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RESEARCH PAPER

Analysis of genetic diversity in gladiolus (*Gladiolus hybridus*) by multivariate analysis under sub-tropical conditions of Punjab (India)

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Abstract : The present study was under taken to analyze the genetic diversity in fifty seven genotypes of gladiolus through multivariate analysis. The genotypes were grouped into five different clusters with highest inter cluster distance reported between IV and V and lowest between II and IV. The highest intra cluster distance was observed within cluster II and lowest within cluster V. Based on cluster means, the important cluster was observed to be cluster IV for leaf breadth, number of days taken to sprouting, heading, colour bud show and opening of first floret, stem, spike and rachis diameter, equatorial and polar diameter of corm and spike length and cluster III for leaf length, number of leaves per plant and durability of floret. Hence, selection of parents from clusters III and IV could be utilized for hybridization with parents of other clusters to achieve more improvement in vigour and yield. The results of principal component analysis showed that first 3 principal component axes explained 68.77 per cent of total variation in the germplasm. The greater part of this variation was loaded from equatorial and polar diameter of corm, days taken to opening of 1st floret and colour bud show, spike and stem diameter.

Key Words : Gladiolus, Genetic diversity, Mahalanobis D^2 static, Principal component analysis

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INTRODUCTION

Gladiolus is a tender, herbaceous perennial and one of the most important bulbous cut flower crops grown for its beauty, majestic blooms or colourful florets. As a popular decorative plant, it is grown in herbaceous borders, beddings, pots and bowls. Its export to international markets in European countries can prove more remunerative especially during winter season. Gladiolus is very rich in varietal wealth and there is addition of new varieties every year (Kumar and Yadav, 2005). However, a large number of new varieties are

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mainly imported from foreign countries and the performance of these varieties depend upon climatic conditions of the region under which they are grown. As a result, cultivars which perform better in one region may not perform same in other regions of varying climatic conditions (Swaroop and Janakiram, 2010). The main emphasis in gladiolus improvement has been on the development of cut flower varieties having attractive colour with long spikes, more number of well spaced large sized florets and good corm multiplication ability. So, development of varieties with good quality traits and well adapted to the Indian conditions is much needed in the recent times. In order to formulate gladiolus crop improvement programmes, understanding about the nature and degree of genetic divergence available in the germplasm can play a pivotal in selecting suitable parents for successful hybridization programme. On the other hand, principal component analysis (PCA) identifies plant traits that characterize the distinctness among selected genotypes and is also extended to the classification of a population into groups of distinct orders, and thus guide in the choice of parents for hybridization (Chakravorty *et al.*, 2013). Therefore, present investigation was undertaken to examine the nature and magnitude of genetic divergence present in fifty seven genotypes of gladiolus.

Material and Methods

The present research study was carried out at the research farm of Punjab Agricultural University Ludhiana, India for two seasons (2012-2013 to 2013-2014). Fifty seven genotypes were used for the study. Planting of uniform sized corms with a spacing of 30 x 20 cm was done during 2nd week of October each year. The experiment was conducted under Randomized Block Design, replicated three times and pooled data of two years were analyzed as per the method suggested by (Gomez and Gomez, 1984). The observations were recorded on randomly selected plants from each plot for 14 characters namely leaf breadth, leaf length, number of leaves /plant, days taken to sprouting, days taken to heading, days taken to colour bud show, days taken to opening of first floret, durability of floret (day), spike length (cm), stem diameter (mm), spike diameter (mm), rachis diameter (mm), equatorial corm diameter (cm) and polar diameter of corm (cm). Plot means over replications were used for statistical analysis. Genetic diversity was studied using (Mahalanobis, 1936) generalized distance (D^2) extended by (Rao,1952). Trait variability analysis was performed by principal component analysis (PCA) method, with the number of principal components being chosen based on the screen test (Kovacic, 1994). Agglomerative Hierarchical cluster analysis was used to determine differences and similarities among the genotypes, and the distance measure used was Euclidean distance as the parameter that best reflects the differences existing among the genotypes (Kendall, 1980). All statistical analysis carried out was based on fourteen agro-morphological quality traits using R-software package and SAS 9.2 software SAS Institute (SAS Institute, 2011).

Results and Discussion

Based on D^2 value estimates of genetic divergence, gladiolus genotypes were grouped into five distinct clusters (Fig. 1) indicating wide range of variation for growth, flowering and corm traits present in germplasm. Cluster I and II comprised of one (1.75%) and 3 genotypes (5.27%), respectively, while as cluster III has 6 genotypes (10.53%) mainly dominated by indigenous bred cultivars. In this cluster, Punjab Glance, PG-9-2 and PG-6-16 show close similarity to each other as they are off-springs of same female parent (Happy end). Cluster IV is the biggest cluster comprised of 28 genotypes (49.12%) and is represented by both indigenous and exotic cultivars. Punjab Flame showed resemblance with its parents (Sylvia and White Prosperity) as all the three came together in same cluster. Punjab Pink Elegance and Punjab Dawn share the same cluster as they have Suchitra as common parent. Cluster V comprised of 19 genotypes (33.33%) in which Punjab Lemon Delight, PG-18-1 and PG-23-55 show some degree of similarity with each other because of having same female parentage *i.e.* Jacksonville Gold. Earlier workers (Rashmi *et al.*, 2016) also obtained five clusters in 20 genotypes of gladiolus. The data on intra and inter- cluster distance (Table 1) reflected that cluster II recorded highest intra cluster distance (46.95) followed by cluster III (30.78) while as minimum distance was observed in cluster V (0.00). This indicated that genotypes of cluster II have diverse genetic architecture. Maximum inter cluster distance (70.69) was observed between genotypes of cluster IV and V followed by II and V. The genotypes of cluster II and IV exhibited lowest inter- cluster distance (36.95), indicating resemblance among the genotypes of these groups for various growth and

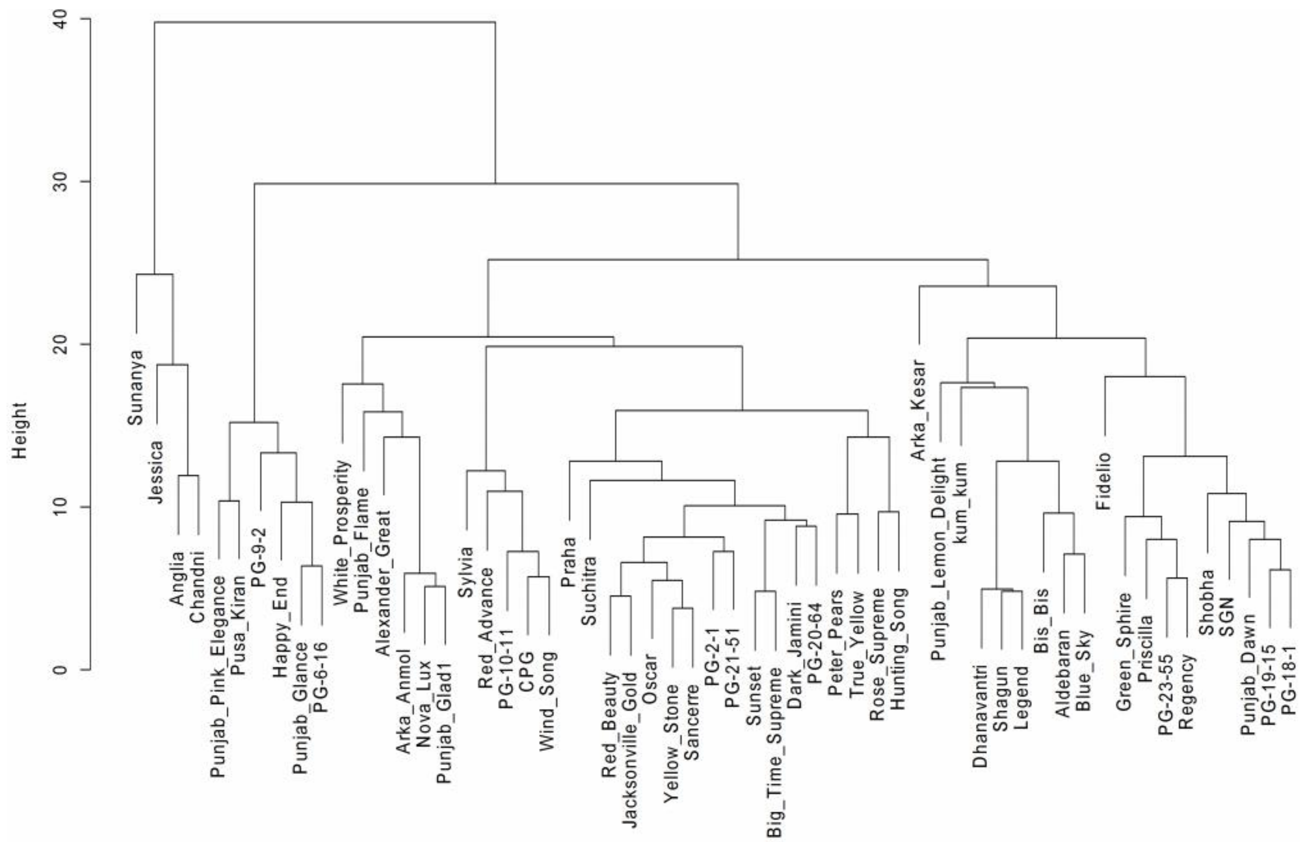

Fig. 1: Dendrogram for 57 gladiolus genotypes

flowering traits. The distribution of genotypes into different clusters showed no uniformity with respect to their origin. Thus, ruling out association between geographical distribution and genetic divergence. Therefore, selection of parents for hybridization should be done on the basis of genetic diversity and not on geographical distribution. Similar results were also reported in gladiolus (Bhajantri and Patil, 2016). Based on cluster means (Table 2), cluster IV showed higher mean values for leaf breadth, days taken to sprouting, heading, colour bud show and opening of first floret, spike length, stem diameter, spike diameter, rachis diameter, equatorial and polar diameter of corm while as cluster II showed minimum values for most of these characters. Thus, it can be interpreted that cluster IV was dominated by late flowering genotypes while cluster II by early flowering genotypes and cluster III by medium flowering genotypes. Thus it can be concluded that genotypes from cluster IV (late flowering type) for leaf breadth, spike length, stem diameter, spike diameter, rachis diameter, equatorial and polar diameter of corm and genotypes from cluster V (medium flowering type) for leaf length, number of leaves per plant and durability of floret could be selected as parents for future hybridization programme. However, based on inter-cluster distance crossing of genotypes between cluster IV and V, II and V and I and V are expected to show maximum heterosis. Crosses involving parents belonging to more divergent

Table 1: Average intra- (bold face) and Inter- cluster distance (D^2) of 57 genotypes

Sr. No.	1	2	3	4	5
1.	24.7	37.46	51.63	55.65	55.66
2.		46.95	43.82	36.95	58.72
3.			30.78	54.24	54.03
4.				23.4	70.69
5.					0.00

clusters would be expected to manifest maximum heterosis and wide variability in germplasm (Singh *et al.*, 1987). The selection of parents should also consider the special advantage of each cluster and each genotype within a cluster depending on specific objective of hybridization (Chahal and Gosal, 2002). Thus, crosses involving parents from cluster V with any other cluster are expected to exhibit high heterosis and can 'produce segregates with high yield potential.

Table 3 represents principal component analysis and percentage contribution of each component to total variation in the germplasm. The eigen values are used to

Table 2: Cluster means for 14 characters in genotypes

Character	Cluster				
	57	40,41,56	1,9,23,33,34,44	2,3,5,6,7,8,10,11,12,13,14, 15,16,17,18,19,26,27,29,30 ,31,35,37,45,49,51,52,53,	4,20,21,22,24,25,28,32,3 6,38,39,42,43,46,47,48,5 0,54,55
Leaf breadth (cm)	1.44	1.85	2.11	2.25	1.98
Leaf length (cm)	20.11	37.77	37.49	37.46	33.50
No. of leaves per plant	6.99	7.27	7.79	7.69	7.29
Days taken to sprouting	7.1	7.56	7.77	8.58	8.44
Days taken to heading	71.35	65.94	66.7	82.21	75.58
Days taken to colour bud show	85.20	84.38	82.51	100.17	94.03
Days taken to opening of 1st floret	89.66	89.06	90.61	107.58	102.31
Durability of floret (day)	1.84	2.72	4.50	4.10	3.35
Spike length (cm)	55.33	42.17	77.65	79.76	63.87
Stem diameter (mm)	13.75	10.56	11.95	14.49	12.38
Spike diameter (mm)	7.95	7.09	8.29	9.04	7.92
Rachis diameter (mm)	5.25	5.26	5.71	6.02	5.32
Equatorial diameter (cm) of corm	6.01	4.59	5.89	6.32	5.83
Polar diameter (cm) of corm	3.04	2.13	3.05	3.17	2.99

Table 3: Latent vectors for fourteen traits

Character	Eigen vectors		
	PRIN 1	PRIN 2	PRIN 3
Leaf breadth (cm)	0.250337	-0.059653	-0.317185
Leaf length (cm)	0.202038	0.053001	-0.412390
No. of leaves per plant	0.226254	-0.127991	-0.381702
Days taken to sprouting	0.098737	0.378917	0.282537
Days taken to heading	0.240849	0.396805	-0.066075
Days taken to colour bud show	0.259550	0.436888	0.086035
Days taken to opening of 1st floret	0.240007	0.450202	0.098462
Durability of floret (day)	0.250807	-0.266312	-0.128217
Spike length (cm)	0.303063	-0.036227	0.005296
Stem diameter (mm)	0.375805	-0.009805	0.131168
Spike diameter (mm)	0.382244	-0.123657	-0.055692
Rachis diameter (mm)	0.303049	-0.173860	-0.109333
Equatorial diameter (cm) of corm	0.246680	-.286544	0.477104
Polar diameter (cm) of corm	0.240443	-.287591	0.453857
Eigen values	5.16	2.98	1.50
Percentage variance	36.84	21.25	10.68
Cumulative %age variance	36.84	58.09	68.77

determine how many factors to retain and sum of these values is normally equal to number of variables. Therefore, in this analysis the first factor retains the information contained in 5.16 of the original variables and third factor retains the information contained in 1.50 of the original variables. The first, second and third principal component accounted for 36.84 per cent, 21.25 per cent and 10.68 per cent of total variation, respectively present in germplasm. The major characters that have maximum contribution towards first, second and third principal component are spike diameter (0.38), days to colour bud show (0.44) and Equatorial diameter of corm (0.48), respectively while remaining characters are contributing either very low or negatively to total variation. Therefore, in the present study, differentiation of the genotypes into different clusters was because of relatively high contribution of few characters rather than small contribution from each character. Similar results were also obtained by earlier in gladiolus (Patra and Mohanty, 2015). The genotypes in the PC1 were more likely to be associated by spike length, rachis diameter, spike diameter, stem diameter, spike length, equatorial and polar diameter of corm, leaf breadth, days taken to heading, days taken to colour bud show, days taken to opening of 1st floret and durability of floret whereas the genotypes in PC2 are associated by days to sprouting, heading, colour bud show and opening of 1st floret (Fig. 2) due to high positive loading of these characters towards their respective components. The traits which contributed more positively towards PC3 were equatorial and polar diameter of corm (Fig. 3). In the component pattern diagram (Fig. 2 and 3) correlation between variables and the principal component depicted that days taken to sprouting, heading, colour bud show and opening of 1st

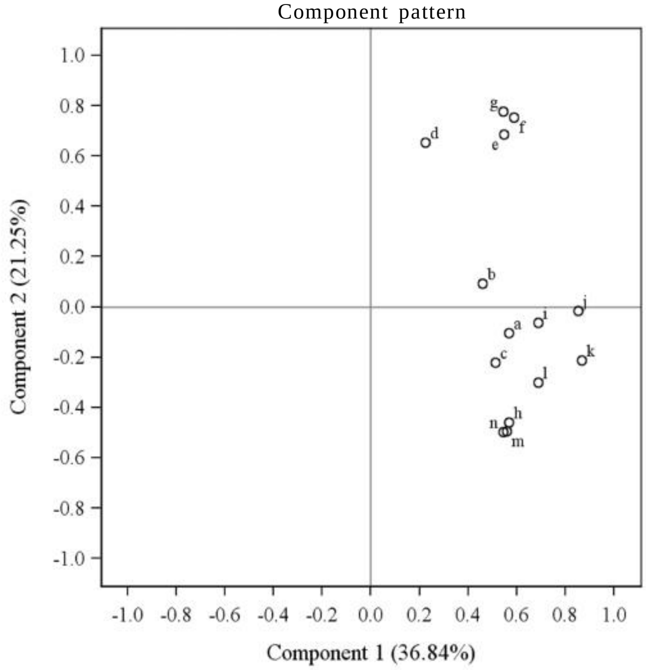

Fig. 2: Relationship among 14 morphological characters in gladiolus germplasm by 2D scatter for first two principal components

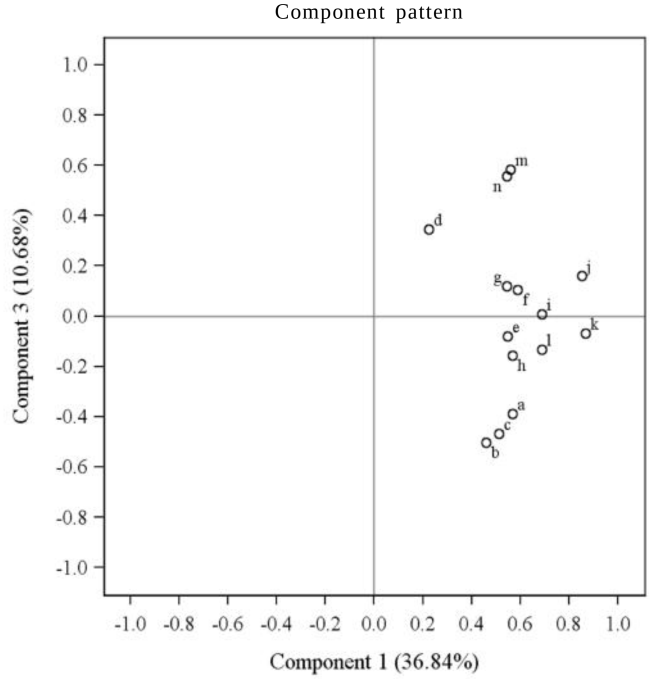

Fig. 3: Relationship among 14 morphological characters in gladiolus germplasm by 2D scatter for first and third principal components

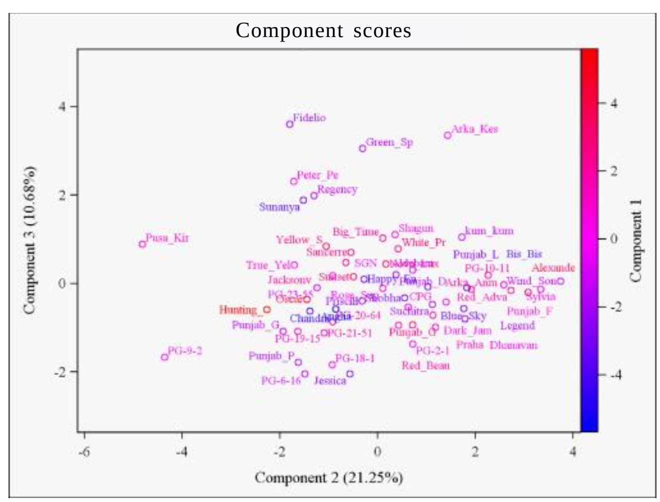

Fig. 4: Relationships among 57 gladiolus genotypes shown by a 2D scatter for first three principal components based on morphological characters

floret and leaf length are non-significantly correlated. However, stem diameter, spike length, leaf breadth, number of leaves per plant, spike diameter and rachis diameter are strongly negatively correlated. The coordination of the genotypes on all axes together (Fig. 4) revealed that PG-23-55, PG-6-16, Jacksonville Gold, Arka Kesar and Kum Kum were found to be most distinct genotypes. Usually it is customary to choose one variable from these identified groups. Hence, spike diameter for the first, days to colour bud show for the second and equatorial diameter of corm for the third group are best choices as these characters contributed positively to first three principal components and could be given due consideration while selecting the best genotypes without losing yield potential.

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