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Genetic divergence analysis in gladiolus (*Gladiolus grandiflorus*)

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ABSTRACT

The present investigation was carried out to assess the extent of genetic variability, heritability, genetic advance and genetic divergence using 33 gladiolus (*Gladiolus grandiflorus* Hort) genotypes with 16 characters. Moderate to high GCV and PCV were recorded for almost all the characters under study emphasizing the existence of variation in the population. All the characters (except number of days required for spike initiation, number of days required for first floret opening and number of florets/spike) showed high heritability along with higher/moderate genotypic coefficient of variation and genetic advance indicating that most likely the heritability was due to additive gene effects and the genotypes under study were highly diverse and of great potential with regard to these characters, and therefore, these are more reliable for effective phenotypic selection. The inter-cluster average D^2 value was maximum (25.54) between cluster II and VI followed by between cluster V and cluster VI (24.36). The minimum inter cluster distance was obtained between cluster I and cluster III (12.34), indicated that genotypes of cluster I and cluster III are very close to each other. The clustering pattern showed that genotypes of different geographical areas were clubbed in one group and also the genotypes of same geographical area were grouped into same cluster as well as in different cluster indicating formal relationship between geographical diversity and genetic diversity.

Key words: D^2 analysis, GCV, Genetic advance, Heritability, PCV

Gladiolus (*Gladiolus grandiflorus* Hort.) is one of the largest genera in Iridaceae family, with approximately 300 species (Goldblatt *et al*. 2001). This genus is distributed in Mediterranean Europe, Asia, tropical Africa and South Africa. However, the centre of diversity of genus is located in the cape floristic region. It is one of the most important bulbous cut flower crop, commercially grown in many tropical, sub-tropical and hilly parts of the world, owing to its attractive colour and exquisite florets. Besides their intangible aesthetic value, gladiolus can contribute to the economy earning and saving valuable foreign exchange.

Gladiolus is one of the most important cut flower and the second most popular bulbous ornamental crop of the India. It is also known as 'the queen of bulbous flowers' and suitable for floral arrangements and garden display. Success in selection for new types depends on the extent of genetic variability, heritability, genetic advance and genetic divergence which is a prerequisite for initiating appropriate breeding programme in gladiolus.

MATERIALS AND METHODS

The present experiment was conducted at Floriculture Research Farm, Department of Floriculture and Landscaping, ASPEE College of Horticulture and Forestry, Navsari Agricultural University, Navsari, Gujarat which falls under south Gujarat heavy rainfall zone-I, AES-III. The experimental material consisted of 33 genotypes, viz. Sancerre, American Beauty, Her Majesty, Panjab Dawn, Priscilla, Gunjan, Shagun, Psittascinus Hybrid, Wine and Rose, Spic and Span, Peter Pears, Greenstar, Nova Lux, Eurovision, Rose Supreme, Melody, Phule Prerna, Phule Neelrekham, Sylvia, Friendship, Fedelio, T512, Candyman, Bangladesh, Cheops, Pink Lady, Algarve, Limoncello, Magma, and Meridiona. Healthy and uniform sized corms of 3-4 cm diameter were planted in November 2014 at 7-8 cm depth with a spacing of 30 × 20 cm. All the recommended package of practices was followed to grow a successful crop. Under these programme, 16 characters related to vegetative growth, flower production and quality, and bulb production were estimated.

The experiment was laid out in randomized block design with three replications and 40 plants per treatment. The biometrical observations were recorded on twenty randomly taken plants from each variety in each replication. The mean values obtained were used for determining phenotypic coefficient of variation (Burton and Devane 1953), heritability (Hanson *et al.* 1956) and expected genetic advance (Johnson *et al*. 1955). The genetic divergence analysis was carried out using the Mahalanobis's D^2 statistics (Mahalanobis 1936) and genotypes were grouped in clusters according to Tocher's method as described by Rao

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(1952). The intra and inter cluster distances and variances were worked out as per method suggested by Gomez and Gomez (1983).

RESULTS AND DISCUSSION

The analysis of variance revealed that all the sixteen characters exhibited highly significant indicating considerable amount of genetic variability among the genotypes tested under the study (Table 1). Genetic variability is a basic pre requisite for any crop improvement programme on which ample scope to identify high yielding, early and dwarf genotypes to improve different characters simultaneously, provided the material is subjected to judicious selection pressure.

The analysis of variance permits estimation of phenotypic and genotypic coefficients of variability of various polygenic traits. The genotypic coefficient of variation measures the extent of variability among the different traits caused due to the inherent capacity of the genotype. The genotypic and phenotypic coefficients of variation are required to understand the effect of environment on various polygenic traits. The high values of GCV % and PCV % were found for leaf area (30.33, 31.86), number of spikes/plant (30.35, 35.38), number of cormels/plant (60.11, 60.51), weight of cormels/plant (60.79, 62.38), number of sprout/plant (29.21, 32.62), and weight of corms/plant (30.94, 32.92), respectively. The moderate values of GCV % and PCV % were recorded for plant height (12.78, 13.62), number of days required for sprouting (12.28, 12.75), number of leaves/plant (18.79, 19.10), length of spike (13.53, 14.18), size of corms (18.64, 19.36) and diameter of floret (13.32, 13.87), respectively. The least values of GCV % and PCV % were estimated for number of days required for first floret opening (7.07, 7.59) and number of days required for spike initiation (8.39, 8.81), respectively. The high PCV (7.66%) and low GCV (5.90%) were recorded for number of florets/spike (Table 2).

The estimates of genotypic coefficients of variation in the present study were found to be lower than those of phenotypic coefficient of variation indicating that the apparent variation is not only due to genotype, but also due to the influence of environment. Similar results have been reported by Pratap and Rao (2006) for most of the characters studied. Narrow differences between genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were observed for the number of days required for sprouting, plant height (cm), number of leaves/ plant, leaf area, number of days required for spike initiation, number of days required for first floret opening, length of spike, diameter of floret, number of cormels/ plant and size of corms, indicated the least influence of environment on these characters. Similar results were obtained by Pragnyashree *et al*. (2014) and Pratap and Rao (2006) in gladiolus. Higher difference between GCV and PCV were observed for number of florets/spike, number of sprout per plant, number of spikes/plant, number of corms per plant and weight of corms/plant.

Heritability in broad sense and genetic advance as per cent mean was calculated for 16 characters. Heritability and genetic advance are important selection parameters. Heritability estimates along with genetic advance are more useful in predicting the gain under selection than heritability estimates alone (Robinson *et al.* 1949). However, it is not necessary that a characters showing high heritability will

Table 1 Analysis of variance for sixteen traits in 33 genotypes of gladiolus

Source of variation	DF	No. of days required for sprouting	Plant height (cm)	No. of sprout/ plant	No. of leaves/ plant	Leaf area	No. of days required for spike initiation	No. of days required for first floret opening	No. of florets/ spike
Replication	2	4.756**	42.29**	0.330**	0.71**	48.29	17.89**	39.10**	108.56
Genotypes	32	4.188**	153.37**	0.620**	4.55**	2136.56**	91.26**	88.18**	98.26**
Error	64	0.107	6.66	0.047	0.049	71.63	3.03	4.32	96.24
SEm ±		0.186	1.47	0.12	0.126	4.81	0.99	1.18	5.58
CD (P = 0.05)		0.37	2.93	0.25	0.25	9.61	1.98	2.36	11.14
CD (P = 0.01)		0.495	3.89	0.33	0.34	12.77	2.63	3.13	14.80
	DF	*No of spikes/ plant*	*Length of spike*	*Diameter of floret*	*No. of corms/ plant*	*No. of cormels/ plant*	*Size of corms*	*Weight of cormels/ plant*	*Weight of corms/ plant*
Replication	2	0.076	28.19	0.997**	0.025	9.53	0.37**	9.79	12.09
Genotypes	32	0.55**	247.39**	4.13**	0.206**	1114.37**	2.72**	223.69**	577.39**
Error	64	0.059	7.85	0.11	0.025	17.18	0.069	3.89	24.41
SEm ±		0.14	1.59	0.19	0.0907	2.36	0.15	1.12	2.80
CD (P = 0.05)		0.28	3.18	0.38	0.18	4.71	0.299	2.24	5.61
CD (P = 0.01)		0.37	4.23	0.50	0.24	6.26	0.398	2.98	7.46

** Significant at P=0.01

Table 2 Genotypic and phenotypic co-efficient of variation, heritability and genetic advance as per cent of mean for 16 traits in 33 genotypes of gladiolus

Character	Range	GCV (%)	PCV (%)	Broad sense heritability (%)	Genetic advance/ percent of mean
No. of days required for sprouting	7.07-11.87	12.28	12.75	92.67	24.36
Plant height (cm)	42.77-70.48	12.78	13.62	88.02	24.70
No. of sprouts/plant	1.00-2.80	29.21	32.62	80.22	53.90
No. of leaves/plant	5.53-12.47	18.79	19.10	96.81	38.09
Leaf area	35.24-174.19	30.33	31.86	90.57	59.45
No. of days required for spike initiation	55.67-79.13	8.39	8.81	90.66	16.45
No. of days required for first floret opening	66.40-88.47	7.07	7.59	86.61	13.54
No. of florets/spike	8.60-17.00	5.90	70.66	0.70	1.01
No. of spikes/plant	1.00-2.67	30.35	35.38	73.55	53.61
Length of spike	44.62-82.45	13.53	14.18	91.05	26.60
Diameter of floret	6.99-11.42	13.32	13.87	92.21	26.34
No. of corms/plant	1.00-2.07	18.49	22.05	70.29	31.93
No. of cormels/plant	5.40-89.33	60.11	61.51	95.51	121.01
Size of corms	2.84-8.18	18.64	19.36	92.71	36.97
Weight of cormels/plant	2.59-39.69	60.79	62.38	94.96	122.04
Weight of corms/plant	17.53-75.46	30.94	32.92	88.30	59.89

also exhibit high genetic advance. Estimates of heritability also give some idea about the gene action involved in the various polygenic traits. It is being used in predicting the performance of genotypes in subsequent generations and to decide the appropriate weightage to be given for improving particular character and the breeding method to be followed for improvement of specific character.

In the present study, the magnitude of heritability (Table 2) ranged from 0.70 to 95.52 and genetic advance was ranged from 1.01 to 122.04. The higher magnitude of heritability was exhibited in all the characters, except number of florets/ spike (0.70). High heritability alone is not enough to make efficient selection in the advanced generations and unless accompanied by substantial amount of genetic advance. Burton (1952) pointed out that heritability in combination with intensity of selection and amount of variability present in the population influences the genes to be obtained from the selection. Thus, genetic advance is another important selection parameter. The high heritability was coupled with high genetic advanced which indicated that these characters were least influenced by environmental factors and prevalence of additive gene action in their inheritance and hence, suitable for selection to bring out improvement in the crop (Patra and Mohanty 2014). Under study, the expected genetic advance expressed in percentage of mean was high for all the characters, except number of days required for spike initiation, number of days required for first floret opening and number of florets/spike. The high magnitude of heritability was coupled with high to moderate expected genetic advance, indicated that the predominance of additive gene action for these traits and early generation selection could be practical to improve these characters due to reliability of additive gene action for selection. Similar results found by Pattanaik *et al.* (2015). Low heritability estimates for a character indicated larger role of environmental effect and selection based on phenotypic value may not be effective. Under present study, low heritability was observed for number of florets/plant (0.70), this result was supported by Bichoo *et al.* (2002);

Table 3 The distribution of 33 genotypes of gladiolus into six different clusters on the basis of Mahalanois D^2 Statistic

Cluster	No of genotypes	Genotypes
I	28	Gunjan, Wine and Rose, Shahrjada, Novalux, Eurovision, Shagun, Punjab Dawn, Her Majesty, T512, Magmas, Limoncello, Cheops, Pink Lady, Bangladesh, Algrave, Meridina, Phule Neelrekha, Pusa Suhagin, Pricilla, Chandani, Prince Margaret Rose, Phule Ganesh, Jester Gold, Malcagni, Yellow Stone, Forta Rosa, Ocilla, Green Star
II	1	Snow princess
III	1	Sancerre
IV	1	Psittacinus Hybrid
V	1	Flame Souveniar
VI	1	American Beauty

Table 4 Average Intra and Inter – cluster (D^2) value for 33 genotypes of gladiolus

Cluster	I	II	III	IV	V	VI
I	9.48	14.27	12.34	13.27	13.64	19.79
II		0.00	15.67	16.55	20.52	25.54
III			0.00	14.71	15.92	19.55
IV				0.00	19.17	19.66
V					0.00	24.36
VI						0.00

Pratap and Rao (2006); Lepcha *et al*. (2007); Nimbalkar *et al*. (2007) in gladiolus. All the characters (except number of days required for spike initiation, number of days required for first floret opening and number of florets/spike) showed high heritability along with higher/moderate genotypic coefficient of variation and genetic advance indicating that most likely the heritability was due to additive gene effects and the genotypes under study were highly diverse and of great potential with regard to these characters. Further, improvement in these characters would achieved by phenotypic selection.

Table 5 Cluster means for sixteen characters in thirty-three genotypes of gladiolus

Cluster number	No. of days required for sprouting	Plant height (cm)	No. of sprouts/plant	No. of leaves/plant	Leaf area	No. of days required for spike initiation	No. of days required for first floret opening	No. of florets/spike
I	9.33	54.86	1.41	6.30	86.26	64.20	74.31	14.00
II	10.47	63.08	1.80	5.73	174.19	59.47	70.73	16.67
III	10.73	47.67	1.27	6.47	122.76	68.33	80.13	16.60
IV	11.60	49.27	2.53	7.93	35.24	79.13	88.47	12.27
V	10.47	61.83	1.60	5.87	57.67	58.00	67.20	13.60
VI	8.73	48.08	2.80	12.47	49.97	71.00	82.20	8.60
	No. of spikes/ plant	*Length of spike*	*Diameter of floret*	*No. of corms/ plant*	*No. of cormels/plant*	*Size of corms*	*Weight of cormels/plant*	*Weight of corms/plant*
I	1.25	66.42	8.61	1.29	32.48	5.02	13.56	41.94
II	1.40	71.88	8.56	1.33	89.33	4.98	23.58	47
III	1.20	77.09	11.42	1.27	18.07	5.65	4.03	75.46
IV	2.20	57.22	8.37	1.40	6.40	2.84	39.70	43.50
V	1.53	55.81	8.52	2.07	13.67	8.18	2.59	53.56
VI	2.67	57.76	8.89	1.73	12.87	4.35	15.11	53.96

Table 6 Per cent contribution of sixteen characters towards genetic divergence in gladiolus

Character	Contribution (%)
No. of days required for sprouting	7.77
Plant height (cm)	2.84
No. of sprouts/plant	0.19
No. of leaves/plant	7.95
Leaf area	2.46
No. of days required for spike initiation	5.11
No. of days required for first floret opening	0.00
No. of florets/spike	0.00
No. of spikes/plant	0.00
Length of spike	6.06
Diameter of floret	14.20
No. of corms/plant	0.00
No. of cormels/plant	14.77
Size of corms	8.52
Weight of cormels/plant	20.64
Weight of corms/plant	9.47

On basis of D^2 analysis (Mahalanobis 1936), the thirty-three genotypes were grouped into six clusters (Table 3). The cluster I was very large and comprised of 28 genotypes (Gunjan, Wine and Rose, Shahrjada, Novalux, Eurovision, Shagun, Punjab Dawn, Her Majesty, T512, Magma, Limoncello, Cheops, Pink Lady, Bangladesh, Algrave, Meridina, Phule Neelrekha, Pusa Suhagin, Pricilla, Chandani, Prince Margaret Rose, Phule Ganesh, Jester Gold, Malcagni, Yellow Stone, Forta Rosa, Ocilla and Green Star) and other clusters were solitary, viz. cluster II (Snow Princess), cluster III (Sancerre), cluster IV (Psittacinus Hybrid), cluster V (Flame Souveniar) and cluster VI (American Beauty). The clustering pattern showed that genotypes of different geographical areas were clubbed in one group and also the genotypes of same geographical area were grouped into same cluster as well as in different cluster indicating formal relationship between geographical diversity and genetic diversity.

Intra and inter cluster distance (D^2) were computed for six clusters and presented in Table 4. The inter-cluster average D^2 value was maximum (25.54) between cluster II and VI followed by (24.36) between cluster V and cluster

VI. The minimum inter cluster distance was obtained between cluster I and cluster III (12.34). It indicates that genotypes of cluster I and cluster III are very close to each other. The maximum intra cluster distances was observed in cluster I (9.48) indicating differences in genotypes within the cluster.

A considerable range of variation was found in cluster mean value in respect of all 16 characters given in Table 5. A close perusal of these cluster mean for different characters indicated that cluster II had highest cluster mean for leaf area (174.19), length of spike (77.09), weight of corms/plant (75.46) and diameter of floret (11.42). Cluster II showed the highest clusters mean for plant height (63.08 cm), number of florets/spike (16.67) and number of cormels/ plant (89.33). The cluster VI exhibited maximum mean value for number of leaves/plant (12.47), number of sprouts/plant (2.80) and number of spikes/ plant (2.67), while minimum mean for number of days required for sprouting (8.73). The cluster IV had highest mean value for weight of cormels/plant (39.70) whereas cluster V showed maximum value for size of corms (8.18) and number of corms/ plant (89.33), while minimum mean value for number of days required for spike initiation (58.00) and number of days required for first floret opening (67.20).

The relative contribution of different quantitative characters under evaluation towards the expression of genetic divergence is given in Table 6. The trait weight of cormels/plant contributed maximum (20.64%) towards genetic divergence followed by number of cormels/ plant (14.77%), diameter of floret (14.20%), weight of corms/plant (9.47 %), size of corms (8.52 %) and number of leaves/ plant (7.95 %). 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 II and VI could be expected to exert high heterosis effect in the hybrids when crossed and consequently might generate desirable segregates. The characters which contributed maximum in genetic divergence were, viz. weight of cormels/plant (20.64%), number of cormels/ plant (14.77%), diameter of floret (14.20%), weight of corms/plant (9.47%), size of corms (8.52%) and number of leaves/plant (7.95%) and number of days required for sprouting (7.77%) can be used in selecting diverse parent for hybridization programme.

Thus, apparently contribution of additive gene effects in the expression of these traits was indicated. Consequently, improvement in these characters through direct selection to develop better cultivars of gladiolus can easily be done. High heritability with low genetic advance indicated the contribution of non-additive gene effects. Hybridization and asexual propagation of F_1 can be done to exploit. The clustering pattern showed that genotypes of different geographical areas were clubbed in one group and also the genotypes of same geographical area were grouped into same cluster as well as in different cluster indicating formal relationship between geographical diversity and genetic diversity. From the investigation it was found that inter crossing genotypes from clusters II and VI and cluster II and V might result in wide array of variability for exercising effective selection.

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