

DETERMINATION OF GENETIC DIVERGENCE BY D² ANALYSIS IN BIRD OF PARADISE (*STRELITZIA REGINAE*) PROGENY LINES DURING SUMMER SEASON

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ABSTRACT

In Bird of paradise based on Mahalanobis's D² analysis, genetic divergence studies were conducted in forty progeny lines which were grouped into twelve clusters. The cluster I retained maximum number of progenies (11) followed by Cluster II and III each with 10 progenies respectively and rest of the clusters were of solitary type. The clustering pattern indicated that there was no association between geographical distribution of accessions and genetic divergence. The maximum inter cluster D² value was observed between the cluster VII and VIII (15.38) indicating that crosses may be attempted between the progenies of cluster VII (P-27) and cluster VIII (P-1) to obtain new desirable recombinants in Bird of Paradise. Cluster mean analysis indicated that the maximum number of leaves/plant (9.67) and spathe length (26.0) was recorded in cluster VI. The highest mean stem girth (28.33), flower stalk length (62.33), flower stalk girth (6.40) was recorded in cluster VII. The number of flowers/m² (4.67) and vase life (12.67) was observed maximum in cluster IX. Most of these were important flower attributing characters. This indicates that the progenies included in these VI, VII and IX clusters could effectively be used for the crop improvement program for increasing yield.

INTRODUCTION

Bird of paradise (*Strelitzia reginae*) belonging to the family *Strelitziaceae* is one such flower, which has great potential globally. This slow growing, evergreen perennial is native to the subtropical coasts of southern Africa and is widely grown in warm regions (Hensely *et al.*, 1998). It is highly prized as cut flower due to brilliant colour and unusual appearance of the spectacular flower. Therefore, the crop is cultivated in many parts of the world in order to produce cut flowers for both domestic and international market. They are gaining popularity among the flower growers of India owing to the fact that they can be successfully grown with little care and attention and they do fairly well under partial shade also. Looking at its commercial importance, there is utmost need to develop newer varieties/accessions/hybrids with higher yield. For this purpose the breeders choose genetically distant parents, genetic diversity plays an important role in breeding, because hybrids derived from the lines of diverse origin display more heterosis than those between closely related strains (Lahbib *et al.*, 2010; Srivastava *et al.*, 2014). Mahalanobis D² (Mahalanobis, 1936) is reliable and most frequently used. D² statistic has been employed widely to resolve genetic divergence at inter varietal, subspecies and species levels in classifying problems in crop plants (Murthy and Tiwari, 1967 and Siddique and Swaminathan, 1971). In the process of formulating the bird of paradise improvement programmes, understanding about the nature and degree of

genetic divergence available in the germplasm plays a pivotal role. The progenies derived from diverse parents are expected to show a broad spectrum of genetic variability and provide better scope to isolate superior recombinants.

Therefore, present investigations were undertaken to examine the nature and magnitude of genetic divergence in forty bird of paradise progenies.

MATERIALS AND METHODS

The experimental plant material for the present study comprised of forty progenies of Bird of Paradise (*Strelitzia reginae*) planted at the Horticulture Research Station, Kanabargi Farm (Belgaum), University of Horticultural Sciences, Bagalkot (Karnataka) during summer 2011-12. Forty plants were chosen from the bird of paradise population, from these plants, suckers were removed and planted as plant to progeny rows with ten plants per row with three replication and these were evaluated. The experiment was laid out in RCBD with 3 replications; plants were maintained with the spacing of 1×1 m², observations of forty progeny lines were recorded on five randomly selected plants for twelve morphological characters. The germplasm was subjected to multivariate analysis utilizing Mahalanobis D² statistic as suggested by Mahalanobis (1936) and Rao (1952) using statistical software WINDOSTAT 9.1 developed by INDOSTAT services Ltd. Hyderabad, India. Progenies were grouped into various clusters following Tocher's method as suggested by Rao (1952).

RESULTS AND DISCUSSION

The analysis of variance revealed that the progenies varied significantly for all the twelve morphological characters under present investigations. After computing D^2 value for all the possible pairs, forty progenies were grouped into twelve divergent clusters, shown in Table 1 and illustrated in fig. 1 using Toucher's method (Singh and Choudhary, 1977) which indicated large genetic diversity indicating adequate genetic diversity for selecting superior and diverse parents which can be exploited for any breeding program. Contribution of each character towards genetic divergence was estimated from the number of times that character appeared in first rank. It was observed that stem girth contributed maximum (61.54%) towards genetic divergence followed by plant height (27.05%),

number of bracts (3.21%), number of leaves (3.08%), leaf breadth and flower stalk girth (2.05%), spathe length (0.64%), number of flowers (0.26%) and vase life (0.13%). These characters showed highest contribution in differentiating at intra cluster level. Similar observations have been recorded by Desh Raj and Mishra (2000), Pal *et al.* (2006) in gladiolus crop.

Forty progeny lines were grouped into 12 clusters (Table 2) and among them, cluster I was the largest with 11 genotypes followed by cluster II and III each with 10 progeny lines respectively, and rest of the clusters were of solitary type. The formation of solitary clusters may be due to total isolation preventing the gene flow or intensive natural/human selection for diverse adaptive complexes. These genotypes may be very

Table 1: Per cent contribution of 12 quantitative characters towards diversity in forty Bird of paradise progenies during summer season 2011

Sl. No.	Character	Per cent contribution of total divergence (%)	No. of times ranked 1 st
1	Plant height (cm)	27.05	211
2	Stem girth (cm)	61.54	480
3	Leaf length (cm)	0	0
4	Leaf breadth (cm)	2.05	16
5	No. of leaves/plant	3.08	24
6	No. of suckers	0	0
7	No. of flowers/plant	0.26	2
8	Flower stalk length (cm)	2.05	16
9	Flower stalk girth (cm)	0	0
10	Spathe length (cm)	0.64	5
11	Vase life (days)	0.13	1
12	No. of bracts	3.21	25

Table 2: Grouping of Bird of paradise progenies based on D^2 analysis

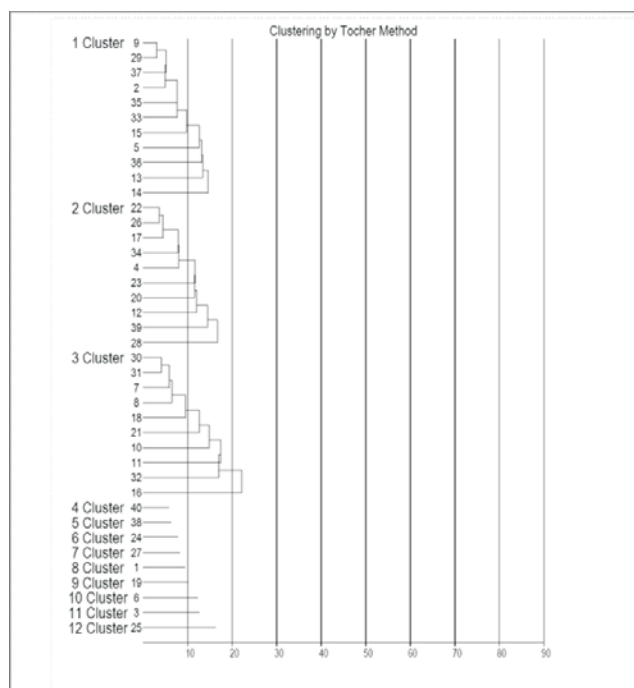
Sl. No.	Clusters	Number of genotypes	Progenies included in the cluster
1	I	11	P-9, P-29, P-37, P-2, P-35, P-33, P-15, P-5, P-36, P-13, P-14
2	II	10	P-22, P-26, P-17, P-34, P-4, P-23, P-20, P-12, P-39, P-28
3	III	10	P-30, P-31, P-7, P-8, P-18, P-21, P-10, P-11, P-32, P-16
4	IV	1	P-40
5	V	1	P-38
6	VI	1	P-24
7	VII	1	P-27
8	VIII	1	P-1
9	IX	1	P-19
10	X	1	P-6
11	XI	1	P-3
12	XII	1	P-25

Table 3: Average intra and inter cluster D^2 values of 12 clusters in Bird of paradise progenies during summer 2011

Sl.No.	Cluster	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII
1	I	3.58	5.24	6.62	4.18	6.77	4.59	8.23	9.61	6.40	7.88	6.21	7.16
2	II		3.75	9.13	6.71	4.61	5.07	5.22	11.38	4.68	4.63	7.51	6.73
3	III			4.19	7.68	11.86	9.43	13.01	5.58	8.49	11.48	10.63	7.24
4	IV				0.00	7.09	4.16	8.88	11.48	8.52	9.47	3.54	9.86
5	V					0.00	4.51	2.86	14.66	7.11	4.99	6.21	9.90
6	VI						0.00	6.21	12.76	7.74	7.76	3.96	9.48
7	VII							0.00	15.38	7.11	4.20	8.20	9.99
8	VIII								0.00	9.37	13.03	14.58	6.64
9	IX									0.00	4.23	10.33	4.03
10	X										0.00	9.92	7.38
11	XI											0.00	12.14
12	XII												0.00

Table 4: Mean values of clusters for different quantitative characters in Bird of paradise progenies during summer 2011

Sl.No.	Characters/ clusters	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII
1	Plant height (cm)	83.17	73.42	80.23	95.17	80.00	87.00	72.67	65.67	61.67	64.67	101.67	58.00
2	Stem girth (cm)	17.15	21.96	9.63	17.03	26.67	21.33	28.33	6.67	19.53	25.57	21.37	15.67
3	Leaf length (cm)	30.60	30.65	32.27	30.00	33.00	29.33	24.00	24.00	32.67	26.00	32.83	24.67
4	Leaf breadth (cm)	9.89	8.22	8.75	11.00	9.17	7.33	7.33	7.67	9.00	8.33	10.83	9.50
5	No. of leaves	7.24	6.93	6.93	7.33	6.00	9.67	7.00	6.33	6.33	4.00	7.33	7.00
6	No. of suckers/m ²	4.06	3.30	3.17	3.33	3.00	4.00	2.67	1.67	3.67	3.67	3.33	3.33
7	No. of flowers	2.06	2.63	2.47	2.33	1.33	2.67	3.33	3.67	4.67	4.00	2.33	2.33
8	Flower stalk length (cm)	48.11	59.82	56.38	37.17	44.33	55.50	62.33	42.17	34.33	53.67	56.00	55.33
9	Flower stalk girth (cm)	4.79	5.03	5.00	5.67	4.40	5.03	6.40	4.70	5.67	4.70	5.13	5.72
10	Spathe length (cm)	20.21	20.90	20.11	18.33	21.33	26.0	18.50	20.17	24.17	18.83	17.67	22.17
11	Vase life (days)	8.88	10.03	9.50	12.00	10.00	8.67	12.33	8.33	12.67	12.00	8.67	8.67
12	No. of bracts	4.39	5.40	5.73	5.67	4.33	3.00	5.67	5.33	7.67	8.33	5.67	5.67

**Figure 1: Dendrogram showing clustering patterns of forty progeny lines of bird of paradise (Tocher's method)**

unique and useful in breeding point of view. Similar conclusions were drawn by Kavitha and Anburni (2009) in African marigold and Rakesh Kumar *et al.*, (2011) in Snapdragon, Kameswari *et al.* (2014) in chrysanthemum.

The divergence within the cluster (intra cluster distance) indicates the divergence among the progenies falling in the same cluster. On the other hand, inter cluster divergence suggests the distance (divergence) between the accession of different clusters. Average inter and intra cluster distances revealed that, in general, inter cluster distances were much higher than those of intra cluster distances, suggesting homogeneous and heterogeneous nature of the germplasm lines within and between the clusters, respectively. The intra and inter cluster D² values among 40 lines are presented in Table 3, revealed that cluster IV, V, VI, VII, VIII, IX, X, XI and XII showed minimum intra-cluster D² value (0) followed by cluster I (3.58), whereas, maximum intra-cluster D² value (4.19) was

shown by cluster III followed by cluster II (3.75) revealing considerable genetic divergence among the lines of this cluster and was due to both natural and artificial selection forces among the progenies (Rathi *et al.*, 2011). Minimum inter-cluster D² value was observed between the cluster V and VI (2.86) followed by cluster IV and X (3.54) and cluster VI and IX (3.96) indicated close relationship among the accessions included in these clusters. Maximum inter-cluster D² value was observed between the cluster VII and VIII (15.38) followed by cluster V and VIII (14.66) and cluster VIII and XI (14.58) indicated that the progenies belonging to these groups were genetically most diverse and the accessions included in these clusters can be used as a parent in hybridization program to get higher heterotic hybrids from the segregating population. Similar results were revealed by Asha *et al.* (2015) in okra; Mehta *et al.* (2004) in brinjal and Vidhya, C. and Kumar, N. (2014) in brinjal. Mehta and Asati (2008) and Meena and Bahadur (2013) in tomato; Nimbalkar *et al.*, (2006) in Dahlia and Bhajantri and Patil (2013) in gladiolus.

Further, for crop improvement, intercrossing among accessions with outstanding mean performance was suggested by Roy and Sharma (1996); Kumar *et al.* (2013), and the reliable conformity for this can be known on the basis of cluster means. The cluster mean values revealed considerable genetic differences between the groups for all the traits under study (Table 4). Progeny lines in cluster I showed maximum performance for number of suckers per plant (4.06), while maximum leaf breadth (11.0) was recorded by cluster IV. The cluster V showed highest leaf length (33.0). The maximum number of leaves per plant (9.67) and spathe length (26.0) was recorded in cluster VI. The cluster VII recorded highest mean stem girth (28.33), flower stalk length (62.33), flower stalk girth (6.40). The yield character (number of flowers per plant- 4.67) and vase life (12.67) was observed maximum in cluster IX, which indicates that the progeny line included in this cluster could effectively be used for the crop improvement program for increasing yield. The cluster X recorded maximum number of bracts (8.33) and cluster XI recorded higher plant height (101.67). These results were in good agreement with the findings of Desh raj and Mishra (2000), Bhajantri and Patil (2013) in gladiolus, Nimbalkar *et al.* (2006) in Dahlia, Manjunath *et al.* (2009) in Anthurium and Kameswari *et al.* (2014) in chrysanthemum. In present study, progeny lines from cluster VII, VI and IX can be chosen for hybridization

programme as cluster VII recorded the high cluster mean values for three important characters followed by cluster VI and IX which showed highest cluster mean values for two characters each. Most of these were important flower attributing characters. These clusters can be preferred in selecting the genotypes for the respective traits as they recorded good means.

The genetic divergence analysis revealed presence of substantial amount of genetic variability among the progeny lines. The pattern of distribution of lines into various clusters in random showing that geographical diversity and genetic diversity are not related to each other. The choice of parents is of paramount importance in breeding programmes where crosses are to be assessed, selection based on extent of genetic divergence has been successfully utilized in different crop species by Nimbalkar *et al.* (2006) and Desh Raj and Misra (2000) in gladiolus. Heterosis is of direct relevance for developing hybrids in both cross and self-pollinated crops. It is increasingly realized that crosses between divergent parents usually produced greater heterotic effect than those between closely related ones (Patil and Apte, 2002, in gladiolus).

In nut-shell

The available diversity present in the existing germplasm indicated the possibility of selecting the right progeny line for developing cut flower varieties. The progenies included in clusters VI (P-24), VII (P-27) and IX (P-19) could effectively be used for the crop improvement program for increasing yield as most of these were important flower attributing characters. The above findings indicated that the smallest inter-cluster D² value was observed between the cluster V and VI (2.86) followed by cluster IV and X (3.54) and cluster VI and IX (3.96) indicated close relationship among the accessions included in these clusters. The lines belonging to these clusters were relatively closer to each other, in comparison to lines grouped in other clusters. This analysis would be useful to avoid selecting parents from genetically homogeneous clusters, and maintain a relatively broad genetic base for breeding.

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