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

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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 23 gladiolus (*Gladiolus hybridus* Hort.) genotypes with 27 characters. Moderate to high GCV and PCV were recorded for almost all the characters except days taken to spike initiation, days taken for colour showing stage, days taken from first floret to last floret opening in a spike, vase life and number of days taken to 50% flowering under study emphasizing the existence of variation in the population. All the characters except days taken from first floret to last floret opening in a spike, days taken to spike initiation, number of days taken to 50% flowering and vase life showed higher and moderate 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 (2116.27) between cluster I and III followed by between cluster II and cluster III (1318.53). The minimum inter cluster distance was obtained between cluster II and cluster IV(143.00), indicated that genotypes of cluster II and cluster IV 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.

Keywords: Gladiolus, genetic diversity, heritability, cluster, genotype

Introduction
Gladiolus is considered to be a high value crop next to rose in floricultural trade. Gladiolus (*Gladiolus hybridus* 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. It 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. The improvement of gladiolus has remained more or less stationary due to lack of good parents. It is a well-known fact that choice of parents is of paramount importance in any successful breeding programme. 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. Very scanty information is available under Banda agro climatic condition in respect of genetic diversity of gladiolus. Therefore, present investigation was undertaken with the following objectives:
1. To assess the genetic variability, heritability and genetic advances existing in the selected genotypes for growth, yield and quality parameters.
2. To study the genetic divergence among different gladiolus genotypes.

Materials and Methods
The present experiment was conducted at Instructional Farm, Department of Floriculture and Landscaping, College of Horticulture, Banda University of Agriculture and Technology, Banda, Uttar Pradesh which falls under Bundelkhand Agro-climatic zone of Zone 8-Central Plateau and Hills Region.

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The experimental material consisted of 23 genotypes, *viz.* Praha, Big Time Supreme, Fidelio, Shabnam, Snow Princess, Flirt, Gunjan, Chandani, Sylvia, White Prosperity, C.P.G., Punjab Lemon Delight, Punjab Pink Elegance, Shagun, Punjab Dawn, Glad-6, Punjab Glance, Nova Lux, American Beauty, Pusa Subham, Green Sapphire, Royal Jubilee and Pusa Kiran. Healthy and uniform sized corms of 3-4 cm diameter were planted in November, 2020 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, 27 characters related to vegetative growth, flower production and quality, and corm production were estimated.

The experiment was laid out in randomized block design with three replications and 36 plants per treatment. The biometrical observations were recorded on fifteen 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) [2], heritability (Hanson *et al.*, 1956) [6] and expected genetic advance (Johnson *et al.*, 1955) [8]. The genetic divergence analysis was carried out using the Mahalanobis's D^2 statistics (Mahalanobis, 1936) [11] and genotypes were grouped in clusters according to Tocher's method as described by Rao (1952) [18]. The intra and inter cluster distances and variances were worked out as per method suggested by Gomez and Gomez (1983) [5].

Results and Discussion
The analysis of variance revealed in Table 1 that all the twenty seven characters except days taken for first floret to last floret opening in a spike exhibited highly significant indicating considerable amount of genetic variability among the genotypes tested under the study. Genetic variability is a basic prerequisite 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. Data presented in Table 2 that the high values of GCV % and PCV % were found for leaf area (31.36, 31.42), number of shoots/ plant (25.64, 31.64), days taken to corm sprouting (24.49, 32.95), number of spike per plant (20.30, 25.33), rachis length (20.26, 22.97), weight of spikes (29.66, 31.59), number of corms per plant (22.31, 27.20), number of cormels per plant (25.96, 31.60), average weight of corms (24.33, 30.31), respectively. The moderate values of GCV % and PCV % were recorded for plant height (10.08, 15.71), stem girth (16.20,18.72), number of leaves per plant (11.75, 14.95), leaf length (11.98, 13.86), length of spikes (10.64, 17.33), girth of spike (12.47, 14.54), number of florets per spike (18.79, 21.65), diameter of florets (10.51, 13.81), diameter of corms (15.65, 21.27) and average weight of cormels (11.71, 17.78), respectively. The least values of GCV (%) and PCV (%) were estimated for days taken to spike initiation (4.60, 8.40), days taken for colour showing stage (4.41, 6.87), days taken from first floret to last floret opening in a spike (5.35, 17.61) and

vase life (4.39, 8.09), respectively. The high PCV (5.90%) and low GCV (2.97%) were recorded for number of days taken to 50% flowering.

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) [17] for most of the characters studied. Narrow differences between genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were observed for leaf area, stem girth, leaf length, girth of spike, rachis length, weight of spike, number of florets per spike, diameter of florets, indicated the least influence of environment on these characters. Similar results were obtained by Swetha *et al*. (2019) [22]; Ishwarraddy *et al.* (2018) [7]; Pragnyashree *et al.* (2014) [16] and Pratap and Rao (2006) [17] in gladiolus. Higher difference between GCV and PCV were observed for days taken to corm sprouting, plant height, number of shoots per plant, number of leaves per plant, leaf width, days taken to spike initiation, days taken for colour showing stage, days taken from first floret to last floret opening in a spike, number of spikes per plant, number of spikes per square meter, number of spikes per ha, length of spikes, vase life, number of corms per plant, number of cormels per plant, diameter of corms, average weight of corms and average weight of cormels.

Heritability in broad sense and genetic advance as per cent mean was calculated for 27 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) [19]. However, it is not necessary that a characters showing high heritability will 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 mentioned in Table 2 which ranged from 6.22 to 99.65 and genetic advance was ranged from 3.07 to 64.50. The higher magnitude of heritability was exhibited in the characters, *viz.* stem girth, number of shoots per plant, number of leaves per plant, leaf length, leaf width, leaf area, number of spikes per plant, number of spikes per sq meter, girth of spike, rachis length, weight of spike, number of florets per spikes, number of corms per plant, number of cormels per plant and average weight of corms. High heritability alone is not enough to make efficient selection in the advanced generations and unless accompanied by substantial amount of genetic advance. The moderate heritability was exhibited in days taken to corm sprouting, plant height, days taken for colour showing stage, number of spikes per ha, length of spike, diameter of florets, diameter of corms and average weight of cormels. Burton (3) 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) [14]. Under study, the expected genetic advance expressed in percentage of mean was high for all the characters, except plant height, days taken to spike initiation, days taken for colour showing stage, days taken from first floret to last floret opening in a spike, length of spikes, diameter of florets, vase Life, number of days taken to 50% flowering and average weight of cormels. 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) [15]. 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 days taken to spike initiation, days taken from first floret to last floret opening in a spike, vase life and number of days taken to 50% flowering, this result was in line of agreement with the findings of Bichoo *et al.* (2002) [1]; Pratap and Rao (2006) [17]; Lepcha *et al.* (2007) [10]; Nimbalkar *et al.* (2007) [13]; Singh and Singh (2018) [18]; Rashmi and Chandrashekhar (2016) [19]; Kumar *et al.* (2019) [9] in gladiolus. All the characters except days taken to corm sprouting, plant height, days taken for colour showing stage, number of spikes per ha, length of spike, diameter of florets, diameter of corms and average weight of cormels, days taken to spike initiation, days taken from first floret to last floret opening in a spike, vase life and number of days taken to 50% flowering 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 be achieved by phenotypic selection.

On basis of D² analysis (Mahalanobis, 1936) [11], the twenty-three genotypes were grouped into five clusters and elaborated in Table 3. The cluster I was very large and comprised of 11 genotypes (Sylvia, C.P.G, Chandani, Punjab Dawn, Flirt, Punjab Pink Elegance, Shagun, Glad-6, Punjab Glance, Shabnam and American Beauty), cluster IV consisted of 7 genotypes (Fidelio, Royal Jubilee, Punjab Lemon Delight, Snow Princess, Pusa Subham, Gunjan and Nova Lux), cluster III comprised of 3 genotypes (Praha, White Prosperity and Green Sapphire) and other clusters were solitary, *viz.* cluster II (Pusa Kiran)) and cluster V (Big Time Supreme). 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 (D²) were computed for five clusters and presented in Table 4. The inter-cluster average D² value was maximum (2116.27) between cluster I and III followed by (1318.53) between cluster II and cluster III. The minimum inter cluster distance was obtained between cluster II and cluster IV (143.00). It indicates that genotypes of cluster II and cluster IV are very close to each other. The maximum intra cluster distances was observed in cluster III (173.26) indicating differences in genotypes within the cluster.

A considerable range of variation was found in cluster mean value in respect of all 27 characters embodied in Table 5. A close perusal of these cluster mean for different characters indicated that cluster III had highest cluster mean for plant height (92.28 cm), number of shoots per plant (2.26), number of leaves per plant (8.63), leaf length (43.34 cm), leaf area (127.19 sq cm), days taken for spike initiation (96.63), days taken for colour showing stage (107.10), weight of spike (75.53 g), diameter of corms (5.32 cm), average weight of corms (67.69 g), average weight of cormels (8.62 g). However, the cultivars included in cluster V showed highest cluster mean for stem girth (14.94 mm), leaf width (31.08 mm), number of spikes per hectare (3.18 lakh), girth of spikes (8.09 mm), diameter of florets (9.81 cm), number of corms per plant (2.24) and number of cormels per plant (38.62). Cluster II exhibited maximum mean value for number of days taken for corm sprouting (16.30), days taken from first floret to last floret opening in a spike (8.63), rachis length (35.91 cm) and number of florets per spike (13.60). Cluster I had highest mean value for number of days taken to fifty per cent flowering (111.90) and Cluster IV showed maximum value for vase life (7.28 days).

The relative contribution of different quantitative characters under evaluation towards the expression of genetic divergence is given in Table 6. The trait leaf area contributed maximum (70.36%) towards genetic divergence followed by diameter of corm (10.28%), number of cormels per plant (5.14%), average weight of corms (4.35%) and number of corms per plant (2.77%), length of spike (1.58%) and diameter of florets (1.19%). 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 I and III 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.* leaf area (70.36%), diameter of corm (10.28%), number of cormels per plant (5.14%), average weight of corms (4.35%) and number of corms per plant (2.77%). can be used in selecting diverse parent for hybridization programme.

Table 1: Analysis of variance (ANOVA) for twenty seven traits in 23 genotypes of gladiolus

Source of variation	DF	No. of days taken to corm sprouting	Plant height (cm)	Stem girth (mm)	No. of shoots / plant	No. of leaves / plant	Leaf length (cm)	Leaf width (mm)	Leaf area (cm²)	Days taken for spike initiation
Replication	2	43.80*	100.09	12.8**	1.08*	3.24*	10.8	23.86	4.97	313.42**
Genotypes	22	43.61**	295.77**	13.08**	0.91**	2.61**	62.65**	73.46**	1616.40**	94.32**
Error	44	9.27	95.42	1.31	0.13	0.44	6.32	7.92	1.87	41.35
SEm ±		1.71	5.51	0.64	0.20	0.37	1.42	1.58	0.77	3.63
CD (P = 0.05)		3.46	11.11	1.31	0.42	0.76	2.86	3.20	1.56	7.32
CD (P = 0.01)		5.01	16.08	1.89	0.61	1.10	4.14	4.63	2.26	10.58

	DF	Days taken for colour showing stage	Days taken for first floret to last floret opening in a spike	No. of spikes / plant	No. of spikes/ meter²	No. of spikes / ha (lakh)	Length of spikes (cm)	Girth of spikes (mm)	Rachis length (cm)	Weight of spike (g)
Replication	2	289.12**	15.83*	0.33*	111.99*	1.13*	67.74	0.20	75.01*	52.64
Genotypes	22	91.01**	2.59	0.45**	112.99**	1.04**	222.40*	2.93**	139.89**	763.25**
Error	44	29.33	1.98	0.07	19.04	0.19	79.09	0.31	12.16	32.65
SEm ±		3.05	0.79	0.15	2.46	0.24	5.02	0.32	1.96	4.66
CD (P = 0.05)		6.16	1.60	0.30	4.97	0.49	10.12	0.64	3.97	6.50
CD (P = 0.01)		8.91	2.32	0.44	7.18	0.72	16.63	0.92	5.74	9.40

	DF	No. of florets / spike	Diameter of the florets (cm)	Vase life (Days)	No. of days taken to 50% flowering	No. of corms / plant	No. of cormels / plant	Diameter of corm (cm)	Average weight of corms (g)	Average weight of cormels (g)
Replication	2	4.66	2.37*	0.76	529.57**	0.065	41.64	0.098	21.33	1.09
Genotypes	22	18.64**	3.50**	0.54*	65.09*	0.80**	179.37**	1.98**	643.67**	3.82**
Error	44	1.83	0.68	0.24	32.27	0.11	24.79	0.43	100.02	1.15
SEm ±		0.76	0.46	0.27	3.20	0.18	2.81	0.37	5.64	0.60
CD (P = 0.05)		1.54	0.94	0.56	6.46	0.38	5.67	0.75	11.38	1.22
CD (P = 0.01)		2.23	1.36	0.81	9.35	0.55	8.19	1.09	16.46	1.77

* denotes significant at P=0.05 & ** significant at P=0.01respectively

Table 2: Genotypic and phenotypic co-efficient of variation, heritability and genetic advance as per cent of mean for 27 traits in 23 genotypes of gladiolus (*Gladiolus hybridus* Hort.).

Character rs	Range	GCV (%)	PCV (%)	Broad sense heritability (%)	Genetic advance as percentage of mean
Days taken to corm sprouting	8.20-24.93	24.49	32.95	55.23	37.49
Plant height	65.49-102.63	10.08	15.71	41.17	13.32
Stem girth	9.33-17.17	16.20	18.72	74.84	28.87
No. of shoots/ plant	1.07-3.00	25.64	31.64	65.65	42.80
No. of leaves / plant	5.87-9.20	11.75	14.95	61.82	19.04
Leaf length	29.10-46.77	11.98	13.86	74.80	21.35
Leaf width	15.76-33.22	18.97	22.14	73.37	33.47
Leaf area	48.22-129.86	31.36	31.42	99.65	64.50
Days taken to spike initiation	79.20-101.17	4.60	8.40	29.92	5.19
Days taken for colour showing stage	91.60-110.48	4.41	6.87	41.20	5.83
Days taken from first floret to last floret opening in a spike	7.03-10.73	5.35	17.61	9.22	3.34
No. of spikes /plant	1.20-2.86	20.30	25.33	64.24	33.52
No. of spikes/ meter²	20.00-45.00	19.17	24.31	62.19	31.14
No. of spikes/ ha (lakh)	2.00-4.43	18.40	23.78	59.87	29.33
Length of spikes	47.03-81.53	10.64	17.33	37.66	13.45
Girth of spikes	5.66-10.09	12.47	14.54	73.54	22.03
Rachis length	23.12-48.37	20.26	22.97	77.77	36.18
Weight of spikes	32.54-87.33	29.66	31.59	88.18	57.39
Number of florets/spike	8.44-17.53	18.79	21.65	75.39	33.62
Diameter of florets	7.76-11.54	10.51	13.81	57.96	16.49
Vase Life	6.37-8.00	4.39	8.09	29.41	4.90
No. of days taken to 50% flowering	102.67-120.67	2.97	5.90	25.31	3.07
No. of corms/plant	1.27-3.33	22.31	27.20	67.29	37.71
No. of cormels/ plant	12.47-46.47	25.96	31.60	67.51	43.95
Diameter of corms	3.46-6.43	15.65	21.27	54.13	23.72
Average weight of corms	28.78-85.97	24.33	30.31	64.43	40.24
Average weight of cormels	5.72-9.92	11.71	17.78	43.43	15.90

Table 3: The distribution of 23 genotypes of gladiolus into five different clusters on the basis of Mahalanobis D² Statistic

Cluster	No. of Genotypes	Genotypes
I	11	Sylvia, C.P.G, Chandani, Punjab Dawn, Flirt, Punjab Pink Elegance, Shagun, Glad-6, Punjab Glance, Shabnam and American Beauty.
II	1	Pusa Kiran
III	3	Praha, White Prosperity and Green Sapphire.
IV	7	Fidelio, Royal Jubilee, Punjab Lemon Delight, Snow Princess, Pusa Subham, Gunjan and Nova Lux.
V	1	Big Time Supreme

Table 4: Average Intra and Inter – cluster (D²) value for 23 genotypes of gladiolus

Cluster	I	II	III	IV	V
I	128.88	215.84	2116.27	384.28	1071.95
II		0	1318.53	143	580.58
III			173.26	937.11	321.06
IV				135.85	348.71
V					0

Table 5: Cluster means for twenty seven characters in twenty-three genotypes of gladiolus

Cluster number	No. of days taken to corm sprouting	Plant height (cm)	Stem girth (mm)	No. of shoots / plant	No. of leaves / plant	Leaf length (cm)	Leaf width (mm)	Leaf area (cm²)	Days taken for spike initiation
I	11.75	75.39	12.08	2.08	6.96	35.00	25.98	74.69	91.73
II	16.30	82.34	10.40	1.76	7.00	31.87	20.30	50.10	90.22
III	10.70	92.28	14.71	2.26	8.63	43.34	30.05	127.19	96.63
IV	15.11	80.12	11.53	1.94	7.01	35.99	21.50	60.50	89.55
V	14.33	87.33	14.94	1.97	7.75	40.08	31.08	99.92	91.46

	Days taken for colour showing stage	Days taken for first floret to last floret opening in a spike	No. of spikes / plant	No. of spikes/ meter²	No. of spikes / ha (lakh)	Length of spikes (cm)	Girth of spikes (mm)	Rachis length (cm)	Weight of spike (g)
I	101.70	8.30	1.87	30.83	3.09	65.42	7.54	30.34	57.33
II	102.97	8.63	1.56	26.11	2.59	62.18	7.24	35.91	40.85
III	107.10	8.11	1.85	30.83	3.03	64.80	7.94	32.71	73.53
IV	102.09	8.43	1.65	27.53	2.73	63.86	7.18	32.05	48.12
V	102.91	8.38	1.93	32.22	3.18	70.21	8.09	31.57	53.67

	No. of florets / spike	Diameter of the florets (cm)	Vase life (Days)	No. of days taken to 50% flowering	No. of corms / plant	No. of cormels / plant	Diameter of corm (cm)	Average Weight of corm (g)	Average Weight of cormels (g)
I	12.30	8.91	7.24	111.90	2.20	29.11	4.57	53.05	8.01
II	13.60	8.65	7.20	111.08	1.98	19.09	4.30	48.38	8.58
III	12.90	10.35	6.91	110.00	2.23	34.19	5.32	67.69	8.62
IV	13.00	9.28	7.28	111.04	2.12	24.60	4.36	56.22	7.52
V	10.77	9.81	7.25	111.88	2.24	38.32	5.04	59.47	8.27

Table 6: Percent contribution of twenty seven characters towards genetic divergence in gladiolus

Character	Contribution %
Days taken to corm sprouting	0.00
Plant height	0.00
Stem girth	0.00
No. of shoots/ plant	0.00
No. of leaves / plant	0.00
Leaf length	0.00
Leaf width	0.00
Leaf area	70.36
Days taken to spike initiation	0.00
Days taken for colour showing stage	0.00
Days taken from first floret to last floret opening in a spike	0.00
No. of spikes /plant	0.00
No. of spikes/ meter2	1.19
No. of spikes/ ha (lakh)	1.98
Length of spikes	1.58
Girth of spikes	0.40
Rachis length	0.79
Weight of spikes	0.00
Number of florets/spike	0.00

Diameter of florets	1.19
Vase Life	0.00
No. of days taken to 50% flowering	0.00
No. of corms/plant	2.77
No. of cormels/ plant	5.14
Diameter of corms	10.28
Average weight of corms	4.35
Average weight of cormels	0.00

Conclusion

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 F1 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 I and III and cluster II and III might result in wide array of variability for exercising effective selection.

The germplasm used in the present study is of diverse nature and can be used in the breeding programme for developing improved varieties. The heritable variability exists in germplasm for leaf area, weight of spike, rachis length, number of florets per spike, stem girth, leaf length, girth of spike and leaf width and selection of genotypes on the basis of these traits would be more fruitful for crop improvement programme. Selection for number of spikes per plant and corm size may play a major role in increasing the yield. Thus, these genotypes deserve to be considered as potent parents for further utilization in gladiolus improvement programme.

Due to their high heritability, variability, and genetic advancement exhibiting additive gene effect, the genotypes Pusa Shubham, Punjab Lemon Delight, Pusa Kiran, Praha and Shabnam produced higher spike yield per sq meter indicating that these genotypes may be shown for higher yield and indicating good response to selection. These genotypes can be utilized to selectively increase yield and component attributes.

Declaration

The authors declare that they have no conflict of interest to this work.

Authors' Contribution

Conceptualization of research (KST, RP); Designing of the experiments (KST, RP); Contribution of experimental materials (KST, RK); Execution of field/lab experiments and data collection (KST, RP); Analysis of data and interpretation (KST, RP, RK, AKS); Preparation of the manuscript (KST, RK, AKS, RP).

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