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Genetic Variability, Heritability and Scope of Improvement for Yield Components in Glory Lily (*Gloriosa superba* L.)

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ABSTRACT

Genetic variability, heritability (%) in a broad sense and genetic advance as per cent of mean (GA) were studied among 21 morpho-economic traits in 18 genotypes of glory lily (*Gloriosa superba* L.) during two seasons (2007 and 2008). The highest dry seed yield/plant was recorded for GS 15 followed by GS 06, GS 18 and GS 03. Promising genotypes were identified for multiple desirable morpho-economic traits *viz*., plant height, number of leaves, number of flowers/plant, number of pods/plant, number of seeds/pod and fresh yield/plant were GS 15, GS 06, GS 18 and GS 03 which can be utilized directly or included in a hybridization programme as a donor for the improvement of respective traits in desirable genotypes. The highest phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were recorded for fresh seed yield/plant followed by dry seed yield/plant and fresh pod yield/plant in both seasons. The higher estimates of heritability and genetic advance as per cent of mean were obtained per plant for number of leaves, fresh pod yield and fresh seed yield. Thus, selection for these traits is likely to accumulate more additive genes leading to further improvement in their performance.

Keywords: genetic advance, genotypic variation, h^2, phenotypic variation, seed yield

INTRODUCTION

Gloriosa superba (Liliaceae) is found naturally in Africa and Southeastern Asia. It is currently distributed extensively throughout the tropics and globally as a pot plant (Acharya 2006). It is also observed that its natural distribution spreads mainly in tropical Asia *viz*., India, Sri Lanka, Malaysia, Burma (Jayaweera 1982). It is one of the major medicinal plants in India cultivated for its seeds which are exported to developed countries for pharmaceutical use. In India, it is usually found in Himalayan foot-hills, Central India, Tamil Nadu, Andhra Pradesh and Bengal. Seeds and tubers contain valuable alkaloids *viz*., colchicine and colchicoside as the major constituents, which are used to treat gout and rheumatism. Due to the action of colchicoside on spindle fibre formation during cell division, the plant has been identified as a potential anti-cancerous drug. In the Indian systems of medicine, the tubers are used as tonic, antiperiodic, antihelmenthic and also against snake bite (Gupta 2005).

Gloriosa was found in the wild on natural fences a decade back but now it has been domesticated for economic gain in as much as all parts of the plant find a diverse usage in Indian systems of medicine. Though *G. superba* has an extensive natural distribution and selective cultivation, the species has become endangered due to over exploitation of its tubers and poor seed germination (Sivakumar and Krishnamurthy 2002). Having a huge demand for the seeds of *G. superba* in the international market, breeding work for improvement in this species is of great importance as less effort have been made in this direction. Hence the present investigation, in which an attempt was made to study the genetic variability in germplasm accessions for morpho-economic traits in order to gather knowledge of various yield component characters towards seed yield for crop improvement in *G. superba* genotypes.

MATERIALS AND METHODS

The materials consisted of 18 genotypes (**Table 1; Fig. 1**) collected in 2007 from different places of Tamil Nadu and Andhra Pradesh and subjected to diversity analysis. A field experiment was conducted in a randomized block design with three replications at the Medicinal Plants Unit, Botanical Garden, Tamil Nadu Agricultural University, Coimbatore during season I (2007) and II (2008). Each plot consisted of three rows of 5 m length with an inter-row and intra-row spacing of 150 cm and 30 cm respectively. Recommended agronomical practices and plant protection measures were followed to ensure a normal healthy crop (Farooqui and Khan 1991).

Agro-morphological observations were recorded on five randomly selected plants on each accession per replication for plant height (cm), stem girth (cm), number of leaves/plant, number of branches/plant, days to flowering, days to 50% flowering, number

Table 1 Genotype details of *Gloriosa superba* collected in 2007.

Name of germplasm	Accessions
Nallampalayam cultivated	GS 01
Kallimanthayam cultivated	GS 02
Sathyamangalam wild	GS 03
Aruppukotai wild	GS 04
Aruppukotai cultivated	GS 05
Kankayam cultivated	GS 06
Kallimanthayam wild	GS 07
Ottanchadram cultivated	GS 08
Moolanur cultivated	GS 09
Jeyankondam cultivated	GS 10
Udangudi cultivated	GS 11
Viralimalai cultivated	GS 12
Pudukottai cultivated	GS 13
Andhra cultivated – I	GS 14
Andhra wild	GS 15
Z-Melur cultivated	GS 16
Poondurai wild	GS 17
Andhra cultivated – II	GS 18

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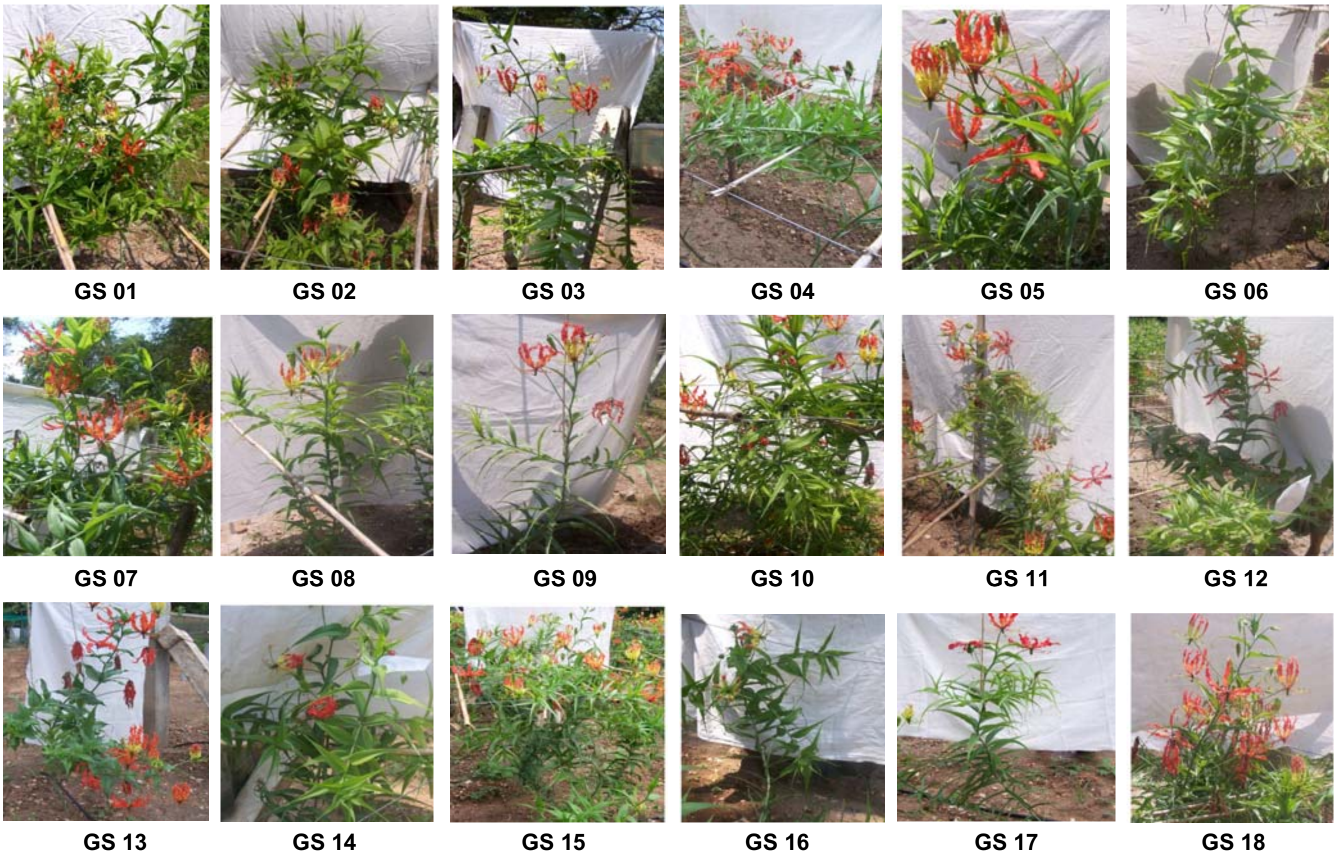

Fig. 1 Morphological variation in *Gloriosa superba* genotypes.

of flowers/plant, number of pods/plant, pod setting percentage, pod length (cm), pod girth (cm), number of seeds/pod, fresh pod weight (g), fresh seed weight/pod (g), fresh pod yield/plant (g), fresh seed yield/plant (g), fresh seed recovery (%), dry seed recovery (%), 100 fresh seed weight (g), 100 dry seed weight (g) and dry seed yield/plant (g).

The statistical parameters like mean, standard error and critical difference for all the observations were assessed by adopting standard methods of analysis as suggested by Panse and Sukhatme (1978). Heritability (%) as broad sense (h^2) was estimated according to Hanson (1955). Phenotypic and genotypic co-efficient of variation were estimated as per Burton (1952). Genetic advance as % of mean was estimated according to Johnson (1955).

RESULTS

The mean performance revealed a significance difference among genotypes for all the traits studied. In the pooled season the highest mean of dry seed yield/plant was recorded for GS 15 followed by GS 06, GS 18 and GS 03. A minimum of 128.20 and a maximum of 620.00 number of leaves/plant were observed in GS 17 and GS 15, respectively. The number of pods/plant was maximum in GS 15 (44.67) and minimum in GS 17 (5.33). The dry seed yield/plant was 4.97 and 93.90 g in GS 17 and GS 15, respectively (**Table 2**).

The genotypic coefficient of variation (%) was found to be less than phenotypic coefficient of variation (%) for all the traits studied (**Table 3**). The maximum PCV (81.52 and 85.16% in season I and II, respectively) and GCV (81.48 and 85.12% in season I and II, respectively) were observed for fresh seed yield/plant while minimum PCV (4.32 and 7.97% in season I and II, respectively) and GCV (4.27 and 7.94% in season I and II, respectively) were recorded for days to 50% flowering.

In both seasons, the heritability value was recorded as maximum for number of leaves/plant (100.00%). The lowest heritability value was recorded for dry seed recovery percentage (83.00%) in season I and pod girth (88.00%) in season II.

In season I, the genetic advance as percentage of mean was highest for fresh seed yield/plant (167.79%) followed by dry seed yield/plant (159.82%) and fresh pod yield/plant (158.66%). The lowest value was recorded for days to 50% flowering (8.68%). In season II, the GA as percentage of mean ranged from 16.30% (days to 50% flowering) to 175.28% (fresh seed yield/plant).

DISCUSSION

The variability of genetic stocks could be increased by increasing the collection from diversified origin and geographical distribution. The mode of origin and subsequent adaptations to varied environments are the primary causes for heritable variations found among genotypes (Anshebo 2002). The phenotypic and genotypic variances, estimated from the total variance were used to assess the variability among the genotypes. The genotypic coefficient of variance helps to measure the range of diversity in a character and provides the means to compare genetic variability in quantitative characters. The genotypic coefficient of variance along with phenotypic coefficient of variation was used to ascertain the value of diversity among the genotypes.

Genetic variability in glory lily genotypes

Among the various characters observed for this study, higher variability range was observed for plant height, number of leaves/plant, number of branches/plant, number of flowers/plant, number of pods/plant, number of seeds/pod and dry seed yield/plant. Thus, there existed immense scope for selection based on these characters. Wider variations in all these characters and their relative contribution to the seed yield were reported in *Vigna radiata* (Pandey and Kole 2007) and *Pisum sativum* (Kumar 2008). The traits that recorded relatively less variability were stem girth, days to flowering, days to 50% flowering, pod length, pod girth and hundred dry seed weight. The relative contribution of these

Table 2 Mean performance of different glory lily genotypes for morpho-economic traits (Pooled).

GP	PH	NLP	NBP	DF	D50%F	NFP	NPP	NSP	FPW	FSWP	FPYP	FSYP	DSWP	DSYP	PDI
GS 01	155.70	449.23	13.67	37.67	29.00	28.00	21.33	7.00	148.60	39.33	5.80	123.63	1.70	36.27	44.34
GS 02	174.17	460.70	16.00	37.00	28.33	30.67	23.00	8.00	181.73	42.67	6.70	154.27	1.80	41.40	60.22
GS 03	169.37	457.63	15.00	38.00	28.00	30.00	23.33	7.50	175.77	49.67	6.23	145.43	1.80	42.00	42.87
GS 04	74.50	130.50	4.00	40.33	31.00	9.67	6.67	3.90	26.93	31.00	3.00	20.03	0.77	5.07	48.92
GS 05	112.93	245.37	5.00	33.33	29.33	18.67	10.33	5.90	60.27	47.00	4.47	46.13	1.43	14.80	64.48
GS 06	177.00	617.30	17.00	36.00	27.00	54.00	43.00	7.70	341.00	72.00	6.83	293.70	1.87	80.23	61.54
GS 07	165.43	454.70	13.67	35.33	28.00	30.00	22.67	7.50	168.50	62.00	6.03	136.73	1.73	39.30	21.73
GS 08	114.80	248.10	4.67	36.67	29.33	19.00	14.00	5.70	80.20	54.67	4.33	60.63	1.50	21.00	45.50
GS 09	105.23	238.23	4.00	38.67	30.00	17.67	11.67	5.00	60.33	47.00	4.00	46.70	1.17	13.60	57.70
GS 10	139.19	374.30	6.00	35.67	29.00	20.00	12.67	6.20	77.23	54.00	4.93	62.50	1.57	19.83	42.18
GS 11	110.93	243.60	4.00	36.00	30.00	18.00	11.00	5.60	60.50	36.00	4.20	46.20	1.33	14.67	40.38
GS 12	144.37	381.20	6.67	44.00	29.00	23.00	13.67	6.70	91.17	58.33	5.53	75.63	1.60	21.87	39.64
GS 13	141.63	377.70	7.00	40.33	29.00	21.67	13.67	6.50	89.30	52.00	5.43	74.23	1.60	21.87	54.68
GS 14	161.10	451.90	13.67	37.00	28.00	29.00	22.67	7.10	160.20	59.00	5.97	135.23	1.70	38.53	30.24
GS 15	180.63	620.00	17.67	36.00	26.33	56.33	44.67	8.20	374.93	77.33	7.40	330.27	2.10	93.90	33.25
GS 16	108.87	240.73	5.00	41.00	30.00	17.33	12.33	5.50	68.23	48.33	4.27	52.63	1.20	14.80	35.83
GS 17	54.97	128.20	3.33	40.67	31.00	8.33	5.33	3.90	21.30	31.67	2.97	15.83	0.93	4.97	38.25
GS 18	173.57	614.23	16.33	37.00	28.00	53.33	41.00	7.70	319.77	68.33	6.70	274.67	1.80	73.80	52.77
CD (0.05%)	1.42	0.32	0.76	1.30	0.58	0.89	1.32	0.19	8.06	3.81	0.23	7.82	0.08	3.56	0.22

PH, plant height; NLP, number of leaves/plant; NBP, number of branches/plant; DF, days to flowering; D50%F, days to fifty per cent flowering; NFP, number of flowers/plant; NPP, number of pods/plant; NSP, number of seeds/pod; FPW, fresh pod weight; FSWP, fresh seed weight/pod; FPYP, fresh pod yield/plant; FSYP, fresh seed yield/plant; DSWP, dry seed weight/pod; DSYP, dry seed yield/plant; PDI, per cent disease index.

Table 3 Estimates of variability and genetic parameters of *Gloriosa superba* genotypes during and seasons I and II.

Characters	Season I PCV %	Season II PCV %	Season I GCV %	Season II GCV %	Season I h^2	Season II h^2	Season I GA	Season II GA	Season I GA (% mean)	Season II GA (% mean)
Plant height	27.03	27.05	27.02	27.05	99.00	99.00	76.22	76.13	55.67	55.71
Stem girth	14.00	16.27	13.97	16.24	99.00	99.00	0.19	0.22	28.73	33.41
No. of leaves/plant	41.79	41.75	41.79	41.75	100.00	100.00	322.07	320.10	86.09	86.02
No. of branches/plant	57.27	56.60	57.21	56.54	99.00	99.00	11.29	11.35	117.71	116.33
Days to flowering	6.85	10.22	6.74	10.15	97.00	98.00	5.17	7.94	13.67	20.77
Days to fifty per cent flowering	4.32	7.97	4.27	7.94	99.00	99.00	2.51	4.75	8.68	16.30
No. of flowers/plant	52.95	54.49	52.94	54.48	99.00	99.00	29.36	29.96	109.04	112.20
No. of pods/plant	61.55	64.03	61.51	63.99	99.00	99.00	24.83	25.54	126.62	131.73
Pods setting percentage	10.98	14.31	10.77	14.13	96.00	97.00	15.30	19.84	21.78	28.76
Pod length	19.84	28.07	19.82	28.05	99.00	99.00	2.58	3.73	40.81	57.76
Pod girth	17.79	20.44	16.65	19.51	87.00	91.00	2.40	2.87	32.09	38.36
No. of seeds/ pod	25.41	25.32	25.28	25.23	98.00	99.00	26.78	26.52	51.82	51.77
Fresh pod weight	20.25	23.05	20.22	23.03	99.00	99.00	2.68	3.05	41.60	47.40
Fresh seed weight/pod	24.92	29.75	24.88	29.71	99.00	99.00	2.69	3.24	51.15	61.13
Fresh pod yield/plant	77.07	79.04	77.04	79.01	99.00	99.00	220.89	225.34	158.66	162.70
Fresh seed yield/plant	81.52	85.16	81.48	85.12	99.00	99.00	195.24	206.22	167.79	175.28
Fresh seed recovery	5.44	8.45	5.21	8.28	91.00	95.00	8.33	13.53	10.30	16.72
Dry seed recovery	7.66	17.01	6.99	16.68	83.00	96.00	3.85	10.18	13.13	33.71
100 fresh seed weight	18.74	19.99	18.73	18.40	99.00	84.00	3.59	3.17	38.59	34.88
100 dry seed weight	13.43	13.53	13.43	13.53	99.00	99.00	0.73	0.73	27.66	27.86
Dry seed yield/plant	77.76	80.33	77.67	80.21	99.00	99.00	53.08	55.63	159.82	165.00

PCV, phenotypic co-efficient of variation; GCV, genotypic co-efficient of variation; h^2, heritability (broad sense); GA, genetic advance

traits to seed yield had been reported in *Silybum marianum* (Ram 2005), *Pongamia pinnata* (Kaushik 2007) and *Vigna radiata* (Makeen 2007).

Genotypic and phenotypic coefficient of variation of glory lily genotypes

The estimate of genotypic and phenotypic variance was worked out for the 21 characters of *G. superba*. In the present investigation, the GCV (%) was highest for fresh seed yield/plant followed by dry seed yield/plant, number of pods/plant, number of branches/plant, number of flowers/plant and number of leaves/plant. These results conform to the earlier findings of Shukla (2003) in fennel and Kumar (2008) in *Pisum sativum.* Low GCV was recorded for plant height, stem girth, days to flowering, days to 50% flowering, fresh seed recovery and dry seed recovery. This is line with the findings of Sharma (1990) in fenugreek, Ibrahim and Hussein (2006) in *Hibiscus sabdariffa* and Nya and Eka (2007) in *Talinum triangulare.*

The small difference between PCV and GCV estimate for all characters indicated that variability was primarily due to genotypic difference providing scope for selection between populations. The characters that had close GCV and PCV values indicated low contribution of environmental variances for the characters *viz*., plant height, number of leaves/plant, number of branches/plant, number of flowers/plant, hundred fresh seed weight and 100 dry seed weight. These results were similar to earlier findings of Mathur (2003) in *Centella asiatica* and Sethi (1991) in palmrosa and Sharma (1990) in fenugreek.

The difference between genotypic and phenotypic variances indicates the contribution of environmental variance (Ram and Singh 1993). The smaller the difference in values between phenotypic and genotypic variance, the lesser will be the environmental effect on the character. Similarly, the higher the values, the greater will be the environmental effect. These results were similar to earlier findings in isabgol by Lal (1999) and *Ocimum sanctum* by Ahmad and Khaliq (2002). The presence of comparatively little difference between PCV and GCV estimates for all characters indicated that variability was primarily due to genotypic differences and that scope for selection based on these components would be much greater in *G. superba*.

Heritability and genetic advance as percentage of mean of glory lily genotypes

Heritability and genetic advance as percentage of mean are the two important parameters of which h^2 is used to estimate the expected genetic advance through selection. A relative comparison of heritability estimates and expected genetic advance as the percentage of mean will give an idea about the nature of gene action governing a particular character (Johnson 1955). According to Burton (1952), heritability estimates also have a bearing on the population response to selection. Heritability denotes the additive genetic variance in per cent of the total variance (Wright 1921). High estimates of heritability for certain traits suggest that they are under genetic control. The higher the value of genetic advance, better and surer the progress will be on the mean in the succeeding generation under directional selection.

In the present investigation, many characters except days to flowering, pod setting percentage, pod girth, number of seeds/pod, fresh seed recovery percentage/plant and 100 fresh seed weight registered high heritability indicating that these traits could be governed by additive genes (Panse and Sukhtame 1978), and therefore these characters could be readily fixed by selection. These results confirmed the findings of Rishi (1984) in *Dioscorea*, Krishnamoorthy and Madalageri (2002) in ajowan, Shukla (2003) in fennel, Ibrahim and Hussein (2006) in *Hibiscus sabdariffa*, Mahalakhsmi (2006) in *Phyllanthus amarus* and Kaushik (2007) in *Pongamia pinnata*.

Medium heritability estimates were recorded for days to flowering, pod setting percentage and number of seeds/pod. For these traits, the environment and non-additive gene effect constituted a major portion of the total phenotypic variance, and thus improvement for these characters cannot be made by selection. The above finding confirms an earlier report of Makeen (2007) in mungbean.

Even though heritability estimates represent the heritable portion of variation, they do not indicate the effectiveness with which selection of a phenotype could be made based on the phenotypic performance (Johnson 1955), and thus high heritability could not be considered as an indication of greater genetic gain. The results of the present study have clearly highlighted that despite high heritability, the genetic advance as percentage of mean was low for many characters except plant height, number of leaves/plant, fresh seed weight/pod, fresh seed yield/plant and dry seed yield/plant. High heritability linked with high genetic advance as percentage of mean of these traits indicates that the expressions of these characters are governed by additive genes and improvement could be possible through selection. A high heritability value along with high genetic advance as per cent of mean is more useful in predicting genetic progress that would result from selecting the best individuals. A similar finding was reported by Lal (1999) in *Plantago ovata*, Megeji (2002) and Singh (2003) in opium poppy and Yadav in coriander (1999a) and ginger (1999b).

In the present investigation, high heritability and low genetic advance as percentage of mean were observed for stem girth, days to flowering, days to 50% flowering, pod length, fresh pod weight, fresh seed weight/pod, 100 fresh seed weight and 100 dry seed weight suggesting that high heritability was not always an indication of high genetic advance. Thus, it appears that during selection of a new genotype, heritability and genetic advance as percentage of mean should be considered together. The presence of high heritability and low genetic advance is attributed to the effects of non-additive genes (Panse and Sukhatme 1978). In the present study, fresh pod yield/plant and fresh seed yield/plant had higher estimates of genetic advance than heritability. Hence, selection on this character could be highly reliable. Thus the present study suggested that a good amount of variation was observed for various characters under study and recorded obvious breeding value as their heritability and genetic advance as a percentage of mean.

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