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Short Communication

Classificatory analysis for genetic diversity in dahlia

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The experimental material constituted 18 varieties of dahlia and the experiment was conducted in randomized block design with five replications during 1998-99 winter season. Recommended package of practices were followed to raise the crop. Observations were recorded on three random competitive plants from each replication for plant height, stem diameter, number of primary branches, internode length, number of leaves, length and width of leaf, leaf area, plant spread, days to first bud initiation, bud development period, bud development at colour break stage, days from colour break to opening, days to first flowering, days to full opening of flower, bloomlife of flower, number of flowers per plant, ornamental crop duration, diameter of main flower, diameter of secondary flower, diameter of last flower, stalk length of main flower, stalk length of secondary flower, stalk diameter of main flower, stalk diameter of secondary flower, number of ray florets in main flower and secondary flower, length, width and thickness of petal, number of tubers per plant, weight of tubers per plant, length and thickness of largest tuber, length and thickness of smallest tuber. Mahalanobis' D^2 statistic was used to quantify genetic diversity among the genotypes and clustering by Tocher's method was done following Rao [1]. Canonical analysis was carried out according to Anderson [2]. For numerical classificatory analysis, the general similarity coefficient (S_G) of Gower [3] was used as a measure of resemblance between different operational taxonomic units or OTUs (entries included in the study) and S_G values were calculated as per Sneath and Sokal [4]. Based on the matrix of the S_G values, phenograms (dendrograms) were constructed using the UPGMA (unweighted pair group method using arithmetic average) technique in one of the SAHN (sequential, agglomerative, hierarchic, non-overlapping) clustering methods [4] and the clusters were identified at appropriate phenon levels.

Significant differences among the 18 genotypes of dahlia were found for all the characters except for bloomlife of flower and number of tubers per plant. The major contributors to genetic diversity (D^2) were stalk diameter of secondary flower followed by number of ray florets in the main flower, length of petal and number of ray florets in the secondary flower. The restricted role of other characters may be attributed to the fact that most of the test entries were commercial varieties. Following the Tocher's method, the 18 entries were grouped into six clusters and the clustering was in broad agreement with the grouping obtained by using the first two canonical vectors which accounted for more than 99 per cent of total variation. Cluster-1 comprised five varieties having less number of large sized flowers with late flowering, moderate bloomlife and short ornamental crop duration. Cluster II included six varieties with medium to high number of medium to large sized flowers. Cluster III consisted of four varieties which were marked for their late flowering with comparatively lesser number of small sized flowers. Cluster IV, V and VI were monotypic clusters quite distinct from others. Cluster IV included only Jyotsna a tall variety with medium flowering period bearing a

Table 1. Composition of clusters/sub-clusters identified from the dendrogram

Cluster	No. of entries	Sub-cluster group	No. of entries	Variety/varieties
I	12	IA_1	3	Kenya Gerua, Kenya Bicolor, Kenya White
		IA_2	3	Chaitan, Blackout, Cryodon Monarch Red
		IA_3	1	Donald Vandemark
		IB	2	Kelvin Rose, Vigour
		IC	1	Tenzing Norgay
		ID	1	Croydon Monarch Blue
		IE	1	Thelma Davidson
II	3	IIA	1	Monarch Sport
		IIB	1	Cryodon Apricot
		IIC	1	Tatan
III	1		1	Buddha
IV	2	IVA	1	Jyotsna
		IVB	1	Gloriosa Samalatal

good number of small sized flowers while cluster V contained Buddha which was characterized by short plant height with a long ornamental crop duration bearing more number of small flowers having moderate bloom life. Cluster VI contained the pompon type, Gloriosa Samalatal which was of medium height with maximum number of flowers of very small size and better longevity.

In the numerical taxonomic approach, the genotypes were classified using all the 36 characters to calculate similarity coefficients (S_G). The dendrogram shows that at 70 per cent phenon level, all the genotypes were broadly grouped into four clusters i.e. cluster 1 comprising 12 varieties, cluster II consisting of three, cluster III having one and cluster IV with two (Table 1, Fig. 1). At 75 percent phenon level cluster I, the largest cluster was further classified into five sub clusters (IA, IB, IC, ID and IE) and cluster IV into two (IV A and IV B). IA and IB were multivariety sub clusters containing seven and two genotypes respectively, while the other three were single-variety clusters. Similarly, IV A and IV B were also single variety sub-clusters. When phenon line was drawn at 80 percent level, the sub-cluster IA was further divisible into three groups, IA_1 and IA_2 containing three genotypes each and IA_3 with one and cluster II comprising three genotypes was dissociated into three sub- clusters (II A, II B and II C) each containing single variety. Thus, it was possible to distinguish subtle differences between the genotypes grouped in different clusters and/or sub-clusters at different phenon levels.

A comparison of clustering patterns based on different methods shows that grouping of genotypes into clusters through D^2 analysis, canonical analysis and through dendrogram was almost same. D^2 analysis followed by Tocher's method of grouping and canonical analysis brought out six clusters each, similar in their constitution. Grouping of genotypes through D^2 analysis corresponds to that obtained through dendrogram to the extent of 66.7 per cent i.e. 12 genotypes out of 18 remained in the same cluster. It was seen that all the five genotypes of cluster I, four out of six genotypes of cluster II and three out of four of cluster III in D^2 analysis were in one major cluster (cluser I) of dendrogram. The discrepancy for the remaining genotypes could be attributed to the difference in the method of analysis. D^2 analysis is done on the basis of uncorrelated means of genotypes while in numerical taxonomic approach, the analysis was not free from correlation among the genotypes. However, it was observed that Kenya Geura, Kenya Bicolor and Kenya White of sub-cluster IA_1, Croydon Monarch Red in sub-cluster IA_2 and Thelma Davidson in sub-cluster IE were together in cluster I of D^2 analysis as well as dendrogram. These gneotypes differentiated into three sub-clusters at 80 per cent phenon level. Kelvin Rose, Vigour, Tenzing Norgay and Croydon Monarch Blue of cluster II in D^2 analysis were although included in cluster I of dendrogram at 70 per cent phenon, they further dissociated into three sub- clusters (IB, IC and ID) at 75 per cent phenon level. Similarly, Monarch

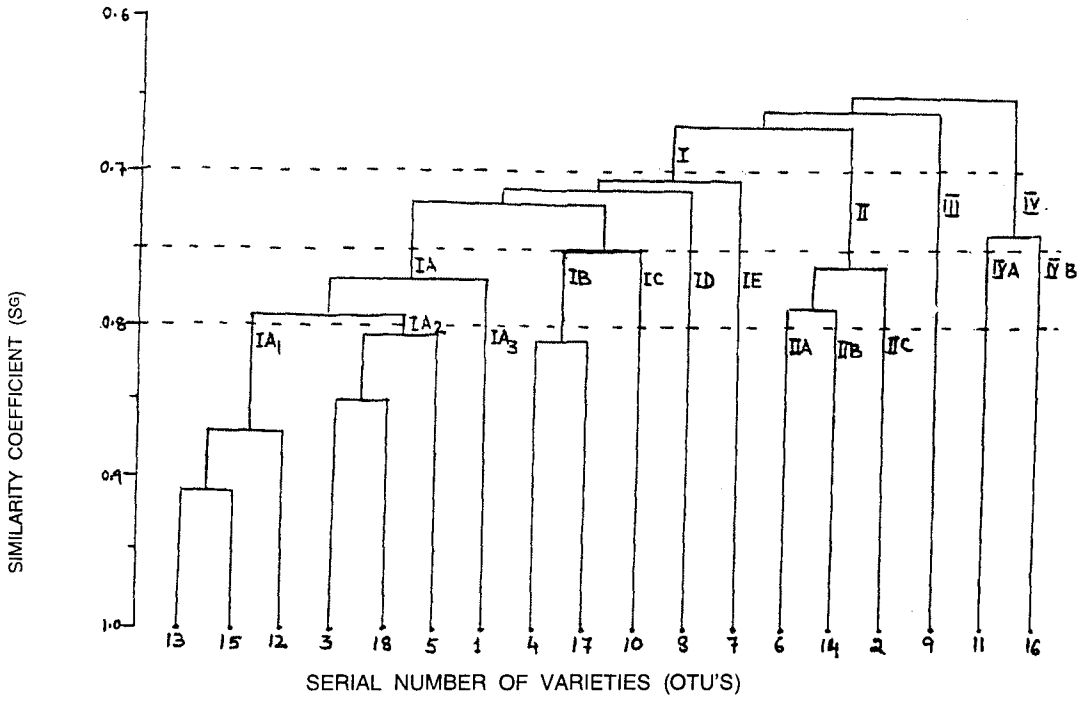

Fig. 1. Dendrogram based on similarity coefficient (S_G) of 36 characters in 18 dahlia varieties

Sport and Croydon Apricot included in cluster II in both the methods were further divisible into single-variety clusters (II A and II B) at 80 per cent phenon. On the other hand, the variety Buddha, Jyotsna and Gloriosa Samalatal forming single- variety clusters in D^2 analysis also maintained their identity in UPGMA method of numerical taxonomic approach at 75 per cent phenon level.

Thus, in a broad sense all the three methods of classifying genotypes into different groups were comparable but dendrogram clustering gave an additional advantage of identifying sub-cluster of the major groups at different phenon levels so that each small group can be more critically analysed.

The varieties Kenya White, Kenya Gerua and Kenya Bicolor in cluster I with less number of large sized flowers and short ornamental crop duration and Kelvin Rose, Monarch Sport, Croydon Apricot and Vigour in cluster II with less number of moderately large flowers, longer ornamental crop duration and earlier flowering habit were identified for garden display. On the other hand, the variety Gloriosa Samalatal in cluster VI having more number of small flowers display. On the other hand, the variety Gloriosa Samalatal in cluster VI having more number of small flowers with longer ornamental crop duration and earliness for flowering was found suitable for both garden display and cut-flower arrangement. Further improvement in dahlia could be achieved by combining more number of large sized flowers with earliness to flower and longer ornamental crop duration through development of F_1 hybrids between the varieties thus identified and subsequently propagated by asexual means for maintaining their hybridity.

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