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Variability for qualitative and quantitative traits in Glory lily (*Gloriosa superba* L.)

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ABSTRACT

Glory lily (*Gloriosa superba* L.) is one of the major medicinal plants of India cultivated for its seeds which are exported to developed countries for pharmaceutical use. Identifying germplasm is an important component for efficient and effective management of plant genetic resources. Variability for qualitative and quantitative traits was investigated in 18 genotypes of *G. superba* collected from different regions of Tamil Nadu and Andhra Pradesh. For qualitative traits, these genotypes were subjected to diversity analysis based on NBPGR descriptors. Fourteen qualitative and twenty quantitative traits of *G. superba* were evaluated to assess morphological variations among the genotypes collected. In qualitative traits, a large number of genotypes of the 18 clustered together, at 77% similarity in two clusters. Dendrogram constructed on the basis of twenty quantitative traits for the same set of genotypes did not reveal any clear pattern in grouping, and the genotypes were grouped into seven different clusters. Cluster analysis based on qualitative and quantitative traits revealed a different group of genotypes for each of the data-set. This clearly indicated that less variation existed between genotypes with respect to morphological traits. These easily observable morphological traits are useful tools for preliminary evaluation, because, they offer a fast and reliable approach for assessing extent of diversity in *G. superba* genotypes.

Key words: *Gloriosa superba,* morphological traits, cluster analysis

INTRODUCTION

Gloriosa superba L., a climber belonging to the family Liliaceae, is a major high-value medicinal crop. 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, the plant is usually found in the Himalayan foot-hills, Central India, Tamil Nadu, Andhra Pradesh and Bengal. Seeds and tubers contain valuable alkaloids, viz., colchicine and colchicoside as major constituents, and are used for treating 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-cancer drug. In the Indian Systems of Medicine (ISM), the tubers are used as tonic, antiperiodic, antihelmenthic and also against snake-bite (Gupta *et al*, 2005). *Gloriosa* could be found in the wild on natural fences a decade back, but now, it has been domesticated for economic gain (as all parts of the plant find diverse uses in ISM). Though *G. superba* enjoys extensive natural distribution and selective cultivation, the species is now endangered due to over-exploitation of its tubers and poor seed-germination. Growing demand for seeds of *G. superba* in the international market and wide popularity of the plant among farmers makes it necessary to induce variability and develop lines with high-yield, high colchicine content, dwarf stature and leaf-blight resistance. In this medicinal plant, knowledge of genetic variability existing within the species will greatly aid exploitation of the variability directly as cultivars and, indirectly, as its use as base material in breeding programmes.

MATERIAL AND METHODS

Eighteen accessions, collected from different regions of the important *Gloriosa* growing states viz., Tamil Nadu and Andhra Pradesh, were grown in the field in a randomized block design with three replications, at the Medicinal Plants Unit, Botanical Garden, Tamil Nadu Agricultural University, Coimbatore, during 2007 - 2008 (Table 1). Planting was done in plots with three 5 m long rows, with inter-and intra-row spacing of 150 cm and 30 cm, respectively. The plots were irrigated at weekly intervals. Recommended agronomic practices and plant protection measures were followed to

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ensure a normal, healthy crop. Diversity, in terms of morphological variations among the genotypes collected, was documented as per Singh *et al* (2003). Morphological characters identified in the descriptor for *Gloriosa superba* (Saravanan and Buvaneswaran, 2003) such as habit, stem-branching, tuber shape, leaf arrangement, lamina margin, lamina colour, flower shape and biotic-stress susceptibility, were used for morphological characterization. Observations were made on five randomly-selected plants of each genotype for qualitative and quantitative traits.

Qualitative traits depicting an array of characters were converted into binary characters (Sneath and Sokal, 1973) based on variations present in each trait. The presence or absence of a phenotype was given the score of 1 and 0, respectively. Quantitative data generated on various traits were standardized to zero mean and a unit variance. Sequential Agglomerative Hierarchical Non-overlapping (SAHN) clustering was performed on Squared Euclidean distance matrix using dice coefficient for quantitative and binary data, respectively, using Unweighted Pair Group Method with Arithmetic Averages (UPGMA). Analysis of data was done using NTSYSpc Version 2.02 (Rohlf, 1994).

RESULTS AND DISCUSSION

All the accessions collected were climbers, as reported earlier by Le Roux and Robbertse (1994). All other characters, however, showed great variation among accessions. For instance, leaf-shape variation included ovate, lanceolate and linear. Based on tuber-shape, of the 18 accessions studied, 10 had L-shape and 8 had V-shape. Leaf arrangement was mostly opposite, but alternate arrangement was also seen. Leaf lamina colour in *Gloriosa* was predominantly pale-green or dark-green. However, a few accessions showed dark-green lamina with pale-green streaks. As for leaf-blight susceptibility, most accessions showed no visible sign of susceptibility, while and others exhibited either low or high susceptibility (Table 2).

Cluster analysis grouped 18 genotypes in two major clusters where similarity coefficients ranged from 50.5 to 100 (Fig 1). The maximum number of genotypes figured in cluster I, having 10 genotypes with a high degree of similarity (64-100%). This clearly indicated that less variation existed between genotypes with respect to morphological traits. Minimal variation between genotypes for morphological characters can be attributed to low divergence due to a greater gene flow between populations

Table 1. Details of *Gloriosa superba* genotypes collected in 2007

Sl.No.	Germplasm collected	Genotype designation
1.	Nallampalayam cultivated	GS 01
2.	Kallimanthayam cultivated	GS 02
3.	Sathyamangalam wild	GS 03
4.	Aruppukotai wild	GS 04
5.	Aruppukotai cultivated	GS 05
6.	Kankayam cultivated	GS 06
7.	Kallimanthayam wild	GS 07
8.	Ottanchadram cultivated	GS 08
9.	Moolanur cultivated	GS 09
10.	Jeyankondam cultivated	GS 10
11.	Udangudi cultivated	GS 11
12.	Viralimalai cultivated	GS 12
13.	Pudukottai cultivated	GS 13
14.	Andhra cultivated – I	GS 14
15.	Andhra wild	GS 15
16.	Z-Melur cultivated	GS 16
17.	Poondurai wild	GS 17
18.	Andhra cultivated -II	GS 18

Wild : Sourced from natural habitat
Cultivated : Sourced from farmers' fields in the respective location

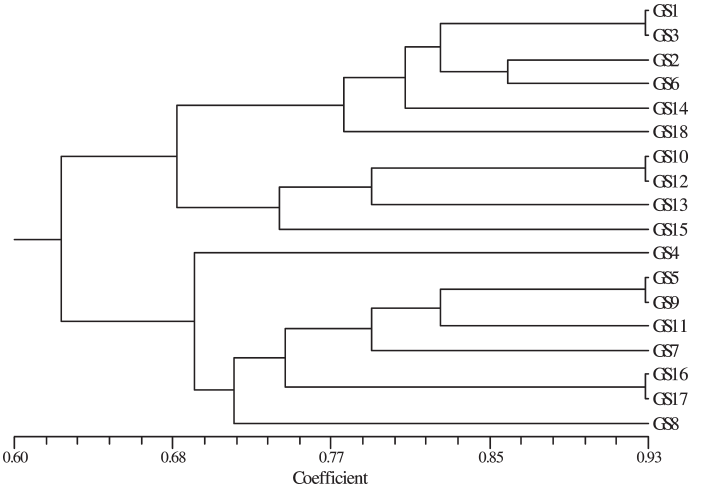

Fig 1. Dendrogram of *Gloriosa superba* genotypes for qualitative traits using UPGMA based on Jaccard's coefficient

(eg., pollination, new introductions etc.) (Doulaty Baneh *et al*, 2007).

Additionally twenty phenotypic quantitative characters were evaluated to assist diversity comparison. Per cent variation for individual traits varied from 0.05 (number of leaves per plant) to 13.55 (hundred fresh-seed weight) (Table 3). Of the twenty traits observed, hundred fresh-seed weight showed highest variation, ranging from 5.88 g (GS 17) to 12.49 g (GS 15). Pod girth, dry-seed yield per plant and dry-seed recovery also showed considerable amount of variation. A minimum of 125.26 and maximum of 621.18 numbers of leaves per plant were observed in GS

Table 2. Phenotype variants observed for various qualitative traits across 18 *Gloriosa superba* genotypes

Trait	Score	Phenotype	No. of genotypes
Plant habit	1	Annual stem with perennial rootstock	18
	2	Biennial	-
	3	Perennial	-
Mode of reproduction	1	Asexual	18
	2	Sexual	-
	3	Asexual & sexual	-
Plant growth habit	1	Climbing	9
	2	Erect	9
Stem branching	1	Profuse	8
	2	Sparse	10
Tuber shape	1	'V' shape	8
	2	'L' shape	10
Stem pubescence	1	Glabrous	18
	2	Sparse	-
	3	Medium	-
	4	Dense	-
Leaf arrangement	1	Alternate	4
	2	Opposite	14
Lamina margin	1	Ovate	5
	2	Lanceolate	10
	3	Linear	3
Leaf base	1	Obtuse	18
Apex of upper leaf	1	With tendril	18
	2	Without tendril	-
Lamina colour	1	Pale green	9
	2	Dark green	6
	3	Dark green with pale green streaks	3
Flower colour	1	Yellow and Red	-
	2	Yellow	-
	3	Red	18
	4	White	-
Flower shape	1	Linear	10
	2	Narrow lanceolate	8
Biotic-stress susceptibility (Leaf blight)	1	Very low or no visible sign of susceptibility	11
	3	Low	5
	5	Intermediate	-
	7	High	2
	9	Very high	-

17 and GS 15, respectively. The number of pods per plant was maximum in GS 15 (46.17), and minimum in GS 17 (4.33). Dry-seed yield per plant was 4 g and 97.78 g in GS 17 and GS 15, respectively. In the present study, variation in mean performance of the genotypes may be due to interaction between environment and genotype as reported by Chandran (1987). Comparatively small difference between characters indicated that variability was primarily due to genotypic differences, and scope for selection based on these components would be much greater in *G. superba*.

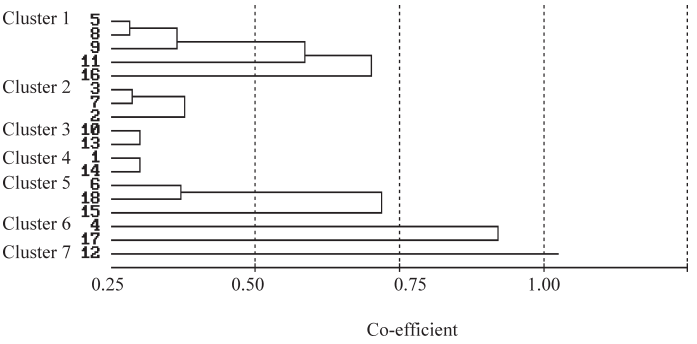

Fig 2. Dendrogram of *Gloriosa superba* genotypes for quantitative traits using UPGMA based on Squared Euclidean Distance of standardized data mean

Dendrogram construction based on twenty quantitative traits for 18 genotypes showed the genotypes to be grouped into seven different clusters (Fig 2). Cluster I had the maximum number of genotypes (five genotypes). Cluster to cluster composition revealed that clusters I, III, IV, V and VI comprised cultivated genotypes of *G. superba* from Tamil Nadu. Cluster II and VII included wild genotypes from Tamil Nadu. On the contrary, clusters V and VI were composed of cultivated genotypes types from Andhra and Tamil Nadu. The distribution pattern of genotypes of diverse origin in a single cluster indicates that genetic diversity observed within *G. superba* was not related to geographic origin. Differences noted in plant characters probably occurred over time, with free movement of plant material from location to location, and due to spontaneous induced mutations over time. Thus, for crop improvement *Gloriosa* plants should be selected on the basis of quantified degree of divergence as opposed to geographic origin of the genotype. These easily-observable morphological traits are a useful tool for preliminary evaluation, because, they offer a fast and reliable approach for assessing extent of diversity in *G. superba* genotypes.

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Table 3. Mean, range, coefficient of variation and standard deviation for vegetative / reproductive quantitative traits in Glory lily

Traits	Mean	Range	CV (%)	SEd	CD (0.05)
Plant height	136.78	54.49 - 180.93	0.63	0.49	0.97
Stem girth	0.67	0.49 - 0.90	1.60	0.006	0.012
No. of leaves per plant	373.09	125.26 - 621.18	0.05	0.11	0.22
No. of branches per plant	9.68	3.33 - 18.17	4.75	0.26	0.52
Days to 50% flowering	29.02	27.00 - 32.50	1.20	0.20	0.39
No. of flowers per plant	26.81	7.33 - 57.83	2.03	0.26	0.52
No. of pods per plant	19.50	4.33 - 46.17	4.11	0.44	0.89
Pod setting percentage	69.61	57.22 - 79.80	3.87	1.51	3.00
Pod length	6.40	4.60 - 8.07	1.50	0.05	0.10
Pod girth	7.50	4.14 - 8.58	10.57	0.45	0.90
Number of seeds per pod	51.46	30.65 - 77.83	3.85	1.22	2.43
Fresh pod weight	6.44	3.70 – 8.57	1.74	0.06	0.12
Fresh seed weight per pod	5.28	2.69 - 7.84	2.64	0.07	0.15
Fresh pod yield per plant	138.86	16.47 - 400.16	3.66	2.79	5.53
Fresh seed yield per plant	117.01	11.95 - 362.34	4.39	2.80	5.54
Fresh seed recovery	80.91	71.65 - 90.41	2.94	1.31	2.60
Dry seed recovery	29.78	22.71 - 35.41	5.75	0.96	1.90
100 fresh seed weight	9.21	5.88 - 12.49	13.55	0.50	0.99
100 dry seed weight	2.65	2.14 - 3.34	0.75	0.01	0.02
Dry seed yield per plant	33.47	4.00 - 97.78	7.55	1.30	2.58

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