



International Journal of Environment and Climate Change

Volume 13, Issue 11, Page 1479-1486, 2023; Article no.IJECC.107331

ISSN: 2581-8627

(Past name: British Journal of Environment & Climate Change, Past ISSN: 2231-4784)

Assessing Genetic Variability, Heritability and Genetic Advance for Morphological Traits in Different Gladiolus (*Gladiolus grandiflorus* L.) Genotypes

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Authors' contributions

This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.

Article Information

DOI: 10.9734/IJECC/2023/v13i113299

Open Peer Review History:

This journal follows the Advanced Open Peer Review policy. Identity of the Reviewers, Editor(s) and additional Reviewers, peer review comments, different versions of the manuscript, comments of the editors, etc are available here: <https://www.sdiarticle5.com/review-history/107331>

Original Research Article

Received: 11/08/2023

Accepted: 17/10/2023

Published: 20/10/2023

ABSTRACT

Gladiolus, commonly known as the gladiola or simply "gladiolus," is a popular flowering plant known for its striking and vibrant flowers. It belongs to the genus *Gladiolus* and is part of the family Iridaceae. The present investigation was carried out at the Horticultural Research Centre of Sardar Vallabhbhai Patel University of Agriculture and Technology, Meerut, Uttar Pradesh during Rabi

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season (Mid Nov - April) 2020-21 to determine the extent of genetic variability, heritability and genetic advance for twenty-five genotypes of *Gladiolus*. For all of the traits, the analysis of variance indicated extremely significant variations between genotypes. Number of spikes per plant had the highest phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV), (35.81 and 23.41, respectively). For all of the traits studied, the phenotypic coefficient of variation (PCV) was higher than the genotypic coefficient of variation (GCV), while the differences were very small, indicating that the environmental influence on traits was low. The heritability estimates ranged from 42.75 (number of spikes per plant) to 99.01 (spike weight). This indicated that environmental variables had the least influence on these features. For most features, the estimated genetic progress as a percentage of mean varied from moderate to high. This finding, together with the high heritability values observed, suggested that additive gene action may exist and that simple selection for such traits may be used to improve them.

Keywords: *Gladiolus*; genetic variability; heritability; genetic advance; phenotypic and genotypic.

1. INTRODUCTION

Gladiolus (*Gladiolus grandiflorus* L.), also referred to as the "Queen of bulbous flowers," is a plant native to South Africa and a member of the Iridaceae family with the somatic chromosome number $2n = 2x = 30$. The gladiolus is a beautiful cut flower with fascinating spikes and florets of bright colors, attractive shapes and a range of sizes that open up gradually from the bottom to the top. Since the beginning of civilization gladiolus flowers have been connected to people. They stand for beauty, peace and love. It is often referred to as a "Sword lily" because of the foliage's sword-like form. *Gladiolus* leaves are narrowly linear, flattened at the sides and sheathed at the base. The stem is herbaceous. The flowers are actinomorphic, bisexual, with three stamens on the petaloid perianth and have a fully developed ovary [1]. A food-storing underground stem known as a "corm" serves as the gladiolus's means of reproduction. Small new corms and cormels or cormlets are formed from the base as the new offspring corm develops on top of the old one. The main method of gladiolus reproduction is by the use of corms and cormels. Almost everywhere in the world, hills and plains are where it is extensively grown. India has the second-largest total area under floriculture in the world only behind China. In India, gladiolus is produced over an area of 9.37 thousand hectares, yielding 707 million spikes. *Gladiolus* cultivation is ideal according to India's agro climatic conditions. 66,671,000 spikes of cut flowers were produced across an area of 1,460,000 ha, with an output productivity of 45665.07 spikes in India [2]. West Bengal, Himachal Pradesh, Sikkim, Karnataka, Uttar Pradesh, Tamil Nadu, Punjab and Delhi are

among the Indian states where it is commercially grown. Having genetic diversity is a requirement for crop enhancement programs. Selecting genotype only on their performance cannot increase yield, a complex quantitative feature. It can therefore be enhanced by employing selection for other features that are highly heritable and related to yield. The degree and kind of diversity present in the base population determines how well any breeding program is progressing. Therefore, the selection of elite genotypes, which ultimately rely on knowledge of variability and genetic diversity of the germplasm, is essential to the success of any plant breeding work. The percent of variability (phenotypic and genotypic) present in a population for a certain characteristic is measured by the genotypic and phenotypic coefficient of variation. Heritability measures how easily a trait may be passed down from one generation to the next generation. When establishing whether the phenotypic variations between genotypes are genetic or the consequence of environmental conditions, the concept of heritability is crucial. On the other side, genetic advance measures the anticipated genetic gain from the population's use of selection. The best illustration of the effectiveness of selection is provided by heritability and genetic advance. The knowledge of the nature and degree of genetic variability existing in a population for desirable features, and their relationship and relative contribution to yield, forms the fundamental condition for incorporating desirable traits to maximize economic yields. In front of these considerations, the current inquiry was created to determine the phenotypic and genotypic coefficient of variations, heritability, and genetic advance in order to determine the degree of genetic variability in *Gladiolus* cultivars.

2. MATERIALS AND METHODS

The current study was conducted during the Rabi season (Mid Nov - April) 2020-21 at the Horticultural Research Center of Sardar Vallabhbhai Patel University of Agriculture and Technology in Meerut, Uttar Pradesh. Meerut is located at 29 degrees 01 minutes latitude in the North, 77 degrees 45 minutes longitude, and has an altitude of 277 meters above Mean Sea Level (MSL), representing the North Western plain zone. The research involved 25 *Gladiolus* genotypes, including varieties like Pusa Bindiya, White Prosperity, Pusa Jyotsana, Hunting Song, Eurovision, Pusa Kiran, Pusa Shanti, Mayur, Pusa Manmohak, Pusa Red Ralentine, Ber lew, Oscar, Surya Kiran, Suchitra, Ber lew-II, Local Orange, Rose Suprime, Traderhorn, Novalux, Red Beauty, Pink Friendship, Shobha, Pusa Vidushi, Anjali and Legend. These genotypes were collected from various regions across India (Table 1). The experiment followed a Randomized Complete Block Design (RCBD) with three (3) replications. For each replication,

observations were recorded for 16 different characteristics from five randomly selected plants within each treatment. These characteristics included Days to 50% corm sprouting, days to complete corm sprouting, plant height (in centimeters), the number of leaves per plant, length and width of the longest leaves, stem girth (in centimeters), days to spike emergence, flowering duration, the number of spikes per plant, spike length (in centimeters), spike weight (in grams), the number of florets per plant, flower diameter (in centimeters), fresh weight of corm (in grams), and corm yield (in quintals per hectare). Genotypic and phenotypic coefficients of variation were calculated using the formulas of Burton [3] and Johnson et al. [4]. Heritability and genetic advance were determined following the methods of Allard [5] and the estimation of genetic advance as a percentage of the mean was conducted following the procedure described by Johnson et al. [4]. The expected genetic advance was also determined using the method proposed by Johnson et al. [4].

Table 1. The details of germplasm with their source

Sr. No.	Germplasm	Source
1.	Pusa Bindiya	IARI, NEW Delhi
2.	White Prosperity	SVPUA&T, Meerut
3.	Pusa Jyotsana	IARI, NEW Delhi
4.	Hunting Song	IARI, NEW Delhi
5.	Eurovision	IARI, NEW Delhi
6.	Pusa Kiran	IARI, NEW Delhi
7.	Pusa Shanti	IARI, NEW Delhi
8.	Mayur	IARI, NEW Delhi
9.	Pusa Manmohak	IARI, NEW Delhi
10.	Pusa Red Ralentine	IARI, NEW Delhi
11.	Ber lew	IARI, NEW Delhi
12.	Oscar	IARI, NEW Delhi
13.	Surya Kiran	IARI, NEW Delhi
14.	Suchitra	IARI, NEW Delhi
15.	Ber lew-II	IARI, NEW Delhi
16.	Local Orange	SVPUA&T, Meerut
17.	Rose Suprime	IARI, NEW Delhi
18.	Traderhorn	IARI, NEW Delhi
19.	Novalux	SVPUA&T, Meerut
20.	Red Beauty	SVPUA&T, Meerut
21.	Pink Friendship	IARI, NEW Delhi
22.	Shobha	IARI, NEW Delhi
23.	Pusa Vidushi	IARI, NEW Delhi
24.	Anjali	IARI, NEW Delhi
25.	Legend	IARI, NEW Delhi

3. RESULTS AND DISCUSSION

3.1 Analysis of Variance

Analysis of variance (ANOVA) results shown in Table 2 show highly significant genotype differences for all traits, including days to 50% corm sprouting, days to completely corm sprouting, plant height at 30, 60, and 90 days, number of leaves per plant at these intervals, length of longest leaf, width of longest leaf, stem girth, days to spike emergence, flowering duration, number of spikes per plant, spike length, spike weight, number of floret per spike inflorescence. These results were in agreement with the findings of Kumar and Kulkarni [6]; Bhujbali et al. [7]; Patra and Mohanty [8]; Emna and Faouzi [9]; Kumar et al. [10]; Rashmi et al. [11]; Ramzan et al. [12]; Singh et al. [13]; Momin et al. [14]; Ishwar raddy et al. [15] and Kumar et al. [16].

3.2 Phenotypic and Genotypic Coefficients of Variation

We calculated the Phenotypic Coefficient of Variation (PCV) and the Genotypic Coefficient of Variation (GCV) for all sixteen studied traits and presented the results in Table 3. In all the examined traits, the PCV was higher than the GCV. Nonetheless, the differences were minor, indicating a limited influence of the environment on these characteristics. The highest GCV was observed for the number of spikes per plant (23.41). We also obtained moderate GCV values for flowering duration (15.59), days to 50% corm sprouting (14.96), days to complete corm sprouting (13.91), the number of leaves per plant at 30 days (13.41), the width of the longest leaf (13.03), floret diameter (11.45), fresh weight of corm (11.43), the number of florets per spike (11.33), stem girth (10.92), and spike weight (10.86). In contrast, the lowest GCV was observed for the number of leaves per plant at 60 days (9.36), length of the longest leaf (9.04), corm yield (8.75), plant height at 30 days (8.87), the number of leaves per plant at 90 days (8.24), plant height at 60 days (6.82), spike length (5.81), days to spike emergence (5.32), and plant height at 90 days (4.88). The highest phenotypic coefficient of variation was found for the number of spikes per plant (35.81). We also obtained moderate PCV values for days to 50% corm sprouting (17.08), flowering duration (16.33), the number of leaves per plant at 30 days (16.02), days to completely corm sprouting (14.79), weight of the longest leaf (14.54), floret diameter (12.63), the number of florets per spike (12.53), the number of leaves per plant at 60 days

(12.16), fresh weight of corm (11.58), stem girth (11.27), spike weight (10.91), and the number of leaves per plant at 90 days (10.61). Meanwhile, the lowest PCV was observed for corm yield (9.54), length of the longest leaf (9.12), plant height at 30 days (8.77), plant height at 60 days (6.99), stem girth (5.91), days to spike emergence (5.56), and plant height at 90 days (4.99). Further the present findings exhibited that the estimate of Phenotypic coefficient of variation (PCV) were magnitudinally higher than their corresponding Genotypic coefficient of variation (GCV) for all the traits studied. This suggests that phenotypic expression of the genotypes was least influenced by factors and desirable improvement can be achieved through simple selection procedures. These results were in consonance with the findings of Patra and Mohanty [8]; Kumar et al. [10]; Rashmi et al. [11]; Ramzan et al. [12]; Nainwal et al. [17]; Verty et al. [18]; Kaushik et al. [19]; Swetha et al. [20]; Balaram and Jankram [21] and Kispota et al. [22].

3.3 Heritability

All the characters under study showed high heritability (>30%). The results obtained on heritability in a broad sense for yield and attributing characters has been presented in Table 3. The estimated heritability ranged between 42.75 (number of spike per plant) to 99.01 (spike weight). Heritability values in order of highest to lowest was observed for spike weight (99.01) followed by length of longest leaf (98.05), fresh weight of corm (97.47), spike length (96.91), plant height at 90 days (95.48), plant height at 60 days (95.27), stem girth (94.00), plant height at 30 days (93.35), days to spike emergence (91.44), flowering duration (91.14), days to completely corm sprouting (88.39), yield of corm (84.02), floret diameter (82.16), number of floret per spike (81.74) and length of longest leaf (80.35), days to 50% corm sprouting (76.73), number of leaves per plant at 30 days (70.03), and number of leaves per plant at 90 days (60.31), number of leaves per plant at 60 days (59.18) and the number of spikes per plant (42.75). This suggests that these traits were least influenced by environmental factors. In other words it could be concluded that the phenotypic expression for these traits were true representative of its genotype. Such high heritability estimates have been reported by Bhujbali et al. [7]; Patra and Mohanty [8]; Mishra et al. [23]; Kumar et al. [10]; Nainwal et al. [17]; Singh et al. [13]; Verty et al. [18] and Kaushik et al. [19].

Table 2. Analysis of variances (ANOVA) for sixteen characters of twenty-five genotypes in *Gladiolus (Gladiolus grandiflorus L.)*

Source of variation	D.F.	Days to 50% corm sprouting	Days to completely corm sprouting	Plant height			Number of leaves per plant			Length of longest leaf	Width of longest leaf
				At 30 days	At 60 days	At 90 days	At 30 days	At 60 days	At 90 days		
Replication	2	0.67	0.62	1.98	1.97	1.67	0.60	1.50	1.15	10.07	0.14
Treatment	24	2.04**	6.27**	36.04**	51.69**	59.50**	1.53**	1.46**	1.81**	82.72**	1.71**
Error	48	0.19	0.26	0.84	0.84	0.92	0.19	0.27	0.33	0.54	0.13
Source of variation	D.F.	Stem girth (mm)	Days to spike emergence	Flowering duration	Number of spike per plant	Spike length (cm)	Spike weight (g)	Number of florets per spike	Floret diameter (cm)	Fresh weight of corm (g)	Yield of corm (q / ha)
Replication	2	8.48	13.91	1.51	0.05	7.61	6.26	0.60	0.37	8.35	0.86
Treatment	24	43.58**	46.07**	31.38**	0.40**	69.31**	187.31**	10.36**	5.19**	79.56**	66.89**
Error	48	0.91	1.39	0.98	0.12	0.73	0.62	0.72	0.35	0.68	3.99

*, ** significant at 5% and 1% level, respectively

Table 3. Estimates of Means, GCV (%), PCV (%), Heritability h^2 % (BS), Genetic advance and Genetic advance as percentage of mean for sixteen characters in *Gladiolus (Gladiolus grandiflorus L.)*

Characters	Mean		Heritability (%)	G.A.	G.A. % mean	GCV (%)	PCV (%)	
	Min.	Max.						
Days to 50% corm sprouting	3.65	7.01	76.73	1.42	27.00	14.96	17.08	
Days to completely corm sprouting	7.81	12.60	88.39	2.74	26.94	13.91	14.79	
Plant height	At 30 days	34.42	48.21	93.35	6.82	16.86	8.47	8.77
	At 60 days	53.45	67.29	95.27	8.28	13.71	6.82	6.99
	At 90 days	84.27	98.45	95.48	8.89	9.81	4.88	4.99
Number of leaves per plant	At 30 days	3.81	6.96	70.03	1.15	23.11	13.41	16.02
	At 60 days	5.25	8.27	59.18	1.00	14.83	9.36	12.16
	At 90 days	6.98	10.15	60.31	1.13	13.19	8.24	10.61
Length of longest leaf	48.33	68.47	98.05	10.68	18.43	9.04	9.12	
Width of longest leaf	3.95	7.79	80.35	1.34	24.06	13.03	14.54	
Stem girth (mm)	26.74	39.44	94.00	7.53	21.82	10.92	11.27	
Days to spike emergence	66.41	79.30	91.44	7.60	10.48	5.32	5.56	
Flowering duration	15.48	25.91	91.14	6.26	30.66	15.59	16.33	

Characters	Mean		Heritability (%)	G.A.	G.A. % mean	GCV (%)	PCV (%)
	Min.	Max.					
Number to spike per plant	1.00	2.00	42.75	0.41	31.53	23.41	35.81
Spike length (cm)	72.62	89.45	96.91	9.70	11.79	5.81	5.91
Spike weight (g)	58.29	88.48	99.01	16.17	22.25	10.86	10.91
Number of florets per spike	12.26	18.87	81.74	3.34	21.09	11.33	12.53
Floret diameter (cm)	8.77	13.66	82.16	2.37	21.37	11.45	12.63
Fresh weight of corm (g)	35.91	52.87	97.47	10.43	23.24	11.43	11.58
Yield of corm (q / ha)	42.23	61.05	84.02	8.65	16.51	8.75	9.54

GCV = Genotypic Coefficient of Variation, PCV = Phenotypic Coefficient of Variation and BS = Broad Sense

3.4 Genetic Advance as Percentage of Mean

Genetic advance as percent of mean depicted in Table 3 was found high (>20%) for number of spike per plant (31.53) followed by flowering duration (30.66), days to 50% corm sprouting (27.00), days to completely corm sprouting (26.94), width of longest leaf (24.06), fresh weight of corm (23.24), number of leaves per plant at 30 at days (23.11), spike weight (22.25), stem girth (21.82), floret diameter (21.37) and number of floret per spike (21.09). while the moderate genetic advance (<20% to >10%) was observed for length of longest leaf (18.43), plant height at 30 days (16.86), yield of corm (16.51), number of leaves per plant at 60 days (14.83), plant height at 60 days (13.71), number of leaves per plant at 90 days (13.19), spike length (11.79) and days to spike emergence (10.48), respectively. while the lowest (<10%) was observed for plant height at 90 days (9.81). Results obtain from the study revealed that high heritability coupled with high genetic advance for width of longest leaf, stem girth, flowering duration, spike weight, number of floret per spike, floret diameter and fresh weight of corm indicating that the heritability is due to additive gene action and simple selection for such traits could be practiced for improving them. Similar results were obtained by Bhujbali et al. [7]; Patra and Mohanty [8]; Mishra et al. [23]; Kumar et al. [10]; Nainwal et al. [17]; Singh et al. [13]; Verty et al. [18]; Kaushik et al. [19]. Ishwarraddy et al. [15]; Kumar et al., [16] and Swetha et al., [20].

4. CONCLUSION

The study conducted an analysis of various traits in a set of breeding materials and found significant genotype differences for all sixteen traits viz., days to 50% corm sprouting, days to corm sprouting, plant height, number of leaves per plant, length of longest leaf, width of longest leaves, stem girth, days to spike emergence, flowering duration, number to spike per plant, spike length, spike weight, number of florets per plant, flower diameter, fresh weight of corm yield of corm and yield of corm. The study also assessed the Phenotypic Coefficient of Variation (PCV) and Genotypic Coefficient of Variation (GCV) for these traits. It was observed that the PCV values were consistently higher than the GCV values, indicating that environmental factors had a limited impact on these traits. This suggested that selection procedures could be straightforward for improving these

characteristics. In terms of heritability all traits showed high heritability estimates in broad sense. This indicated that genetic factors played a significant role in the expression of these traits. Some traits, like the number of spikes per plant and flowering duration showed a high genetic advance making them suitable for selection and improvement. The results indicated that the traits under examination were influenced by genetic factors to a significant degree and were less affected by the environment. This suggested that simple selection procedures could be effective for enhancing these traits. The findings were consistent with prior research, emphasizing the potential for trait improvement through breeding and selection strategies.

ACKNOWLEDGEMENT

I am grateful to my advisor as well as all of the faculty members of Department of Horticulture and Department of Genetics and plant breeding, Sardar Vallabhbhai Patel University of Agriculture and Technology, Meerut, Uttar Pradesh for their unwavering support and advice throughout the entire experimental research study.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

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