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Multivariate Analysis of Genetic Diversity in Chrysanthemum Germplasm

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ABSTRACT

Sustainable production of crops relies on germplasm improvement and genetic diversity. The use of multivariate techniques is an important strategy for germplasm classification and study of genetic relationships among genotypes. The data collected for 97 genotypes of chrysanthemum germplasm from All India Coordinated Research Project on Floriculture report 2016-17 (AICRP report 2016-17) were evaluated for eight quantitative traits through cluster and principal component analysis. The first three PCs with eigen values >1 contributed 83.01% of the variability amongst genotypes. The characters contributing more positively with PC1 were no of flower per plant, no of branches and flowering duration. The cluster analysis sequestrated 97 genotypes into 4 clusters based on between-group linkage method in which euclidean distance has been used as dissimilarity measure. The cluster III and IV were more clearly separated than cluster I and II. The cluster analysis revealed that considerable variation existed in few genotypes that could be implicated in selection of chrysanthemum for the development or improvement of cultivars and germplasm.

Key words: *Genetic Diversity, Chrysanthemum germplasm, Cluster analysis and Principal component analysis*

INTRODUCTION

Chrysanthemums are flowering plants of the genus Chrysanthemum in the family *Asteraceae*, sometimes known as mums or chrysanths. In the 15th century BC Chrysanthemums were first cultivated in China as a flowering herb. In this genus, most of cultivars and hybrids are developed for horticultural purposes. The flowers heads occurs in various forms like daisy, pompons or buttons. The modern cultivated chrysanths are elegantly showier than their wild relatives. The chrysanthemum flowers are used for culinary purposes. The flowers are pulverized, and the active components, called *pyrethrins*. Pyrethrins attack the nervous systems of all insects, and inhibit female mosquitoes from biting. In sub-lethal doses, they have an insect-repellent effect. The presence of genetic diversity is being considered as the first step towards crop improvement programmes in direction of developing high yielding, economically and ecologically sustainable varieties and hybrids. The enormous amount of variability among chrysanthemum cultivars is because of its wide genetic base.

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The extent of heritable characters and their direct/indirect inter-relationships among them shifts the interest of researchers to plan manipulations in the direction of achieving better quantity of production as well as quality production.

The key to reliable and sustainable improvement in production conjointly with the quality is germplasm improvement and genetic diversity. In the classification of germplasm and analysis of genetic relationships among breeding material, the important strategy is multivariate statistical algorithms[8]. Cluster and principal component analysis based on morpho-physiological data, yield and quality, stability of performance, heterosis, and combining abilities, used as a tool in assessment of tomato cultivars and hybrids[3]. More wider the base of genetic diversity of populations, more is the success of any breeding method. Wheat germplasm comprising of 50 genotypes were evaluated for seven quantitative traits through cluster and principal component analyses. The cluster analysis sequestrated 50 genotypes into 5 clusters based on Ward's method. The cluster analysis revealed that considerable variation existed among genotypes that could be implicated in selection of wheat for the development or improvement of cultivars and germplasm. The parental types which could result into superior hybrids can be selected on the basis of Hierarchical cluster analysis. The Hierarchical Cluster analyis groups the entries of germplasm on the basis of their degrees of similarity and dissimilarity among them. The inter crossing among gladiolus genotypes included in diverse clusters is likely to produce potential hybrid which could be maintained and multiplied through asexual reproduction[10]. Clustering was used to study the genetic diversity and identification of cultivars of chrysanthemum genotypes on the basis of morphological characters[11].

Principal component analysis (PCA) is to evaluate the magnitude of genetic diversity among the crop germplasm and to reduce a large number of observed traits into a smaller set of traits that have the maximum contribution in separating the maize genotypes[4]. The principal component analysis reveals the high level of genetic variation and the traits contributing for the variation. Therefore the population panel can be utilized for trait improvement in breeding programs for the traits contributing for major variation[9].

Present study was conducted to decipher the extent of genetic variation and relationships among chrysanthemum genotypes based on quantitative traits using multivariate analysis and to identify the set of morpho-agronomic attributes which could be further utilized in breeding programs.

MATERIAL AND METHODS

The material for the present investigations consisted of 97 existing germplasm collection at Hyderabad centre. Data regarding 8 quantitative traits viz., Plant height (cm), No. of branches, Bud appearance, Diameter of floret (cms), No. of flowers/ plant, Average flower wt.(g), Wt. of flowers (g), Vase life (Days) and Flowering duration (Days) collected from All India Coordinated Research Project on Floriculture report 2016-17.

Hierarchical Clustering technique begins by either a series of successive mergers or of successive divisions. Consider a natural process of grouping

• Each unit is an entity to start with

• Merge those two units first which are most similar (least dij) – now becomes an entity

• Examine mutual distance between (n-1) entities

• Merge those two that are most similar

• Repeat the process and go on merging till all are merged to form one entity

• At each stage of agglomerative process, note the distance between the two merging entities

• Choose that stage which shows sudden jump in this distance (Since it indicates that two very dissimilar entities are being merged). This could be subjective.

A number of different rules or methods have been suggested for computing distance between two clusters. In fact, the various

hierarchical clustering algorithms or methods differ mainly

With respect to how the distance between the two clusters are computed. Here we used between-group linkage method (Average linkage) – This works on the principle of average distance. (Average of distances between unit of one entity and the other unit of the second entity and euclidean distance has been used as dissimilarity measure.

Principal component analysis simplifies the complex data by transforming number of correlated variables into a smaller number of variables called principal components. The first principal component accounts for maximum variability in the data as compared to each succeeding component. Scatter diagram was plotted to show the variation pattern. Mean value of each variable were standardized prior to cluster and principal component analysis to avoid the effects due to difference in scale.

RESULTS AND DISCUSSION

Cluster analysis sequestrated 97 genotypes of Chrysanthemum into 4 clusters (Fig. 1). Members of each cluster are presented in Table 1. Cluster I consisted of 75 genotypes, cluster II of 10 genotypes, cluster III of 9 genotypes,and cluster IV of 3 genotypes. Though cluster analysis grouped genotypes together with greater morphological similarity, the clusters did not necessarily include all genotypes from same origin. Zubair *et al.*[12], Ahmad *et al*.[1], and Ali *et al*.[2], also reported lack of association between morphoagronomic traits and origin. The mutual relationship between these clusters is represented diagrammatically by taking average intra and inter- cluster Euclidean^2 distances. The cluster III and IV were more clearly separated than cluster I and II. The cluster analysis revealed that considerable variation existed in few genotypes that could be implicated in selection of chrysanthemum for the development or improvement of cultivars and germplasm.

Principal component analysis simplifies the complex data by transforming the number of correlated variables into a smaller number of variables called principal components. The first principal component accounts for maximum variability in the data with respect to succeeding components[7]. The analysis had grouped the estimated wheat variables into three main components. The first three PCs with eigen values >1 contributed 83.01% of the variability amongst genotypes (Table 2). The Table 3 reveals that the characters contributing more positively with PC1 were no of flower per plant, no of branches and flowering duration. The scree plot (figure 2) displays the number of the principal component versus its corresponding eigenvalue. The scree plot orders the eigenvalues from largest to smallest. The eigen values of the correlation matrix equal the variances of the principal components.

A matrix of simple correlation coefficients between the selected traits were computed and presented in Table 4. Results revealed that no of flower per plant have positive association with weight of the flower and days of flowering.

Table 1: Cluster Membership

Cluster no	Genotypes
Cluster 1	Ace, Agnipath, Anjali, Anmol, Apurva singer,Arka ravi**,** Asha, Basanthi, Bc-47-101, Beauty, C.chirstal, Chandrika, Cloverlea star,Co-1, Co3, Coffee,Cucubion, D, Dolly orange, Dolly pink ,Farr, Filtration, Freedom, Garden beauty, Geetanjali, Harvest house, IIHR-13, Julie, Kalyani mauye, Kotai no koari, Lalima, Lohagreen, M1o, Meera, Modella, Moharaj, Mr.whitney, Neelim, Pankaj, Paragoan yellow, PAU-a-43, PAU-a-64, PAU-b-107,PAU-b-43,PAU-D-1, Plants & seeds, ice, Poonam, Poornima, Preet singer, Punjab Anuradha, Punjab gold, Pusa cenetary, Raja, Rajahmundry, Rajat, Rathalam selection, Ravi kiran, Reagon Emperor, Red gold, Red queen, Red stone, Rose day, Royal purple, Rupanjali, Sabita, Salora, Seedling red, Shintome, Shova, Silper (white), Sizuka, Skaters valtz, Skater's waltz, Snow ball, Snow sem, Sony, Star pink, Statesmen, Sukai sport, Swapna, Terry, UHFS-77, Vasantika, White, Winter queen, Yellow bonsai, Yellow gold, Yokari
Cluster 2	Agnishika, Garden beauty, Mother Theresa, PAU-a-43, PAU-b-107, PAU-b-43, PAU-D-1, Rekha, Swapna, White
Cluster 3	Akitha, Aparajitha, Autumn joy, Bc-32-20, Bc-6-11, Rathalam selection, Rupanjali, Shintome, Snow sem
Cluster 4	B.mallika, Reagon Emperor, Winter queen

Table 2: Principal Component Analysis (PCA)- Total variation explained

Component	Initial Eigen values			Extraction Sums of Squared Loadings		
	Total	% of Variance	Cumulative %	Total	% of Variance	Cumulative %
1	3.402	42.523	42.523	3.402	42.523	42.523
2	2.213	27.660	70.183	2.213	27.660	70.183
3	1.026	12.829	83.012	1.026	12.829	83.012
4	.661	8.257	91.270			
5	.341	4.263	95.532			
6	.187	2.342	97.875			
7	.109	1.368	99.243			
8	.061	.757	100.000			
Extraction Method: Principal Component Analysis.						

Table 3: PCA Component Matrix

	Component		
	1	**2**	**3**
Plant height (cm)	.160	.655	-.263
No. of branches	.863	.005	-.088
Bud appearance	.122	.001	.964
Diameter of floret (cms)	-.481	.794	.079
No. of flowers per plant	.956	.123	.030
Average flower weight g)	-.315	.879	.105
Wt. of flowers (g)	.710	.604	.021
Flowering duration-Days	.931	.003	.030
Extraction Method: Principal Component Analysis.			
3 components were extracted.			

Table 4: A matrix of correlation coefficients (r) for the estimated variables

	Plant height	**No.of branches**	**Bud appearance**	**Diameter of floret**	**No.of flowers/ plant**	**Av. flower wt.**	**Wt. of flowers**	**Fl. duration**
Plant height	1							
No.of branches	0.143	1.000						
Bud appearance	-0.075	0.036	1					
Diameter of floret	0.330 **	-0.359 **	-0.010	1.000				
No.of flowers/plant	0.159	0.792 **	0.120	-0.338 **	1			
Av. flower wt.	0.336 **	-0.254	0.011	0.826 **	-0.179	1		
Wt. of flowers	0.357 **	0.532 **	0.055	0.109	0.769 **	0.356 **	1.000	
Fl. Duration	0.138	0.705 **	0.129	-0.420 **	0.866 **	-0.297 **	0.658 **	1

**Significant at 1% level of probability

Figure 1: Dendrogram of Chrysanthemum genotypes

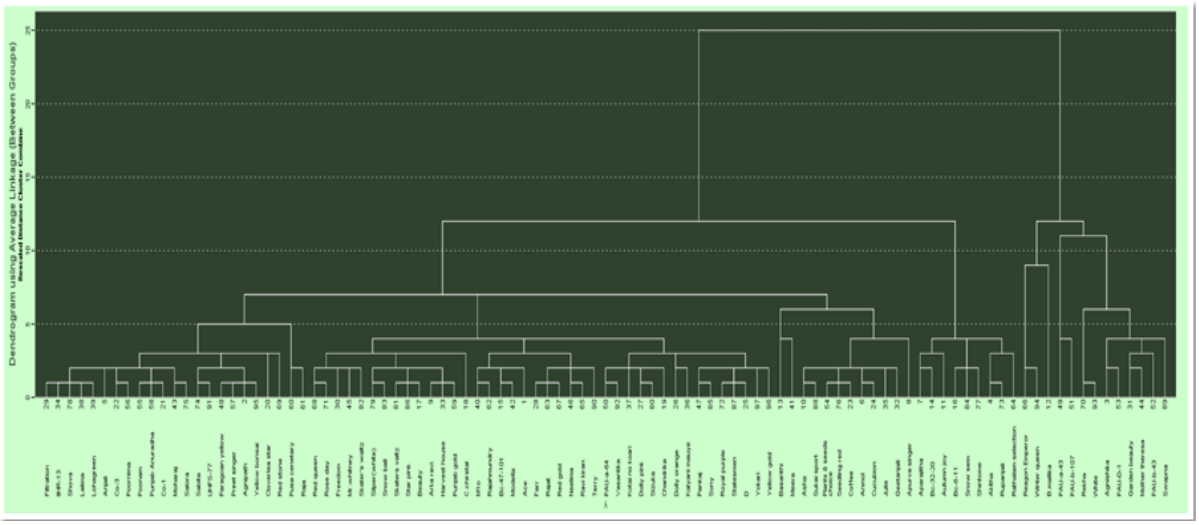
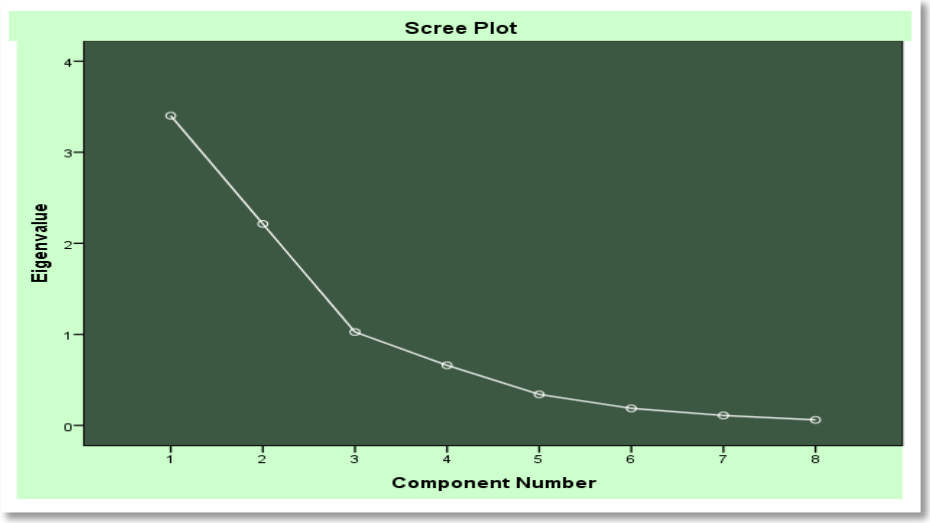


Figure 2: Scree plot



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