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## GENETIC VARIABILITY AND HERITABILITY IN GLADIOLUS (*GLADIOLUS GRANDIFLORA* L.) FOR YIELD TRAITS

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### ABSTRACT

Variability within a crop species is crucial for effective selection, as it forms the basis for identifying traits that can be improved through breeding. In the present study, forty gladiolus (*Gladiolus grandiflora* L.) genotypes were evaluated for thirty-one key traits to estimate genetic variability, genetic parameters and trait associations. The results indicated that the phenotypic coefficient of variation (PCV) was generally higher than the genotypic coefficient of variation (GCV), suggesting the influence of environment on trait expression. Traits such as number of spikes per plant (GCV: 38.06), number of corms per clump (GCV: 33.48), days for floret opening (GCV: 29.88) and vase life (GCV: 29.63) exhibited high GCV values, demonstrating substantial genetic variability. Heritability estimates were notably high for spike length (99.95%), plant height (99.86%), and days to first floret opening (99.77%). The highest genetic advance as percent of the mean was observed for number of spikes per plant (75.23%) and number of corms per clump (61.64%), indicating presence of additive gene action. Genetic advance values were also significant in traits like number of spikes per plant showing a high genetic advance of 1.11 and number of corms per clump displaying a genetic advance of 1.09 further supporting potential for improvement through selection. Genotypic coefficients variation were higher than phenotypic coefficients variation, suggesting that trait associations were mainly governed by genetic factors. Days to first floret opening had most significant positive direct effect on number of spikes per plant, highlighting this trait, along with the number of spikes per plant, as key targets for yield improvement through selection.

**Keywords :** Genetic variability, Heritability, Genotypic coefficient of variation (GCV), Phenotypic coefficient of variation (PCV), Trait association, Additive gene action.

### Introduction

The gladiolus (*Gladiolus grandiflorus* L.) stands out as a lucrative crop for farmers, offering ease of cultivation and short life cycle. Widely recognized as "sword lily," gladiolus holds significant importance as a cut flower in both domestic and international markets. Originating from South Africa, it belongs to Iridaceae family and exhibits wide range of ploidy levels, with chromosome numbers ranging from  $2n=30$  to 120, reflecting its heteroploid nature. The genus comprises approximately 300 species, including both wild and garden-origin varieties, with regions such as Mediterranean, the Middle East, Western Asia, and Madagascar, particularly South Africa, being home to diverse wild species (Kispotta *et al.*, 2017). In India,

gladiolus cultivation thrives in various states including West Bengal, Himachal Pradesh, Sikkim, Maharashtra and Karnataka as well as in the north-eastern states owing to favourable climatic conditions. Its attractive spikes and wide variety of florets in terms of colour, size, and form make it a popular choice for cut flowers, garden displays, and exhibitions (Bhujbal *et al.*, 2013). The commercial potential of gladiolus lies not only in its beauty but also in its ability to develop new corms which is propagating material from the basal internodes of flowering plants. Heritability and genetic advance are critical for any crop improvement program. While heritability estimates can guide breeder by indicating proportion of phenotypic variance due to genetic factors, it is combination of

high heritability and genetic advance as a percentage of mean that allows for more efficient selection. In gladiolus, phenotypic expression is governed by both genetic makeup and environmental factors. Thus, understanding the genetic variability, heritability, and genetic advance of key traits is crucial for development of high-yielding, regionally adapted gladiolus varieties. In the Vidarbha region of Maharashtra, where information on genetic variability and performance of gladiolus cultivars is limited, studying these factors becomes essential for enhancing growth, flowering, yield, and vase life. Therefore, present investigation aims to evaluate performance of different gladiolus varieties for these traits, providing valuable insights into their commercial potential and adaptability.

### Material and Methods

The present study was conducted at the experimental field of the Department of Floriculture and Landscape Architecture, Dr. P.D.K.V., Akola, during winter season of 2021-22 and 2022-23. The soil type at the location was light to medium black soil, uniform in texture and maintained free from weeds and diseases to ensure optimal crop growth. Gladiolus plants were cultivated using standard practices, including field preparation involving ploughing and multiple rounds of criss-cross harrowing. Raised beds were laid out and mulch was applied to all treatments. Observations were recorded from five randomly selected plants in each plot and data was statistically analyzed using a Randomized Block Design (RBD) to compare means of various traits. The experiment utilized D<sup>2</sup> analysis and a Randomized Block Design with forty gladiolus genotypes, each treatment being replicated twice. The layout and planting were randomized for each replication to ensure unbiased results. Detailed information about the experimental design is as follows:

**1:** Genotypic and phenotypic coefficients of variation were computed using the formulas suggested by Burton and De Vane (1953):

$$\text{Genotypic coefficient of variation (GCV)} = \frac{V_g}{\bar{X}} \times 100$$

$$\text{Phenotypic coefficient of variation (PCV)} = \frac{V_p}{\bar{X}} \times 100$$

Where,

$V_g$  = Genotypic variance

$V_p$  = Phenotypic variance

$\bar{X}$  = General mean of the character

PCV and GCV were categorized as low (0–10%), moderate (10–20%), and high (above 20%) as per Sivasubramanian and Menon (1973).

**2:** Heritability in broad sense refers to the proportion of genetic variance to the total observed variance in the population. It has been estimated as per the formula given by Lush (1940).

$$\text{Heritability (h}^2\text{)} = \frac{V_g}{V_p} \times 100$$

Where,

$V_g$  = Genotypic variance

$V_p$  = Phenotypic variance

**3:** Genetic Advance as per cent Mean (GAM) : Genetic advance as per cent mean was worked out for each character adopting the formula given by Johnson *et al.* (1955).

$$\text{GA (as \% of mean)} = \frac{GA}{\bar{X}} \times 100$$

Where,

GA: Genetic advance =  $k \times \sigma_p \times h^2$

K: Selection differential which is equal to 2.06 at 5% intensity of selection (Lush, 1940)

$\sigma_p$ : Phenotypic standard deviation

$h^2$  : Estimated heritability, and

$\bar{X}$  : General mean of the character

### Results and Discussion

The data presented in Table 1 revealed that genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) values were in proximation to each other for all the characters studied. Genetic parameters such as genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability, and genetic advance are valuable biometrical tools used to assess genetic variability (Aditya *et al.*, 2011). Significant differences observed among the traits indicate considerable level of variability exists within the studied genotypes. GCV helps quantify the variability among different genotypes for various traits, reflecting the inherent genetic potential. Both GCV and PCV are necessary to evaluate the influence of environmental factors on polygenic traits (Naresh *et al.*, 2015).

#### Genotypic Coefficient of Variation (GCV)

The genotypic coefficient of variation (GCV) is a measure used in genetics and breeding to evaluate the extent of variability in a specific trait caused by genetic

factors. It is a statistical tool that helps quantify the genetic diversity within a population for a particular characteristic, expressed as a percentage of the mean. The genotypic coefficient variance value is categorized as low (0-10%), moderate (10-20%) and high (20% and above) given by Sivasubramanian and Madhavamenon (1973). Wide range of genotypic coefficient of variation (GCV) was observed for characters ranging leaf area per plant (45.08) to length of single floret (6.97). High magnitude GCV was recorded for leaf area per plant (45.08), number of cormels per plant (41.36), average weight of single corm (38.07), weight of corms per plant (37.20), spikes per hectare (32.22), spikes per plot (32.10), number of spikes per plant (31.95), leaf area (30.96), number of corms per plant (28.75), weight of cormels (28.35), polar diameter of corms (26.98), number of tillers per plant (25.53), days required for sprouting of corms (24.31), days required for 50% sprouting corms (22.53) and number of leaves per plant (22.32). Higher GCV indicates greater genetic diversity and thus more scope for selection and breeding. While moderate range of genetic variation was observed for width of leaves (18.45), length of leaves (17.09), equatorial diameter of corms (17.64), number of florets per spike (14.19), diameter of spike (14.15), rachis length (13.88), vase life (13.35), blooming period in field (12.69), diameter of single floret (12.58), height of plants at 30 days (11.99), length of spike (11.62), and days required for emergence of first spike (10.42). Moderate GCV indicates moderate genetic variability; selection may have less effect in improving the trait. Low GCV was observed for days required for opening of first pair of florets (7.95), days required for fifty per-cent flowering (7.39), distance between two florets (9.17) and length of single floret (6.97). Low GCV indicates narrow range of genetic variation, suggesting that selection may have a minimal impact on enhancing the trait. Similar findings were also reported by Kumar *et al.* (2013), Naresh *et al.* (2015) and Bhujabal *et al.* (2013) in gladiolus.

### Phenotypic Coefficient of Variation (PCV)

The Phenotypic Coefficient of Variation (PCV) is a statistical measure that quantifies the total variability in a trait within a population, taking into account both genetic and environmental influences. It provides an understanding of how much a phenotypic trait varies in relation to its mean. PCV reflects overall variability in a trait, making it useful for comparing traits or populations. PCV is always equal to or greater than GCV because environmental influences add to total variation. The phenotypic coefficient variance value is categorized as low (0-10%), moderate (10-20%) and

high (20% and above) given by Sivasubramanian and Madhavamenon (1973). Wide range of phenotypic coefficient of variation (PCV) was observed for characters ranging from leaf area per plant (45.90) to days required for 50% flowering (10.03). High magnitude of PCV was recorded for leaf area per plant (45.90), number of cormels per plant (42.24), average weight of single corm (39.23), weight of corms per plant (38.10), spikes per hectare (33.71), spikes per plot (33.29), number of spikes per plant (33.44), leaf area (32.09), number of corms per plant (31.03), weight of cormels (29.72), polar diameter of corms (28.14), number of tillers per plant (28.09), days required for sprouting of corms (26.51), days required for 50% sprouting corms (24.17) number of leaves per plant (23.85) and width of leaves (20.91). High PCV indicates a high level of overall variability in the trait, which may or may not be mostly genetic. Further analysis (like heritability) is needed to separate genetic and environmental contributions. While moderate PCV was observed for equatorial diameter of corms (19.41), length of leaves (18.87), number of florets per spike (16.41), diameter of spike (16.27), rachis length (16.04), vase life (15.91), blooming period in field (15.27), diameter of single floret (15.38), height of plants at 90 days (14.41), length of spike (14.15), and days required for emergence of first spike (13.20), distance between two florets (12.64), length of single floret (11.59) and days required for opening of first pair of florets (10.69). Moderate variability in the trait, with moderate scope for improvement through selection, unless the trait is strongly influenced by genetics. In this study, the phenotypic coefficient of variation (PCV) exceeded the genotypic coefficient of variation (GCV) for all traits, indicating that the apparent variation is influenced not only by genotype but also by environmental factors. This aligns with findings from previous studies on gladiolus by Pratap and Rao (2006), Kumar *et al.* (2011), Mishra *et al.* (2014), and Naresh *et al.* (2015). The differences between GCV and PCV offer valuable insights into the influence of both genetic and environmental factors on trait expression.

### Heritability

Heritability in broad sense and genetic advance were calculated for thirty- one traits. Both are important for selection, as combining them provides a better prediction of selection gain than heritability alone. However, it is not necessary that a character showing high heritability will also exhibit high genetic advance. Heritability also provides insights into the gene action of polygenic traits, helping to predict how genotypes will perform in future generations. This

information aids in determining the appropriate emphasis for improving specific traits and selecting the best breeding methods for trait enhancement. Heritability value is categorized as low (less than 30%), moderate (30-60%) and high (more than 60%) as given by Johnson *et al.* (1955). The high heritability in broad sense was observed for the characters like leaf area per plant (96.48%), number of cormels per plant (95.91%), weight of corms per plant (95.31%), average weight of single corm (94.17%), leaf area (93.06%), spikes per plot (92.09), polar diameter of corms (91.95%), spikes per hectare (91.33%), number of spikes per plant (91.30%), weight of cormels (90.97%), number of leaves per plant (87.63%), days required for 50% sprouting of corms (86.88%), number of corms per plant (85.83%), days required for sprouting of corms (84.10%), number of tillers per plant (82.60%), equatorial diameter of corms (82.56%), length of leaves (82.05%), width of leaves (77.86%), diameter of spike (75.61%), number of florets per spike (74.81%), rachis length (74.78%), vase life (70.40%), blooming period in field (69.04%), height of plant (69.24%), diameter of single floret (66.93%), length of spike (67.46%) and days required for emergence of first spike (62.53%). Moderate heritability was observed for characters like days required for 50% flowering (54.32%), days required for opening of first pair of florets (55.29%), distance between two florets (52.70) and length of single floret (36.19%). High heritability coupled with high genetic advance compared to the mean value observed for this trait indicated presence of larger number of fixable additive factors which help in improvement of this trait through simple selection procedures. The present findings are in accordance with the findings of Bhujbal *et al.* (2013) and Naresh *et al.* (2015) in gladiolus.

#### Genetic Advance as per cent Mean (GAM)

In the present investigation, the genetic advance estimates were found to be high for leaf area per plant (91.22%), weight of corm per plant (74.81%), average corm weight (76.10%), number of cormels per plant (83.45%), weight of cormels per plant (55.70%), number of corms per plant (54.87%), number of spikes per plant (62.89%), number of spikes per plot (63.77%), spikes per hectare (63.42%), days required for sprouting of corms (45.93%), number of leaves per plant (43.04%), number of tillers per plant (47.80%), days required for 50% sprouting of corms (43.26%),

leaf area (61.52%), leaf width (33.54%), leaf length (30.97%), spike diameter (25.34%), rachis length (24.72%), number of florets per spike (25.29%), vase life of spike (23.07%), blooming period in fields (21.71%), diameter of single floret (21.20%) and plant height at 90 days (20.55%). Moderate genetic advance estimates were observed for spike length (19.66%), days required for the emergence of the first spike (16.96%), distance between two florets (13.72%), days required for opening of first pair of florets (12.17%), days required for 50% flowering (11.22%) and length of single floret (8.64%).

The success of any crop improvement program largely depends on extent of variability present in base population for traits targeted for improvement. To effectively plan a breeding program, it is crucial to assess genetic variability and understand relationships between key traits. In this regard, comparing coefficients of variation at both genotypic (GCV) and phenotypic (PCV) levels becomes essential. The GCV provides insight into extent of genetic variation, while heritability estimates help in evaluating how much of this variation is primarily heritable. If heritability is coupled with significant genetic advance as per cent of mean, these estimates become more reliable. The phenotypic coefficient of variation (PCV) was higher than the genotypic coefficient of variation (GCV) for all the traits studied indicating that apparent variation is not only due to genotype, but also due to influence of environment. Similar results were reported by Pratap and Rao (2006), Kumar *et al.* (2011), Mishra *et al.* (2014), Naresh *et al.* (2015) in gladiolus. The difference between GCV and PCV gives us an idea about role of genotypic and environment on the character (Bhujbal *et al.*, 2013).

High phenotypic variation across all traits in this study pointed to the role of environmental factors in the observed variability. The ultimate success of a breeding program depends on choosing the right genotype. Since phenotypic variance includes genotypic, environmental and genotype-by-environment interaction components, it serves as a reliable metric for character variability. However, gene actions such as additive, dominance and epistatic interactions also influence the phenotype. Thus, differentiating the observed variability into PCV and GCV is crucial for understanding how much of this variability can be attributed to genetic factors alone

**Table 1:** Analysis of chrysanthemum genotypes for floral and yield and quality parameters

	Characters	Range	Mean $\pm$ SEM	Genotypic variance	Phenotypic Variance	GCV (%)	PCV (%)	ECV	H <sup>2</sup> (broad sense)	GA	GAM
1	Days required for sprouting of corms	3.10-8.65	5.62 $\pm$ 0.42	1.87	2.22	24.31	26.51	10.57	84.10	2.58	45.93
2	Days required for 50% sprouting of corms	5.25-15.00	9.23 $\pm$ 0.57	4.32	4.97	22.53	24.17	8.76	86.88	3.99	43.26
3	No of tillers per plant	1.25-4.05	2.22 $\pm$ 0.18	0.32	0.39	25.53	28.09	11.72	82.60	1.06	47.80
4	Height of plant @90 days(cm)	61.28-110.23	81.77 $\pm$ 4.62	96.15	138.86	11.99	14.41	7.99	69.24	16.81	20.55
5	No. of leaves per plant	8.31- 20.81	13.75 $\pm$ 0.82	9.42	10.75	22.32	23.85	8.39	87.63	5.92	43.04
6	Width of leaves (cm)	2.25-4.65	3.13 $\pm$ 0.22	0.33	0.43	18.45	20.91	9.84	77.86	1.05	33.54
7	Length of leaves (cm)	42.14-87.34	60.82 $\pm$ 3.41	106.45	129.74	17.09	18.87	8.00	82.05	19.25	31.90
8	Leaf area (cm) <sup>2</sup>	45.78-182.91	100.69 $\pm$ 6.02	971.86	1044.32	30.96	32.09	8.45	93.06	61.95	61.52
9	Leaf area per plant (cm <sup>2</sup> )	597.46-3181.81	1405.42 $\pm$ 85.53	401423.29	416053.59	45.08	45.90	8.61	96.48	128.02	91.22
10	Days required for emergence of first spike	46.45-76.00	62.55 $\pm$ 3.58	42.51	68.18	10.42	13.20	8.10	62.35	10.61	16.96
11	Days required for opening of first pair of florets	57.10-87.25	75.43 $\pm$ 3.81	35.92	64.98	7.95	10.69	7.15	55.29	9.18	12.17
12	Days required for 50% flowering	62.75-92.50	80.62 $\pm$ 3.86	35.50	65.36	7.39	10.03	6.78	54.32	9.05	11.22
13	No. of spikes per plant	1.10-3.55	1.76 $\pm$ 0.12	0.32	0.35	31.95	33.44	9.86	91.30	1.11	62.89
14	Spikes per hectare	1.22-3.95	1.95 $\pm$ 0.14	0.40	0.43	32.22	33.71	9.93	91.33	1.24	63.42
15	Length of spike (cm)	65.28-113.31	85.42 $\pm$ 4.87	98.49	146.00	11.62	14.15	8.07	67.46	16.79	19.66
16	Diameter of spike (mm)	4.82-10.52	7.82 $\pm$ 0.44	1.22	1.62	14.15	16.27	8.04	75.61	1.98	25.34
17	No. of florets per spike	8.15-17.51	13.66 $\pm$ 0.80	3.76	5.03	14.19	16.41	8.24	74.81	3.45	25.29
18	Distance between two florets	3.94-6.49	5.18 $\pm$ 0.32	0.23	0.43	9.17	12.64	8.69	52.70	0.71	13.72
19	Diameter of single floret (mm)	5.21-10.64	8.22 $\pm$ 0.51	1.07	1.60	12.58	15.38	8.84	66.93	1.74	21.20
20	Length of single floret (cm)	7.96-11.72	9.16 $\pm$ 0.60	0.41	1.13	6.97	11.59	9.25	36.19	0.79	8.64
21	Blooming of period in field	8.35-18.25	13.49 $\pm$ 0.81	2.93	4.24	12.69	15.27	8.49	69.04	2.93	21.71
22	Vase life	6.40-11.55	8.05 $\pm$ 0.49	1.16	1.64	13.35	15.91	8.66	70.40	1.86	23.07
23	Spikes per plot	33.00-106.50	52.91 $\pm$ 3.30	288.55	310.29	32.10	33.29	8.81	92.09	33.74	63.77
24	Rachis Length	48.40-91.10	66.07 $\pm$ 3.76	84.05	112.38	13.88	16.04	8.06	74.78	16.33	24.72
25	No of corms per plant	1.15-3.95	1.98 $\pm$ 0.16	0.32	0.38	28.75	31.03	11.68	85.83	1.09	54.87
26	No. of cormels per plant	15.25-81.10	40.20 $\pm$ 2.43	276.46	288.24	41.36	42.24	8.54	95.91	33.54	83.45
27	Weight of corms / plant(g)	26.40-134.45	70.28 $\pm$ 4.10	683.35	716.95	37.20	38.10	8.25	95.31	52.57	74.81
28	Weight of cormels / plant(g)	11.00-42.95	24.41 $\pm$ 1.54	47.88	52.63	28.35	29.72	8.93	90.97	13.60	55.70
29	Diameter of corms (mm) (Vertical)	7.30-27.39	17.33 $\pm$ 0.98	21.86	23.77	26.98	28.14	7.98	91.95	9.24	53.30
30	Diameter of corms (mm horizontal)	30.86-68.50	51.10 $\pm$ 2.93	81.26	98.42	17.64	19.41	8.11	82.56	16.87	33.02
31	Average weight of single corm(gm)	13.20-71.35	35.31 $\pm$ 2.36	180.66	191.84	38.07	39.23	9.47	94.17	26.87	76.10

## Conclusion

This study demonstrates that the phenotypic coefficient of variation (PCV) consistently exceeded the genotypic coefficient of variation (GCV) for all traits, underscoring the influence of environmental factors on trait expression. Despite this environmental effect, the presence of high GCV and PCV for key traits suggests significant genetic variability within the gladiolus genotypes. High heritability coupled with substantial genetic advance for these traits indicates that additive gene action plays a dominant role, making them promising candidates for selection in breeding programs. The observed variability across genotypes, along with the high potential for improvement, highlights the importance of targeted selection and genetic diversity in achieving crop improvement. By

leveraging this genetic variability, future breeding efforts can effectively enhance yield and other agronomic traits in gladiolus.

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## Competing Interests

No authors have competing interests and no conflicts of interest.

## Authors' Contributions

Conceptualization of research (Dr. P.K. Nagre and Shri N.S. Gupta); Designing of the experiments (Dr. P.K. Nagre and Shri N.S. Gupta ); Contribution of

experimental materials (Shri N.S. Gupta, Dr. Manisha Deshmukh and Shri N.G. Rathod); Execution of field/lab experiments and data collection (Apoorva Guddaraddi); Analysis of data and interpretation (Apoorva Guddaraddi); Preparation of the manuscript (Apoorva Guddaraddi).

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