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EVALUATION OF GENETIC VARIABILITY, HERITABILITY AND GENETIC ADVANCES IN GLADIOLUS (*GLADIOLUS HYBRIDUS* L.) GENOTYPES

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ABSTRACT
Assessment of genetic variability, heritability and genetic advances of 20 gladiolus genotypes were evaluated. The presence of high amount of variability was observed for number of cormels per plant and weight of corms in the 20 gladiolus genotypes. The heritability of different field characters was categorized as very high which ranged between 31.84% (Leaf length) to 94.44% (Weight of corms). The traits like rachis length, number of spikes per plant, weight of spike, number of florets per spike, number of corms per plant, number of cormels per plant, weight of corm, yield of corms kg per hectare and yield of corms tons per hectare exhibited high heritability (>75%) coupled with high genetic advance over per cent mean (>30%) which indicated the prevalence of additive gene action in expression of these traits and there by further improvement of these traits could be made by selection. It was concluded that highly significant varietal differences indicated the presence of high amount of variability.

INTRODUCTION

Gladiolus (Gladiolus hybridus L.) is an ornamental bulbous plant native to South Africa (Sharma and Sharma, 1984). The genus gladiolus is classified in the family Iridaceae (Ankit *et al.,* 2015). It is an elegant cut flower grown for its magnificent spikes. With changing life style and increased urban affluence, floriculture has assumed a definite commercial status in recent times and it has emerged as an important agri-business venture. In this regard gladiolus has gained much importance as it is the 'Queen of bulbous flowers'. The latin word 'Gladius' means sword and hence, it is often called as 'sword lily' because of the shape of its leaves (Lewis *et al.,*1972). Popularity of this crop as a cut flower is increasing day by day because of its attractive flower spikes and availability in wide range of colors of the florets, varying number of florets and their size, wide range of keeping quality and adaptability to different seasons. These characters have made it very attractive for use as a cut flower, vase and bouquet preparation, growing in herbaceous borders, beddings, rockeries and pot cultivation. The major gladiolus producing countries are the United States (Florida and California), Holland, Italy, France, Poland, Bulgaria, Brazil, India, Australia and Israel. The fascinating spike bears a large number of florets with varying sizes and forms with smooth ruffle of deeply crinkled sepals (Jyoti Sharma *et al.,* 2013). Gladiolus is very rich in varietal wealth and every year there is an addition of new varieties (Kumar and Yadav, 2005). The key for any success of any genetic breeding program lies in the availability genetic variability for desired traits (Heller, 1996). Planning and execution of a breeding programme for the development of new varieties depends, to a great extent upon the genetic magnitude of genetic variability. So information on nature and magnitude of variability existing in the plant material and association among the various characters is a prerequisite for improvement in the yield and other characters. The presence and magnitude of genetic variability in a gene pool is the pre-requisite of a breeding programme. The objective of the present investigation was to quantify the magnitude of genetic variability heritability & genetic advances in the present genotypes and to identify important yield-attributing characters to provide useful information for developing high yielding gladiolus genotypes.

MATERIALS AND METHODS

The present investigation was carried out at Experimental block of Department of Floriculture and Landscape Architecture, College of Horticulture, Mudigere (UAHS, Shivamogga) during 2014-15. The experiment was laid out in randomized block design with three replications, consisted twenty gladiolus genotypes. The investigation was conducted in open field condition at a spacing of 30 x 20 cm. Observations were recorded on five selected plants from each variety in each replication. The experimental observations were taken on different morphological traits. The mean values of five randomly selected plants from each cultivar in each replication were used for data analysis.

Genetic parameters

The genetic parameters such as genotypic coefficient of

variation (GCV), phenotypic coefficient of variation (PCV), heritability in broad sense and genetic advance for different characters were worked out for all the genotypes under study following the standard procedures.

Genotypic and phenotypic coefficient of variation

Genotypic and phenotypic coefficients of variation were estimated according to Burton and Devane (1953) based on estimate of genotypic and phenotypic variance.

$$\text{Genotypic coefficient of variation (\%)} = \frac{\sqrt{\sigma 2g}}{X} \times 100$$

$$\text{Phenotypic coefficient of variation (\%)} = \frac{\sqrt{\sigma 2p}}{X} \times 100$$

Where,

x = General mean of the character

s^2g = Genotypic variance

s^2p = Phenotypic variance

Heritabilty estimates

Heritabilty of a charcter on the other hand is an index of its transmissibility. In broad sense, it may be defined as the proportion of genotypic variance to phenotypic variance and heritability percentage in broad sense is calculated by the formulae as suggested by Johnson *et al*. (1995 a and b).

$$\text{Heritability } (h^2) = \frac{\sigma^2 g}{\sigma^2 p}$$

Where,

σ^2g = Genotypic variance and σ^2p = Phenotypic variance

Partitioning of variance

Variance is partitioned into genotypic, phenotypic and in environmental components. In order to form a reliable basis for selection, it is necessary to break up the observed variance and covariance into its heritable (genetic) and non-heritable (non-genetic) components. This was done as per the method suggested by Fisher (1954).

$$\text{Phenotypic variance}(s^2p) = \frac{\text{Genotypic variance} + \text{Environment variance}}{\text{MSS (treatment) - MSS (error)}}$$

Genotypic variance (s^2g) = Number of replications

Environment variance (s^2e) = Error mean sum of squares

Genetic advance (GA)

Genetic advance estimated based on the formula given by Robinson *et al*. (1949)

GA = i x h^2 x óp

where

h^2 = Heritability in broad sense, sp = Phenotypic standard deviation of the trait

i = Selection of differential (i = 2.06) at 5 per cent selection intensity

RESULTS AND DISCUSSION

Significant differences were observed for all the twenty four characters studied among all the Genotypes. The analysis of variance for different quantitative characters for 20 genotypes of gladiolus are presented in Table 1. The results indicated that there was highly significant difference among genotypes for growth, flowering, quality, corms and cormels characters.

Genetic parameters like genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability and genetic advance are useful biometrical tools for determination of genetic variability(Aditya *et al*., 2011). The magnitudes of phenotypic and genotypic coefficient of variation were more or less same indicating little role of environment. The range, mean, phenotypic and genotypic variance, co-efficient of variation, heritability, genetic advance and genetic advance over mean were presented in Fig. 1 and Table 2. In present investigation the perusal of data revealed that most of characters traits under study exhibited moderate to low phenotypic and genotypic variation. The phenotypic coefficient of variation (PCV) was higher than genotypic coefficient of variation(GCV) for all quantitative traits, indicating the predominant role of environment in the expression of the traits. Similar results were obtained by Kumar *et al*. (2011), Sahana *et al*. (2011) and Geeta *et al*. (2015) in gladiolus. The phenotypic coefficient variation (PCV) and genotypic coefficient of variation (GCV) was highest for number of cormels per plant (74.18, 69.91) followed by weight of corms (51.17, 49.73), yield of corms tons per hectare(50.31, 48.60) and number of spike per plant (41.24, 39.78) respectively. Higher GCV and PCV estimates indicate the presence of considerable variability in these traits and scope for selection and improvement.

Heritability values were found to be moderate to high for growth parameters and high for flowering, quantity, yield, corm and cormel parameters. However, High heritability (> 75%) coupled with high genetic advance as per cent mean (>30%) were noticed for the traits viz., duration of flowering, spike length, rachis length, number of spikes per plant, number of florets per spike, weight of the spike, number of corms per plant, number of cormels per plant, weight of corms, weight of

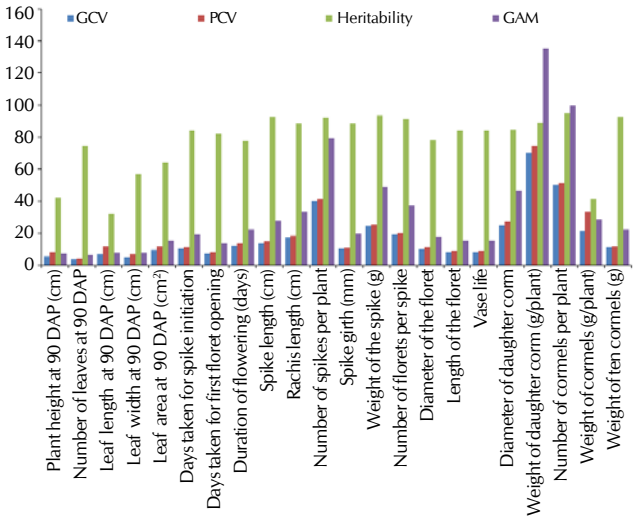

Figure 1: Genotypic coefficient of variation, phenotypic coefficient of variation, heritability and genetic advance over per cent mean for different characters in gladiolus

Table 1: Analysis of variance (mean sum of squares) for growth, flowering, quality, corm and cormel parameters in gladiolus genotypes

Sl. No.	Source of variation/ Characters	Replication	Treatments(Genotypes)	Error	S.Em±	CD (5%)
	Degrees of freedom	2	19	38		
1	Plant height (cm)	68.56	59.46*	18.72	2.50	7.15
2	Number of leaves	0.06	0.29*	0.03	0.10	0.29
3	Leaf length (cm)	33.83	72.84*	30.33	3.18	9.10
4	Leaf width (cm)	0.31	0.15*	0.03	0.11	0.35
5	Leaf area at (cm^2)	187.09	452.01*	70.78	4.89	14.01
6	Days taken for spike initiation	5.94	119.30*	7.10	1.54	4.40
7	Days taken for first floret opening	11.35	84.96*	5.96	1.41	4.03
8	Duration of flowering (days)	6.77	24.12*	2.13	0.84	2.41
9	Spike length (cm)	2.14	286.71*	7.54	1.59	4.54
10	Rachis length (cm)	1.23	226.38*	9.31	1.76	5.04
11	Number of spikes per plant	0.04	1.09*	0.03	0.09	0.27
12	Spike girth (mm)	0.08	1.85*	0.08	0.16	0.46
13	Weight of the spike (g)	20.38	1117.14*	25.91	2.94	8.41
14	Number of florets per spike	1.40	21.34*	0.67	0.47	1.35
15	Diameter of the floret (cm)	0.19	2.87*	0.25	0.29	0.83
16	Length of the floret (cm)	0.52	1.98*	0.12	0.21	0.62
17	Vase life (days)	0.09	1.32*	0.08	0.16	0.46
18	Number of corms per plant	0.05	0.85*	0.05	0.13	0.38
19	Number of cormels per plant	27.09	2087.84*	84.10	5.29	15.16
20	Weight of corms (g/plant)	129.44	7732.99*	148.91	7.05	20.17
21	Weight of cormels (g/plant)	7.41	38.22*	12.29	2.02	5.80
22	Diameter of corm(cm)	0.16	1.15*	0.03	0.1	0.30
23	Yield of corms(kg/plot)	0.05	4.17*	0.10	0.18	0.52
24	Yield of corms (t/ha)	3.84	200.53*	4.69	1.25	3.58

DAP – Days After Planting; * Significant at 5 %

Table 2: Estimates of mean, range, components of variance, heritability and genetic advance for growth, flowering, quality, corm and cormels parameters in gladiolus genotypes

Sl. No	Characters	Mean ± S.Em	Range	components of variance GV	PV	GCV(%)	PCV(%)	h^2(%)	GA	GAM (%)
1	Plant height (cm)	70.79 ± 2.50	64.00-79.40	13.58	32.30	5.21	8.03	42.04	4.92	6.95
2	Number of leaves	8.13 ± 0.1	7.60-8.53	0.09	0.12	3.60	4.17	74.16	0.52	6.38
3	Leaf length (cm)	57.69 ± 3.18	48.93-66.73	14.17	44p.50	6.52	11.56	31.84	4.38	7.58
4	Leaf width (cm)	4.08 ± 0.11	3.67-4.57	0.04	0.07	4.86	6.45	56.76	0.31	7.54
5	Leaf area (cm^2)	124.30 ±4.89	108-149.00	127.07	197.86	9.07	11.32	64.23	18.61	14.97
6	Days taken for spike initiation	61.45±1.54	48.80 - 68.27	37.40	44.50	9.95	10.86	84.04	11.55	18.79
7	Days taken for first floret opening	70.47±1.41	62.40-78.07	26.34	32.29	7.28	8.06	81.56	9.55	13.55
8	Duration of flowering (days)	22.40±0.84	17.60-26.60	7.33	9.46	12.09	13.73	77.50	4.91	21.92
9	Spike length (cm)	69.60±1.59	48.60-90.73	93.05	100.60	13.86	14.41	92.5	19.11	27.46
10	Rachis length (cm)	49.60±1.76	36.67-69.73	72.36	81.66	17.15	18.22	88.60	16.49	33.26
11	Number of spikes per plant	1.5±0.09	1-2.93	0.35	0.38	39.78	41.24	92.10	1.18	79.02
12	Spike girth (mm)	7.68±0.16	6.91-9.99	0.59	0.67	10.00	10.64	88.20	1.49	19.34
13	Weight of the spike (g)	78.21±2.94	42.87-120.13	363.74	389.65	24.39	25.24	93.35	37.96	48.54
14	Number of florets per spike	13.93±0.47	9.27-18.60	6.89	7.56	18.84	19.73	91.20	5.16	37.07
15	Diameter of the floret (cm)	9.59±0.29	7.67-11.19	0.87	1.12	9.73	11.06	77.6	1.69	17.65
16	Length of the floret (cm)	9.75±0.21	8.13-10.82	0.62	0.74	8.07	8.81	83.9	1.49	15.22
17	Vase life (days)	8.01±0.16	6.60 -9.00	0.41	0.49	8.02	8.75	83.93	1.21	15.14
18	Number of corms per plant	2.10±0.13	1.47-3.53	0.27	0.32	24.60	26.95	84.36	97.00	46.27
19	Number of cormels per plant	36.97±5.29	19.60-123.00	667.91	752.01	69.91	74.18	88.81	50.17	135.73
20	Weight of corms (g/plant)	101.12±7.05	50.21-233.15	2528.03	2676.93	49.73	51.17	94.44	100.65	99.54
21	Weight of cormels (g/plant)	13.75±2.02	9.92-22.77	8.64	20.94	21.38	33.27	41.28	3.89	28.29
22	Diameter of corm (cm)	5.53±0.1	4.83-6.41	0.37	0.40	11.06	11.44	92.50	1.22	22.03
23	Yield of corms (kg/plot)	2.40±0.18	1.20-5.60	1.36	1.46	48.47	50.21	93.19	2.32	96.39
24	Yield of corms (t/ha)	16.63±1.25	8.36-38.86	65.28	69.97	48.60	50.31	93.29	1607.60	96.69

cormels, diameter of corm, yield of corms kg per plot and yield of corms tonnes per hectare. This indicates the lesser influence of environment in expression of these characters and prevalence of additive gene action in their inheritance hence, these traits are suitable for selection. Similar results observed by Neeraj *et al*. (2005), Pratap and Rao (2006), Balaram and Janakiram (2009) Bhujbal *et al*. (2013) and Pragynashree *et al*. (2014) in gladiolus. High heritability coupled with moderate genetic advance over per cent mean were observed for days taken for spike initiation, days taken

for first floret opening, diameter of the floret, length of the floret, spike girth, vase life can be exploited through hybridization. However moderate heritability with low genetic advance over per cent was observed for plant height, number of leaves, leaf length , leaf width thereby indicating non-additive gene action *i.e.* the character is highly influenced by environmental effects and selection would be ineffective and which can be exploited through hybridization or heterosis breeding. Similar results observed by Neeraj *et al*. (2005), Nimbalkar *et al*. (2007) and Geeta *et al*. (2015) in gladiolus. Heritability estimate involve the breeding value of the genotype and help to understand the repeatability of performance for character studied. It is being used in predicting the performance of genotypes in subsequent generations and to decide the appropriate weight age to be given for improving particular character and the breeding method to be followed for improvement of specific character.

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