.83	11.35
12	Days to 50 % flowering	83.78	92.85	81.44	90.95
13	Flowering duration	21.60	22.03	21.61	24.90
14	Number of spikes per plant	1.67	1.09	2.00	1.10
15	Spike length (cm)	97.76	100.94	104.02	113.41
16	Spike weight (g)	28.02	40.15	34.63	40.97
17	Rachis length (cm)	40.59	42.43	44.75	61.51
18	Number of florets per spike	11.45	11.77	11.75	13.75
19	Floret diameter (cm)	8.48	7.70	9.62	8.42
20	Vase life	9.20	9.57	9.55	11.30
21	Weight of corm before planting (g)	23.32	15.23	18.16	37.61
22	Number of daughter corms per plant	1.51	1.52	2.57	1.43
23	Daughter corm diameter (cm)	5.05	4.81	5.05	5.88
24	Average weight of daughter corm (g)	42.52	40.94	29.47	63.30
25	Number of cormels per plant	12.12	10.13	14.25	66.99
26	Average weight of cormels (g)	10.10	6.88	41.75	12.46

mean values for five characters (spike length, spike weight, rachis length, number of florets per spike, vase life, number of cormels per plant, weight of corm before planting, weight of daughter corm). Most of these are important flower attributing characters. In breeding programme, parents having high flower quality potential with wide genetic diversity are likely to yield superior segregants within short period.

Apart from selecting genotypes from the clusters having high inter-cluster distance for hybridization, one can also think of selecting parents based on extent of genetic divergence in respect to a particular character of interest. This is to mean that, if breeder's intention is to improve the spike yield, he can select parents which are highly divergent with respect to this character. According to Singh (1998), it is desirable to select suitable and genetically divergent parents, based on information about the genetic variability and genetic diversity present in the available germplasm. In this study, crossing between Copper King and Arka Kesar could get hybrids which are having high spike and corm yield along with good quality characters and early flowering.

Conclusion

On the basis of D^2 analysis, it has been concluded that the environment had significant effect on the clustering pattern of the genotypes and characters contribution for divergence and on the cluster means (Sheikh *et al*., 2004). Hence, these traits need to be given due weightage while selecting parents for improvement programme (Deshraj and Misra, 2000 and Nimbalkar *et al*., 2002). However, the success of breeding programme depends on the genetic diversity among the parents. As a result, for crop improvement through breeding programme, divergence has to be studied for different genotypes and crosses between the genotypes of divergent clusters may be tried. Genetic divergence analysis indicated the right cluster combinations as parents for hybridization to develop progenies with long spike length and keeping quality.

References

Agasimani, A. D. and Patil, V. S. 2015. Studies on genetic divergence in gladiolus (*Gladiolus hybridus* Hort.) genotypes. *Int. J. Farm Sci.* 5(3) : 102-110.

Archana, B. 2013. Genetic variability and improvement studies in gladiolus (*Gladiolus hybrids* Hort.) Doctor of Philosophy in Horticulture, University Of Agricultural Sciences, Dharwad.

Archana, B. and Patil, V. S. 2013. Studies on genetic divergence in gladiolus genotypes (*Gladiolus hybridus)*. Karnataka. *J. Agri. Sci.* 26 (4): 567-569.

Archana, B. and Patil, V. S. 2016. Genetic diversity analysis in gladiolus genotypes (*Gladiolus hybridus* Hort). *J. Appl. Nat. Sci.* **8** (3) : 1416-1420.

Arunachalam, V. 1981, Genetic distance in plant breeding. *Indian J. Genet.* **41**: 226-236.

Deshraj and Misra, R. L. 2000. Genetic divergence for economic characters in gladiolus under different environments. *J. Ornamental Hort. (New Series).* **3**(1) : 37-42.

Kanawjia, A. and Saravanan, S. 2016, Studies on genetic variability and character association in Gladiolus sp. **New Agriculturist. 27**(1) : 139–144.

Kumar, P., Kumar M. and Kumar, A. 2014. Divergence studies in gladiolus (*Gladiolus hybridus* L.) germplasm. *J. Plant Dev. Sci.* **6** (4) : 583-586.

Nimbalkar, C. A., Katwate, S. M. and Patil, M. T. 2002. Genetic divergence and selection of genotypes. Floriculture Research Trend in India. Proceedings of the National Symposium on Indian Floriculture in the New Millenium, Lal Bagh, Bengaluru: 100-104.

Nimbalkar, C. A., Katawate, S. M., Singh, B. R., Bajaj, V. H. and Warade S. D. 2006. Genetic divergence in gladiolus. *J. Ornamental Horti.* **9**(3) : 179-183.

Pal, S. L., Prasad, A. and Singh, R. A. 2006. Analysis of genetic divergence in gladiolus. *Indian J. Horti.* **63**(1): 70-72.

Patra, S. K. and Mohanty, C. R. 2015b. Genetic divergence study in gladiolus. *J. Recent. Adv. Agric.* 3(2) : 356-360.

*Rao, C. R. 1952. *Advanced Statistical Methods In biometric Research, John Wiley and Sons, New York.* 236-272.

Rashmi, R., Chandrashekar, S. Y., Arulmani, N. and Geeta, S. V. 2016a. Genetic divergence studies in gladiolus genotypes (*Gladiolus hybridus* L.). *Res. Environ. Life Sci.* **9**(3): 274-276.

Sharma, S., Dastagiri, M. B. and Reddy, N. 2017, Morphological variation and evaluation of gladiolus (*Gladiolus hybridus* Hort.) cultivars. *J. Horti.* **4**(4):1-5.

Shiekh, Q. M. 2004. *Genetic divergence and stability performance for some economic traits in gladiolus* (*Gladiolus hybrida* L.), Ph.D thesis, University of *Agricultural Sciences and Technology of Kashmir*.

Sheikh, M. Q. and Ahmad, M. 2006, Genetic divergence for certain economic traits. *Indian J. Genet.* **66** (3) : 257-258.

Singh, P. 1998. Cotton Breeding. Kalyani publishers. New Delhi: 191-211.

Singh, R. H. and Choudhary, B. D. 1979. *Biometrical Methods in Quantitative Genetic Analysis.* Kalyani Publishers, Ludhiana.

Swaroop, K. and Janakiram, T. 2010. Divergence studies in gladiolus. *Indian J. Hort.* **67** : 352-355.