Genetic variability in quantitative characters of gladiolus (*Gladiolus* x *hybridus* Hort.)

MAHESH CHOUDHARY*, S.K. MOOND[1], ANOP KUMARI AND B.S. BENIWAL
Department of Horticulture, C.C.S. Haryana Agricultural University, HISAR (HARYANA) INDIA
(Email : balodamahesh@gmail.com)

Abstract : Twelve genotypes of gladiolus were evaluated to determine genetic variability, heritability, genetic advance and genetic gain for twenty six contributing characters. Significant variations were recorded for the various characters studied. Phenotypic and genotypic coefficients of variation were highest for number of cormels and weight of cormels produced per plant, indicating presence of sufficient genetic variability for selection in these traits. High heritability and high genetic advance for number of cormels per plant, weight of cormels per plant, leaf area, number of spikes per plot, number of corms per plot, number of florets remaining open at a time, number of spikes per plant, leaf width, spike diameter, weight of corm, rachis length, vase life of spike, number of corms per plant and plant height indicated the presence of additive gene effects in these traits and their amicability for direct selection. The non additive gene effects were evident in spike length, size index of corms, number of florets per spike, number of days to slipping thus warranting use of heterosis breeding for these characters. The selection on the basis of cormels per plant will be more effective for further breeding programme.

Key Words : Gladiolus, Genetic advance, Genetic gain, Heritability, Variability

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INTRODUCTION

Gladiolus (*Gladiolus* x *hybridus* Hort.) is an important cut-flower crop grown commercially in several parts of the world. However, commercial success of gladiolus cultivation like any other crop depends upon the availability of suitable cultivars to suit the particular climatic conditions and consumer preference of the cultivar. The consumer preferences changes with time. Hence, crop improvement is the need of the time to sustain the availability of desirable cultivars. Improvement through selection depends upon the variability existing in the available genotypes, which may be either due to different genetic constitution of cultivars or variations in the growing environments. Gladiolus is a vegetatively propagated crop through corms and cormels on commercial scale and selection is an easy method for varietal improvement in it. Selection is effective only when the observed variability in the population is heritable in nature.

Genetic variance, heritability and other genetic parameters are reported to be subject to fluctuations with changing environments (Lal *et al.*, 1985 and Misra and Saini, 1988). Genetic variability in a group of germplasm is a pre-requisite for a successful breeding programme. Since, most of the characters influencing yield are polygenic, it is essential for plant breeders to estimate the type of variation available in the germplasm. The type of breeding programme for developing suitable varieties depends largely on the availability of genetic variability in a given species. Heritability estimates give a measure of transmission of characters from one generation to the other, as consistency in the performance of the selection depends on the heritable portion of the variability. Thus, enabling the plant breeder for isolating elite selections in the crop. Hence, the magnitude of the variation and the estimates of the heritability and genetic advance are the important parameters on which the success of selection

* Author for correspondence.
[1]Department of Floriculture and Landscaping, College of Horticulture and Forestry, Jhalarapatan JHALAWAR (RAJASTHAN) INDIA

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lies. With this background in view, the present study was undertaken to assess and estimate the magnitude and nature of variation among twelve genotypes of gladiolus with respect to various vegetative, floral and yield attributes which could be utilized in crop improvement programme.

MATERIALS AND METHODS

The present investigation was conducted at the Instructional Farm, Department of Floriculture and Landscaping, College of Horticulture and Forestry, Jhalawar from October 2008 to May 2009. The investigation was carried on twelve genotypes, laid in a randomized block design with three replications. The evaluated genotypes included Jyotsna, Sancerre, Urmil, TS-14, GS-2, Punjab Dawn, Spic-n-Span, Dhanvantari, Priscilla, Peter Pears, Sabnam and Chandani. Healthy and uniform size corms were planted in a plot size of 1.55 m × 1.10 m at spacing of 40 cm × 25 cm and depth of 6-8 cm. Twenty six parameters covering vegetative, floral and yield attributes were recorded on five randomly selected plants in each plot. The genotypic and phenotypic coefficients of variation were estimated according to the methods of Panse and Sukhatme (1967). Parameters of variability were calculated as per the formula given by Burton and De Vane (1953). Heritability, genetic advance and expected genetic gain were calculated by the formula suggested by Johnson *et al.* (1955). The mean and standard errors were worked out as per standard methods and coefficients of variations were computed.

RESULTS AND DISCUSSION

The analysis of variance reveled that mean square of treatments were significant for most of the characters indicating varietal differences for all the characters studied. The estimates of phenotypic coefficient of variance (PCV) were found higher than genotypic coefficient of variance (GCV) for all the twenty six characters studied indicating that the apparent variation was not only due to genotypes but was also due to the influence of environmental in the expression of genotypes. The results are in agreement with the results of Pratap and Rao (2006). But there was close correspondence between GCV and PCV for certain characters like number of cormels produced per plant, leaf width, leaf area, vase life of spike, number of florets remaining open at a time, weight of cormels produced per plant, weight of corm, plant height, spike length, rachis length, indicating little influence of environment on these characters. In the study, phenotypic and genotypic coefficients of variation were higher for number of cormels produced per plant and weight of cormels produced per plant indicating high variation in these characters, predicting greater scope for improvement of these two characters. The rest of characters *viz.*, number of spikes per plant and per plot, number of corms per plant and per plot, had moderate variability thus amenable for improvement.

The estimates of heritability in broad sense give a measure of transmission of characters from one generation to another, thus giving an idea of heritable portion of variability and enabling the plant breeder in isolating the elite selection in the crop. Heritability and genetic advance increase the efficiency of the selection in a breeding programme by assessing the influence of environmental factors and additive gene action. The estimates of heritability in broad sense specifying the heritable portion of total variation, helps in identification of the appropriate characters for selection. High estimates of heritability in broad sense were obtained for all the characters except corm sprouting percentage and number of days taken for sprouting, reflecting the importance of these traits in selection programme. The magnitude of heritable variability is the most important aspect of genetic constitution of the genotype which has close bearing on the response to selection (Panse, 1957). Similar findings were reported by Lal *et al.* (1985) in gladiolus.

GCV and heritability (broad sense) are not sufficient to determine the amount of variation which is heritable (Burton, 1952). Heritable variation can be determined with greater accuracy when heritability along with genetic advance is studied. Heritability along with genetic gain is more useful criterion in predicting the resultant effects of selecting the best individual (Johnson *et al.,* 1955). High heritability with high genetic advance tells that the character is governed by additive gene action, for that simple selection is advocated. In the present study number of cormels produced per plant showed the high heritability along with maximum genetic gain, followed by weight of cormels produced per plant. Thus, selection on the basis of number of cormels produced per plant and weight of cormels produced per plant would be more effective for further breeding programs, as also reported by Misra and Saini (1988). Negi *et al.* (1982) reported high estimates of heritability along with genetic advance as per cent of mean for weight of cormels produced per corm, number of cormels produced per corm and weight of corm produced. Number of cormels and weight of 10 cormels showed high heritability along with genetic advance, suggesting thereby the basis for selection for further breeding programme (Anuradha and Gowda, 1990). De *et al.* (1993) working on gladiolus also reported that selection on the basis of number of cormels produced per plant would be more effective for further breeding programme.

Spike length, size index of corms, number of florets per spike and number of days to sleeping showed moderate to high heritability but low genetic gain, indicating that high heritability may likely be due to non-additive gene action and for this selection with adequate progeny testing is practiced (Panse, 1957). Lal *et al.* (1985) reported high heritability along with lower genetic advance for plant height, number of leaves per shoot and days to flowering, exhibiting non-additive gene effects.

Table 1: Range, mean, standard error, PCV, GCV, ECV, heritability and genetic gain for 26 characters in gladiolus

Character	Range	Mean	S.E.($\pm$)	PCV (%)	GCV(%)	ECV (%)	H (%)	GG (%)
X_1	7.47-10.56	9.01	0.67	11.90	7.58	9.17	40.59	9.95
X_2	90-100	97.78	4.00	5.09	0.89	5.01	3.06	0.32
X_3	6.37-9.25	7.75	0.53	14.53	11.93	8.30	67.41	20.18
X_4	106.20-154.33	117.82	4.94	12.20	11.07	5.14	82.26	20.68
X_5	42.95-54.89	49.09	2.43	9.18	6.90	6.05	56.53	10.69
X_6	2.63-3.75	3.31	0.15	17.92	17.04	5.57	90.36	33.36
X_7	84.03-155.44	105.53	4.46	20.02	19.33	5.18	93.31	38.47
X_8	59.20-75.33	64.65	2.79	8.67	6.88	5.28	62.94	11.24
X_9	69.33-96.47	80.36	3.37	10.52	9.18	5.14	76.16	16.51
X_{10}	0.701-1.039	0.86	0.04	12.67	11.61	5.07	90.00	21.92
X_{11}	5.11-8.24	6.13	0.37	15.14	13.25	7.33	76.58	23.88
X_{12}	39.07-66.87	50.00	2.40	18.02	17.03	5.87	89.38	33.17
X_{13}	8.73-14.93	11.36	0.78	17.34	15.17	8.40	76.53	27.34
X_{14}	13.33-18.47	14.68	0.65	9.93	8.31	5.43	70.02	14.32
X_{15}	1.13-2.73	1.94	0.15	30.45	29.00	9.32	90.64	56.86
X_{16}	10.67-26.67	18.94	1.21	28.68	27.59	7.82	92.57	54.69
X_{17}	1.55-3.20	2.39	0.18	25.97	24.20	9.41	86.86	46.46
X_{18}	13-30.67	22.75	1.43	27.64	26.56	7.68	92.28	52.55
X_{19}	3.85-4.74	4.25	0.18	7.07	4.79	5.20	45.87	6.68
X_{20}	34.16-77.67	51.94	3.25	23.77	22.50	7.67	89.59	43.88
X_{21}	18.83-120.80	48.44	2.48	72.86	72.59	6.28	99.26	148.97
X_{22}	5.58-21.29	11.57	0.82	37.77	36.75	8.72	94.67	73.66
X_{23}	14.13-19.84	16.33	0.72	10.30	8.79	5.37	72.78	15.44
X_{24}	6.89-9.88	7.72	0.25	11.33	10.60	4.01	87.46	20.42
X_{25}	2.66-4.55	3.54	0.22	16.34	14.43	7.67	78.00	26.26
X_{26}	3.33-5.33	4.30	0.17	16.36	15.61	4.90	91.05	30.69

X_1 = Number of days taken for sprouting of corms, X_2 = Corm sprouting percentage, X_3 =Number of leaves per plant (at slipping stage), X_4 =Plant height (cm), X_5 =Leaf length (cm), X_6 =Leaf width (cm), X_7 =Leaf area (cm^2), X_8 = Number of days to slipping, X_9 = Spike length (cm), X_{10} = Spike diameter (cm), X_{11} = Floret diameter (cm), X_{12} = Rachis length (cm), X_{13} = Duration of flowering (days), X_{14} = Number of florets per spike, X_{15} = Number of spikes produced per plant, X_{16} = Number of spikes produced per plot, X_{17} = Number of corms produced per plant, X_{18} =Number of corms produced per plot, X_{19} = Diameter of corm (cm), X_{20} = Weight of corm (g), X_{21} = Number of cormels produced per plant, X_{22} = Weight of cormels produced per plant (g), X_{23} = Size index of corms, X_{24} = Vase life of spikes (days), X_{25} = Days to wilting of basal floret, X_{26} = Number of florets remaining open at a time.

Selection of individual plants based on number of cormels produced per plant which showed high heritability along with high genetic gain might therefore be effective for crop improvement.

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