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*Original Research Paper*

# Genetic divergence in Chrysanthemum (*Dendranthema* x *grandiflora* Tzvelev) based on morphological traits

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## ABSTRACT

Genetic diversity of thirty-one genotypes of Chrysanthemum were analysed for various growth and flowering related traits. Analysis of variance revealed significant differences among the genotypes for all the morphological traits studied. The clustering pattern based on Mahalanobis $D^2$ statistics categorised genotypes into six distinct clusters. The largest cluster *i.e.* cluster III composed of eleven genotypes followed by cluster II with nine genotypes, cluster I having eight genotypes and cluster IV, V, and VI with one genotype each. The maximum inter-cluster distance was recorded between clusters IV and cluster V (376.87) followed by clusters IV and cluster VI (344.96) and, cluster II and cluster IV (196.81). The maximum intra-cluster distance was observed for cluster III (56.57), followed by cluster II (46.87) and cluster I (29.52). Among all the clusters, genotypes in cluster II recorded highest cluster mean values for number of branches per plant (7.15), number of leaves (119.72) and flowers (91.69) per plant. Among nine characters, number of flowers per plant contributed maximum to divergence (32.26%). Therefore, for chrysanthemum improvement, highly diverse genotypes can be used as parents for crossing to generate high variability.

**Keywords:** Chrysanthemum, genetic diversity, Mahalanobis $D^2$ statistics, morphological traits

## INTRODUCTION

Chrysanthemum is a high-profit floricultural crop belonging to the family Asteraceae and ranked second to rose in market trade (Nguyen et al., 2020), mainly grown for cut flower, loose, pot plant and landscaping. There are approximately 200 species in the genus Chrysanthemum, but most of them are sub-divided into 38 satellite genera of the chrysanthemum complex (Dalda-Sekerci, 2023). More recently, only 41 species have been attributed to the genus Chrysanthemum (Hadizadeh et al., 2022). The cultivated chrysanthemum is originally native of Asia (China and Japan) and northeastern Europe (Baliyan et al., 2014).

Morphological trait measurement is a commonly used index, since it provides a simple technique of quantifying genetic variation, while, simultaneously assessing genotype performance under normal growing environments (Fu et al., 2008). The hybridization of florist chrysanthemum began after 1850 when the practice of culturing chrysanthemum in greenhouses began. Several hundred cultivars have been commercialized, indicating that there are substantial genetic variations that can be manipulated under cultivations to produce a wide array of phenotypic variation (Jo et al., 2015).

Germplasm collection and evaluation have received a lot of attention in India. However, the information for higher flower yield and yield contributing characters is limited. In order to choose diverse parents to complement various breeding programmes, it is necessary to estimate the genetic variation and method of inheritance of various plant traits in chrysanthemum.

In chrysanthemum, the investigation, classification, identification, and diversity analysis of the cultivars became highly challenging due to the large number of cultivars, abundant morphological variation, wide distribution and complex genetic background. Therefore, the present study was carried out to select suitable genotypes for breeding programmes based on the genetic diversity estimation conducted on a group of chrysanthemum genotypes obtained from various locations in India.

**Table 1 : List of thirty-one chrysanthemum genotypes used for diversity study**

| Genotype | Source | Flower form | Growth habit |
|---|---|---|---|
| A1 Collection | Dooblabylekere, Bengaluru | Semi-double | Semi-erect |
| Appu | CSIR-NBRI, Lucknow | Semi-double | Erect |
| Arka Chandrakant | ICAR-IIHR, Bengaluru | Decorative | Spreading |
| Arka Chankdrika | ICAR-IIHR, Bengaluru | Decorative | Erect |
| Arka Kirti | ICAR-IIHR, Bengaluru | Double Korean | Erect |
| Arka Pink Star | ICAR-IIHR, Bengaluru | Semi-double | Spreading |
| Arka Usha Kiran | ICAR-IIHR, Bengaluru | Semi- double | Erect |
| Arka Yellow Gold | ICAR-IIHR, Bengaluru | Decorative | Erect |
| Autumn Joy | PAU, Ludhiana | Decorative | Spreading |
| Coffee | CSIR-NBRI, Lucknow | Semi- double | Spreading |
| Fitonia | CSIR-NBRI, Lucknow | Single | Semi-erect |
| Flirt | CSIR-NBRI, Lucknow | Decorative | Erect |
| Garden Beauty | PAU, Ludhiana | Spoon | Spreading |
| Gulmohar | CSIR-NBRI, Lucknow | Double Korean | Erect |
| Heritage | CSIR-NBRI, Lucknow | Semi-double | Semi-erect |
| Jubilee | CSIR-NBRI, Lucknow | Semi-double | Erect |
| Marigold | Local Collection | Pompon | Erect |
| Mayur | CSIR-NBRI, Lucknow | Semi-double | Erect |
| NBRI Little Kusum | CRIS-NBRI, Lucknow | Pompon | Spreading |
| Pachai Local | Local Collection | Semi-double | Spreading |
| Pink Cloud | CSIR-NBRI, Lucknow | Semi- double | Erect |
| Ratlam Selection | CSIR-NBRI, Lucknow | Decorative | Erect |
| Rekha | CSIR-NBRI, Lucknow | Single | Spreading |
| Shukla | CSIR-NBRI, Lucknow | Semi-double | Semi-erect |
| Statesman | PAU, Ludhiana | Semi-double | Erect |
| Sunil | CSIR-NBRI, Lucknow | Spoon | Erect |
| Vasanthika | CSIR-NBRI, Lucknow | Single | Semi-erect |
| White Dolley | CSIR-NBRI, Lucknow | Pompon | Spreading |
| White Local | Local Collection | Semi-double | Erect |
| White Prolific | CSIR-NBRI, Lucknow | Semi-double | Erect |
| Winter Queen | PAU, Ludhiana | Spoon | Spreading |

## MATERIALS AND METHODS

### Plant material

The present study was carried out in the Division of Flower and Medicinal Crops, ICAR-Indian Institute of Horticultural Research, Bengaluru, during 2019-20 and 2020-21. The experimental site was geographically located at 13°58' N Latitude, 78°E Longitude and at an elevation of 890 meter above mean sea level. In total, thirty-one chrysanthemum genotypes obtained from different locations of India (Table 1) were evaluated for various growth and flowering traits under naturally ventilated polyhouse in completely randomized design with three replications.

The plants of all genotypes were raised through terminal cuttings taken from healthy stock plants. After transplanting, plants were imposed with photoperiod of 15/9 hours for 30 days and 'black in' (dark conditions) until flower bud initiation. Uniform package of practices was followed throughout the experiment to ensure good growth. Five uniformly

**Table 2 : Combined analysis of variance of nine characters for 31 genotypes of chrysanthemum**

| Source of variation | df | Plant height (cm) | No. of branches plant$^{-1}$ | No. of leaves plant$^{-1}$ | Days to bud initiation | Days to first flower opening | Days to optimum flowering | Flower diameter (cm) | No. of flowers plant$^{-1}$ | Flowering duration (days) |
|---|---|---|---|---|---|---|---|---|---|---|
| Treatment | 30 | 8,230.95 ** | 58.67 ** | 13,872.46 ** | 471.52 ** | 3,867.80 ** | 3,852.28 ** | 22.18 ** | 9,507.31 ** | 902.86 ** |
| Error | 62 | 0.25 | 12.81 | 10.19 | 1.00 | 4.74 | 6.02 | 4.22 | 0.08 | 5.29 |

grown plants per replication were tagged for recording observations of various growth and flowering traits, *viz*., plant height (cm), number of branches and leaves per plant, days to bud initiation and first flower opening, number of flowers per plant, optimum flowering (the number of days taken to 50% flowering from the date of 'black in' treatment), flower diameter (cm) and flowering duration (days) to check superiority of genotypes. The data recorded for both the years were pooled and analyzed statistically.

### Quantitative traits data analysis

The mean values of the genotypes in each replication for quantitative characters were used for statistical analysis. The data were processed with the help of the software programme SPAR-1 (Doshi & Gupta, 1991) utilizing various standard statistical procedures. The data recorded on nine different quantitative traits were subjected to the $D^2$statistic of Mahalanobis, and grouping of the genotypes into different clusters was done by using Ward's minimum variance (Rao, 1952) and average intra-and-inter cluster distances were calculated following Tocher's method.

## RESULTS AND DISCUSSION

Analysis of variance indicated highly significant differences among the genotypes for all the characters studied indicating the presence of sufficient amount of variability (Table 2).

### Cluster constellation

Thirty-one genotypes were classified into six clusters on the basis of $D^2$ values calculated from the analysis of nine morphological traits (Fig. 1). Among all the clusters, cluster III being the largest consisted of eleven genotypes, followed by cluster II with nine genotypes, cluster I having eight genotypes and cluster IV, V, and VI with one genotype each (Table 4). The variable number of accessions in different clusters pointed toward the presence of wide range of genetic diversity within as well as between the clusters. Similarly, Bhargav et al. (2023) recorded two clusters in China aster, while, Baliyan et al. (2014) reported four clusters in chrysanthemum, and Kavitha & Anburani (2009) recorded eight clusters in African marigold.

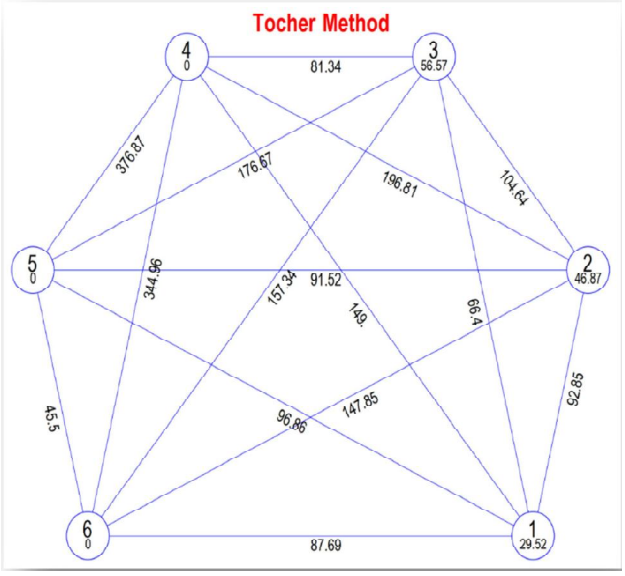


Fig. 1 : Inter and intra cluster distances for thirty-one genotypes in chrysanthemum

The group constellation of thirty-one chrysanthemum genotypes was also plotted in the form of a dendrogram (Fig. 2), where, Euclidian distances in dendrogram highlighted the genetic divergence between and within the clusters. The pattern of distribution of genotypes from various eco-geographical regions into various clusters with different divergence values was random, supporting that genetic diversity and geographical diversity are unrelated. Natural or artificial selection, breeding material exchange, genetic drift, and environmental variation may be the primary factors influencing this genetic diversity in addition to geographic origin. The results of present study are substantiated with the similar conclusions reported on diversity (Kumar et al., 2011; Baliyan et al., 2014) indicated that geographic diversity cannot always be used as an index of genetic diversity. It is quite

possible that many of the genotypes obtained from different geographical regions could share a common ancestor. Moreover, progenies obtained through breeding incorporate genes from varied sources, thus losing the basic geographical identity of the genotype (Bharathi & Jawaharlal, 2014).

Average inter as well as intra-cluster distances in all the genotypes were computed through Mahalanobis ($D^2$) analysis (Table 3). On the basis of $D^2$ values between two genotypes or two clusters, choice of divergent parents can be made for hybridization purpose. The inter-cluster distance ranged from

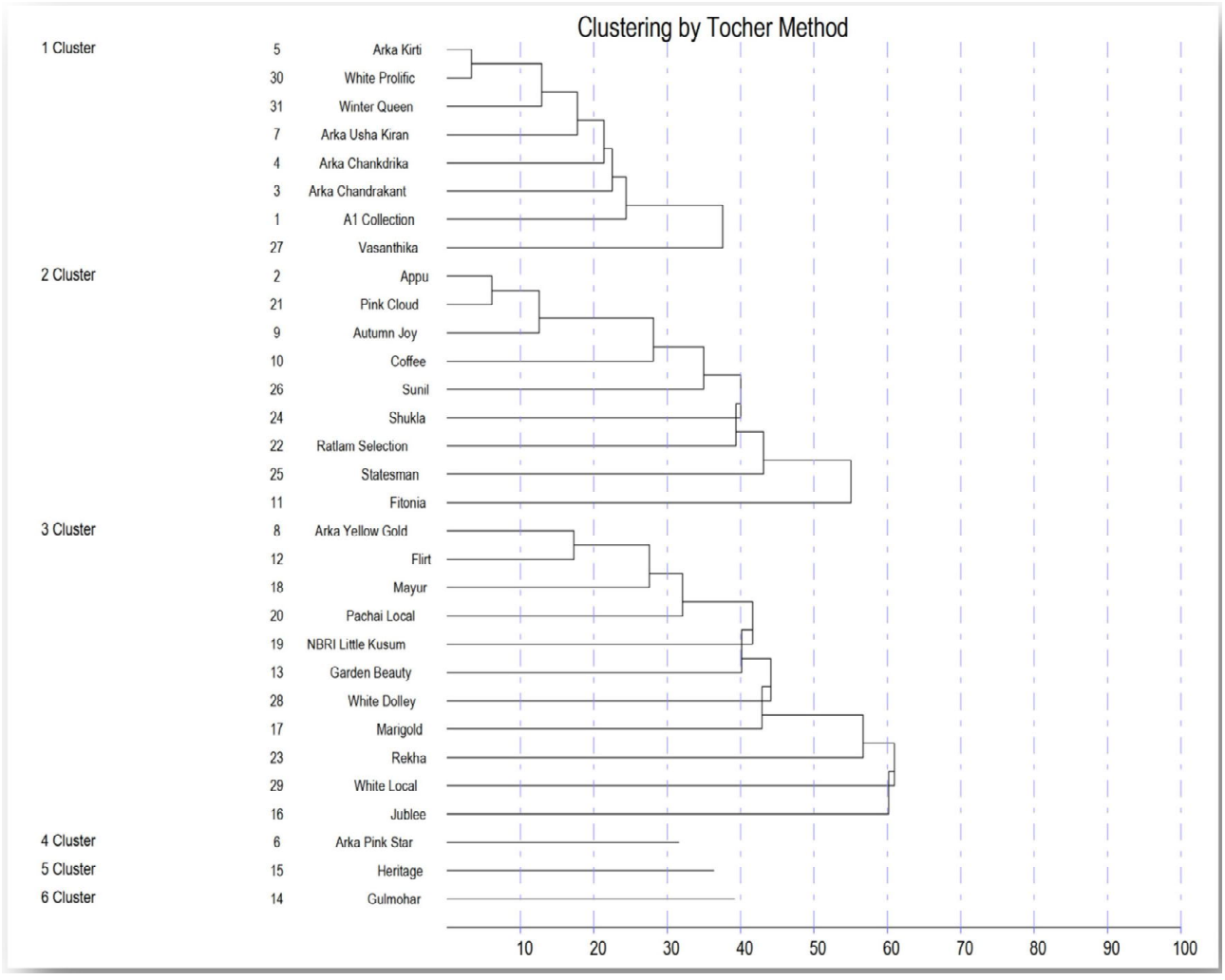


Fig. 2 : Dendrogram showing Euclidean distances based on nine quantitative traits of thirty-one chrysanthemum genotypes

**Table 3 : Average intra and inter-cluster distances computed through $D^2$ analysis**

| Clusters | Cluster distances | | | | | |
|---|---|---|---|---|---|---|
| | I | II | III | IV | V | VI |
| I | **29.52** | - | - | - | - | - |
| II | 92.85 | **46.87** | - | - | - | - |
| III | 66.40 | 104.64 | **56.57** | | - | - |
| IV | 149.00 | 196.81 | 81.34 | **0.00** | - | - |
| V | 96.86 | 91.52 | 176.67 | 376.87 | **0.00** | - |
| VI | 87.69 | 147.85 | 157.34 | 344.96 | 45.50 | **0.00** |

45.5 (cluster V and VI) to 376.87 (cluster IV and V). The maximum (376.87) inter-cluster distance was recorded between clusters IV (Arka Pink Star) and cluster V (Heritage) followed by clusters IV (Arka Pink Star) and cluster VI (Gulmohar) (344.96) and, cluster II (Appu, Pink Cloud, Autumn Joy, Coffee, Sunil, Shukla, Ratlam Selection, Statesman and Fitonia) and cluster IV (Arka Pink Star) (196.81). This clearly indicated that the genotypes present in these clusters contain a wide range of genetic diversity which could be exploited through hybridization program to get better recombinants in the segregating generations. The results suggested that cross combination of genotypes from most divergent clusters IV and V, and IV and IV, respectively would be more vigorous when used as parent in hybridization programme for obtaining wide spectrum of variation among the segregates.

The least intercluster distance was observed between clusters V (Heritage) and cluster VI (Gulmohar) followed by cluster I (Arka Kirti, White Prolific, Winter Queen, Arka Usha Kiran, Arka Chankdrika, Arka Chandrakant, A1 Collection and Vasanthika) and cluster II (Appu, Pink Cloud, Autumn Joy, Coffee, Sunil, Shukla, Ratlam Selection, Statesman and Fitonia). The less inter-cluster distances indicated lower degree of divergence and close genetic makeup of these genotypes (Kaur et al., 2021), making them less suited for use in a hybridization programme between the genotypes in the cluster.

In the present investigation, cluster III (56.57) showed the highest intra-cluster distance followed by cluster II (46.87) and cluster I (29.52). Genotypes belonging to cluster III had the maximum heterogeneity among the assembled genotypes that is also clear from the assembling pattern of the genotypes in the dendrogram (Fig. 2 and Table 4). It means that the genotypes in this cluster were highly diverse for the traits under study. However, null intra cluster distances were recorded in cluster IV, V and VI because of the inclusion of single genotype in each. The lower intra-cluster distances indicated homogenous nature of genotypes within the clusters, while, higher values displayed heterogeneous nature of clusters (Kaur et al., 2021). Lower level of intra- cluster distances explained narrow genetic variation within the cluster. Therefore, the members of same cluster are not expected to yield desirable recombinants. These results for genetic variation within and between the clusters are substantiated with the previous reports (Kavitha & Anburani, 2009; Baliyan et al., 2014). The genetic diversity observed within and between the clusters can be utilized in selection of genetically diverse genotypes which is important for exploitation of heterosis and development of desirable recombinants (Panwar et al., 2014).

***Cluster-wise performance***

The considerable morphological diversity of different clusters could also be explained from the average performance of the genotypes for nine morphological traits (Table 5).

Among all the clusters, genotypes in cluster II had highest cluster mean values for number of branches per plant (7.15), number of leaves per plant (119.72), and number of flowers per plant (91.69). The high yield potential in chrysanthemum is associated with

**Table 4 : Distribution of chrysanthemum genotypes in different clusters through $D^2$ analysis based on quantitative traits**

| Clusters | Number of Genotype(s) | Genotype(s) |
|---|---|---|
| I | 8 | Arka Kirti, White Prolific, Winter Queen, Arka Usha Kiran, Arka Chankdrika, Arka Chandrakant, A1 Collection and Vasanthika |
| II | 9 | Appu, Pink Cloud, Autumn Joy, Coffee, Sunil, Shukla, Ratlam Selection, Statesman and Fitonia |
| III | 11 | Arka Yellow Gold, Flirt, Mayur, Pachai Local, NBRI Little Kusum, Garden Beauty, White Dolley, Marigold, Rekha, White Local and Jublee |
| IV | 1 | Arka Pink Star |
| V | 1 | Heritage |
| VI | 1 | Gulmohar |

**Table 5 : Cluster means for nine quantitative traits in thirty-one chrysanthemum genotypes**

| Clusters | Plant height (cm) | Branches per plant (Nos.) | Leaves per plant (Nos.) | Days to flower initiation | Days to first flower opening | Days to optimum flowering | Flowers per plant (Nos.) | Flower diameter (cm) | Flowering duration (days) |
|---|---|---|---|---|---|---|---|---|---|
| I | 58.02 | 4.35 | 85.54 | 23.61 | 60.55 | 78.29 | 50.11 | 5.65 | 43.75 |
| II | 65.74 | 7.15 | 119.72 | 20.61 | 63.82 | 79.74 | 91.69 | 5.87 | 47.17 |
| III | 50.31 | 7.14 | 93.47 | 19.15 | 52.93 | 69.59 | 54.56 | 4.73 | 41.91 |
| IV | 26.92 | 7.00 | 110.33 | 11.16 | 31.00 | 51.33 | 56.67 | 3.93 | 37.33 |
| V | 92.50 | 5.83 | 101.67 | 28.84 | 88.33 | 104.50 | 67.83 | 5.70 | 47.50 |
| VI | 103.27 | 6.33 | 69.50 | 27.83 | 80.83 | 97.83 | 31.67 | 6.03 | 57.00 |

the number of branches per plant, number of leaves and flowers per plant. However, cluster IV recorded least plant height (26.92), days to flower initiation (11.16), days to first flower opening (31.00), days to optimum flowering (51.33), flower diameter (3.93) and flowering duration (37.33). The clustering pattern could be used to select parents for cross combinations that are expected to generate the highest possible variability for various economic characters. Similar type of observations for morphological variability in chrysanthemum has been reported (Kameswari et al., 2014; Kumar et al., 2016).

In the present study, higher mean for plant height was recorded in cluster VI followed by cluster V, while, number of branches per plant was recorded maximum in cluster II, followed by cluster III. The maximum number of leaves per plant was recorded in cluster II, followed by IV.

Minimum days to flower initiation, first flower opening and optimum flowering was in cluster IV, followed by cluster III. Maximum flower diameter and flowering duration was recorded in cluster VI, followed by cluster II and cluster V, respectively, while, maximum number of flowers per plant was recorded in cluster II, followed by cluster V.

Highly varied genotypes from these clusters may be exploited in a hybridization programme to develop highly desired recombinants for the improvement of yield. Among various groups, the genotype belonging to cluster VI (Gulmohar) and cluster V (Heritage) can be used to develop variety suitable for cut flower purpose. The genotypes were more distinct between cluster IV and III, therefore, hybridization of Arka Pink Star from cluster IV and Arka Yellow Gold, Flirt, Mayur, Pachai Local, NBRI Little Kusum, Garden Beauty, White Dolley, Marigold, Rekha, White Local and Jublee from cluster III may result in earliness to flowering. Similarly, the high yielding genotypes of cluster II can also be utilized in breeding programmes. Additionally, the precise selections for specific characteristics may help in the development of trait-specific high-yielding inbreds. To generate a wide range of variability or segregation for the target traits, the parents for hybridization should be selected from clusters expressing moderate to high $D^2$ values (Kaur et al., 2021).

**Trait-wise contribution to diversity**

The relative contribution of individual characters towards genetic divergence has been computed (Table 6) and revealed that among all the characters,

**Table 6 : Contribution (%) of the traits towards genetic divergence in chrysanthemum genotypes**

| Source | Contribution (%) | Times ranked 1st |
|---|---|---|
| Plant height (cm) | 11.40 | 53 |
| Number of branches per plant | 15.91 | 74 |
| Number of leaves per plant | 10.32 | 48 |
| Days to flower initiation | 2.80 | 13 |
| Days to first flower opening | 13.98 | 65 |
| Days to optimum flowering | 0.43 | 2 |
| Number of flowers per plant | 32.26 | 150 |
| Flower diameter (cm) | 10.11 | 47 |
| Flower duration (days) | 2.80 | 13 |

number of flowers per plant contributed maximum to divergence (32.26%), followed by number of branches per plant (15.91%), days to first flower opening (13.98%) and plant height (11.40%). These characters can be given more emphasis during selection of at least one parent for hybridization program.

Number of leaves per plant, flower diameter, flower duration and days to optimum flowering showed contribution of 10.32%, 10.11%, 2.80% and 0.43%, respectively. The importance of morphological traits in genetic diversity has been substantiated with the findings of Kameswari et al. (2014) and Kumar et al. (2016).

## CONCLUSION

Genetic divergence has been considered as an important factor in selecting genetically diverse parents for efficient and successful hybridization programme. Clustering pattern based on Mahalanobis $D^2$ statistic revealed that diverse geographic origins of the genotypes could not necessarily be an index of variation and the factors such as genetic drift, selection pressure and environment may be responsible for discrepancy of genotypes. Among nine characters, number of flowers per plant contributed maximum to divergence. Therefore, for chrysanthemum improvement, the clustering pattern could be used to select parents for cross combinations that are expected to generate the highest possible variability.

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