Short Communication

Genetic divergence for certain economic traits of gladiolus (*Gladiolus* L.)

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Gladiolus (*Gladiolus* L.) is one of the most important bulbous ornamental crop, valued for it majestic flower spikes with massive florets of brilliant colours, attractive shapes, varying size and excellent keeping quality. The present study was carried out to assess the genetic divergence among the 62 genotypes of gladiolus and to select the suitable genotypes for further utilization in breeding Programme, which were collected from various sources and were evaluated for vegetative, floral, corm and cormel production traits at three locations in a randomized block design with three replications during *kharif* 2002-2003 using Multivariate analysis. The three random locations varied from lower valley basin (1685m, a.m.s.l at 34°N latitude and 74.89°E of longitude) to higher altitude valley basin (2250m, a.m.s.l., 34°N of latitude and 74° E of longitude) of SKUAST-(K).The experimental plot consisted of 2 rows of 4 m length. In each row 28 corms were planted with a spacing of 30 × 15 cm between rows and plants. The biometrical observations were recorded on five randomly selected plants in each replication and data collected were subjected to multivariate analysis utilizing Mahalanobis D^2 statistic [1] and genotypes were grouped into different clusters following Tochers method of cluster formation.

The analysis of variance revealed a significant difference among the 62 genotypes for all the eleven characters indicating the existence of high genetic variability among the genotypes. Based on the relative magnitude of the D^2 values the genotypes were grouped into twelve (12) clusters in pooled over environment (Table 1). It was observed that cluster-I consists of maximum number of genotypes, while the remaining clusters are monogenotypes except, cluster VIII that had 2 genotypes, while pooling the performance of these genotypes across locations the effect of the modifying factors might have been reduced to a greater extent due to balancing of the effects either way around the mean, resulting in the uniform performance of the genotypes on pooled analysis basis. This genetic diversity expressed in pooled over environment might be due to the full expressions of genetic potential of some genotypes for some of the traits. While the effect

Table 1. Distribution of 62 gladiolus genotypes in different clusters in pooled over environment

Cluster	Genotypes included in the cluster	No. of genotypes in the cluster
I	SKG1, 2, 3, 5, 6, 7, 8, 13, 14, 15, 16, 17, 19, 20, 21, 22, 23, 24, 26, 27, 28, 29, 30, 31, 32, 33, 35, 37, 38, 39, 40, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 56, 57, 58, 59, 60, 62	50
II	SKG 55	1
III	SKG 25	1
IV	SKG 11	1
V	SKG 9	1
VI	SKG 10	1
VII	SKG 34	1
VIII	SKG 1, 4	2
IX	SKG 61	1
X	SKG 36	1
XI	SKG 12	1
XII	SKG 41	1
Total		62

on the others were relatively not so pronounced as indicated by the earlier workers [2]. The variation in the grouping of the genotypes in clusters was presumably due to differential response of different traits in different environment.

The distribution of genotypes belonging to same geographical region in different clusters and grouping of genotypes collected from different locations in one cluster is common, but had no tendency to group together in a cluster, revealing that, there was no parallelism in the geographical and genetic diversity. The inclusion of genotypes of different origin together in the same cluster, indicated the ancestral relationship among the accessions. This indicates that genetic drift and selection in different environment can produce greater diversity than the geographic diversity [3].

The inter-cluster and intra-cluster distance of 62 genotypes are presented in Table 2. Maximum intra-cluster distance (D^2 = 8.92) was observed in cluster-I (representing 50 of the 62 genotypes), followed by cluster VIII (D^2 = 7.86). Rest of the clusters showed no estimates as they had only one genotype. Similarly,

Table 2. Average inter- and intra-cluster (bold) distances of 62 genotypes in gladiolus   (Pooled over environment)

Cluster No.	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII
I	**8.92**	11.53	11.70	11.61	12.57	11.99	10.78	19.84	14.71	12.80	12.15	16.05
II		**0.00**	18.01	18.30	18.51	16.02	10.06	26.48	21.81	19.00	15.44	20.87
III			**0.00**	10.72	11.37	13.16	16.11	18.37	8.94	10.98	14.17	16.04
IV				**0.00**	9.48	10.26	15.32	10.13	8.66	9.57	10.73	11.56
V					**0.00**	11.00	14.64	15.09	8.95	10.75	12.45	14.51
VI						**0.00**	16.62	17.39	12.16	11.92	12.09	18.49
VII							**0.00**	22.48	18.90	17.16	15.26	15.32
VIII								**7.86**	13.62	17.96	19.26	12.49
IX									**0.00**	8.67	14.43	15.79
X										**0.00**	10.60	18.68
XI											**0.00**	16.86
XII												**0.00**

Table 3. Cluster wise mean values of 11 characters in gladiolus   (Pooled over environment)

Cluster No.	No. of cultivars	Plant height (cm)	Days to slipping	Spike length (cm)	Days to basal floret opening	No. of florets spike^{-1}	Durability of whole spike (days)	No. of corms plant^{-1}	Weight of corm (g)	Size of corm (cm)	Number of cormels plant^{-1}	Weight of 10 cormels (g)
I	50	115.35	77.37	90.82	84.72	15.93	11.14	1.50	31.31	4.33	44.66	5.00
II	1	133.23	77.35	105.55	82.72	17.55	12.21	1.70	38.41	4.41	83.30	5.80
III	1	112.76	71.63	84.40	75.33	15.22	9.98	1.27	17.79	4.27	33.29	5.06
IV	1	100.01	80.86	75.96	94.20	13.64	10.84	1.60	25.01	3.78	57.70	4.94
V	1	109.14	77.38	85.92	84.38	14.02	9.86	1.91	23.79	4.23	44.07	6.35
VI	1	102.53	83.47	86.19	78.26	13.68	12.88	1.41	31.05	4.60	103.95	6.98
VII	1	123.79	77.49	91.15	92.57	17.02	9.45	2.43	35.05	4.41	21.15	5.37
VIII	2	91.84	97.45	68.31	112.16	12.88	10.88	1.46	17.83	3.43	35.28	6.96
IX	1	104.89	72.46	84.48	81.10	12.54	9.88	1.39	18.67	4.18	27.16	6.29
X	1	106.81	69.73	86.29	77.78	2.01	9.65	1.30	31.79	4.35	30.97	3.78
XI	1	109.28	75.21	81.63	88.78	14.81	9.37	1.27	32.62	4.28	145.73	3.73
XII	1	108.50	92.71	84.05	116.96	15.53	9.78	1.94	19.59	4.01	44.37	6.60

maximum inter-cluster distance (26.48) was observed between cluster II and cluster VIII, followed by the distance between cluster VII and VIII (22.48), and cluster II and cluster VIV (21.81), suggesting vide diversity between these groups. Hybridization between parental lines selected for these clusters are likely to produce most variable progenies through a systemic breeding for high economic yielding (spike length and number of florets spike^{-1}) recombinants. As far as the cluster means are concerned, different characters have higher mean values for different traits indicating that none of the cluster contained genotypes with all desirable character. However, cluster II showed maximum values in all characters, except days to slipping, number of corms plant^{-1} and weight of 10 cormels, whereas cluster VIII had lower mean values in all the characters, except days to slipping, days to basal floret opening, number of corms plant^{-1} and weight of 10 cormels. So recombinations breeding between genotypes of different clusters is needed (Table 3).

With respect to the characters contributing for genetic divergence days to basal floret opening showed for more divergence. While as spike length, number of florets spike^{-1}, weight of corm, number of cormels plant^{-1} also had a major role in deciding the combination of a trait towards total genetic divergence. Thus, based on the D^2 analysis, it has been understood that the environment had significant effect on the clustering pattern of the genotypes, characters contribution for divergence and on the cluster means, hence these traits need to be given due weightage, while selecting parents for improvement programme [4, 5]. However, the success of breeding Programme depends on the genetic diversity among the parents. As a result while breeding new genotype divergence has to be studied under different environment and crosses between the genotypes of divergent clusters may by tried.

References

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