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Genetic Divergence Analysis of Dahlia (*Dahlia variabilis* L.) Genotypes

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Authors' contributions

This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.

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ABSTRACT

The present investigation was carried out to assess the extent of genetic variability, heritability, genetic advance and genetic divergence using 35 dahlia (*Dahlia variabilis* L.) genotypes with 20 characters. Moderate to high GCV and PCV were recorded for almost all the characters under study emphasizing the existence of variation in the population. All the characters (except plant spread and width of the tuber) showed high heritability along with higher or moderate genotypic coefficient of variation and genetic advance indicating that most likely the heritability was due to additive gene effects and the genotypes under study were highly diverse. The inter-cluster average D^2 value was maximum between the cluster V and III (D^2=6704.46) and minimum inter cluster distance was obtained between cluster IV and I (D^2 =1256.64).

Keywords: GCV; PCV; heritability; genetic advance and D^2 analysis

1. INTRODUCTION

Dahlia is one of the popular bulbous flower; grown in many parts India and the world for its beautiful bloom. It is native to Mexico and belongs to the family asteraceae. Plants come in a wide array of sizes or forms from 26 cm to 240 cm in height with flowers ranging from 2.5 cm to

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40 cm in diameter (Vikas *et al*., 2015). The flowers are curvaceous, spiky with single or double forms with different colours. It is easy to grow except in cold conditions or extreme hot dry weather. Dwarf types are suitable for beds and borders (pure or mixed borders). Large flowering dahlias in pots are popular for terrace garden or varandah display. The long stemmed flowers of various forms and colours are used in flower arrangement and cut flowers of pompon and miniature types stay fresh in flower vases for many days and also good for making garlands. Tubers of dahlia were used for the insulin extraction.

Dahlia is being octoploid (2n=8x=64) that have eight sets of homologous chromosomes, whereas most plants have only two sets of chromosome. In addition, dahlias also contain many transposons genetic pieces that move from place to place upon an allele which contributes to their great diversity and it is highly cross pollinated crop with high natural cross pollination contributing to its variability. Genetic diversity is useful for the protection of plant breeder's rights. Moreover, it helps for conservation and management as well as in understanding the genetic relationships between them, which could further be very useful for breeding in supporting the selection of cross combinations from large sets of parental genotypes, thus broadening the genetic base of breeding programme and success in selection for new types depends on the extent of genetic variability, heritability, genetic advance and genetic divergence which is a prerequisite for initiating appropriate breeding programme in dahlia (Manjula et al., 2017) [1]. Keeping these points in view, the present investigation was undertaken with the objective of genetic divergence analysis of dahlia (*Dahlia variabilis* L.) genotypes.

2. MATERIALS AND METHODS

The present experiment was conducted in the Department of Floriculture and Landscape Architecture, College of Horticulture, Sirsi, University of Horticultural Sciences, Bagalkot, Karnataka, India. Experiment was consists of 35 genotypes viz. HUBD-1 (Horticulture University of Bagalkot Dahlia) to HUBD-35 were planted according to randomized block design with two replications and spacing of 60×45 cm. All the recommended package of practices was followed to grow a successful crop. Under these programme, 20 characters related to vegetative, flowering, quality and yield parameters were estimated. The mean values obtained were used for determining phenotypic and genotypic coefficient of variation (Burton and Devane 1953) [2], heritability (Hanson et al. 1956) [3] and expected genetic advance (Johnson et al. 1955) [4]. The genetic divergence analysis was carried out using the Mahalanobis's D^2 statistics (Mahalanobis 1936) [5] and genotypes were grouped in clusters according to Tocher's method as described by Rao (1952) [6]. The intra and inter cluster distance was worked out as per method suggested by Gomez and Gomez (1983) [7].

3. RESULTS AND DISCUSSION

The analysis of variance revealed that all the twenty characters exhibited highly significant indicating considerable amount of genetic variability among the genotypes tested under the study (Table 1). Genetic variability is a basic pre requisite for any crop improvement program on which ample scope to identify high yielding, early and dwarf genotypes to improve different characters simultaneously and provided the material can be subjected to judicious selection procedure.

The analysis of variance permits estimation of phenotypic and genotypic coefficients of variability of various polygenic traits. The genotypic coefficient of variation measures the extent of variability among the different traits caused due to the inherent capacity of the genotype. The genotypic and phenotypic coefficients of variation are required to understand the effect of environment on various polygenic traits. The high values of GCV % and PCV % were found for number of leaves (31.14, 31.80), length of petal (36.08, 36, 82), width of petal (22.43, 22.79), number of petals per flower (37.09, 38.54), shelf life (25.68, 27.07), individual flower weight (36.37,37.26), number of flower per plant (44.87, 45.34), flower yield per plant (51.14, 52.77) respectively. The moderate values of GCV % and PCV % were recorded for plant height (13.10, 14.18), days to first flowering (11.40, 14.25), days to 50 per cent flowering (13.14, 15.27), duration of flowering (11.29, 12.53), stalk length (18.96, 19.63), length of tuber (13.05, 13.99) respectively. The least values of GCV % and PCV % were estimated for plant spread (4.84, 6.22), width of tuber (9.31, 9.88) respectively (Table 2).

Table 1. Analysis of variance for different growth parameters in dahlia genotypes

Sources of variation	Replications	Genotypes	Error	S. Em ±	CD @	CD @
Degrees of freedom	1	24	24		5%	1%
Plant height	111.132	289.383**	20.521	3.203	9.206	12.359
Number primary branches/plant	1.262	1.325**	0.139	0.264	0.76	1.02
Number of leaves	822.857	5117.960**	108.011	7.348	21.12	28.355
Plant spread	0.932	8.792**	2.325	1.078	3.099	4.161
Days to first flowering	4.32	78.502**	10.85	2.33	6.69	8.99
Days to 50% flowering	5.771	239.79*	21.81	3.3	9.49	12.74
Duration flowering	0.001	10.48**	0.27	0.372	1.071	1.439
Length of petal	0.11	3.509*	0.197	0.314	0.904	1.213
Width of petal	0.026	0.363**	0.005	0.054	0.155	0.208
Number of petals per flower	23.54	934.83*	36.383	4.265	12.258	16.457
Shelf life	0.002	1.968*	0.103	0.227	0.653	0.877
Stalk length	0.825	6.811**	0.237	0.344	0.99	1.33
Individual flower weight	0.467	17.635**	0.423	0.46	1.322	1.775
Length of tuber	4.022	203.368**	14.105	2.655	7.632	10.247
Width of tuber	7.774	369.135*	22.147	3.327	9.563	12.839
Number of flowers per plant	51.086	15174.25*	158.639	1.527	4.39	5.898
Flower yield per plant	5109.31	37400.76**	882.473	21	60.37	56.486
Individual tuber weight	0.0347	12.092**	1.34	0.818	2.352	3.158
Number of tubers per plant	0.386	8.538*	0.413	0.454	1.306	1.753
Total tuber weight per plant	258.931	4781.068**	162.252	9	25.886	34.753

**and **indicates significant at 5 % and 1 % level respectively*

Table 2. Estimates of range, genotypic and phenotypic co-efficient of variation, heritability and genetic advance as per cent of mean in dahlia genotypes

Character	Range	GCV (%)	PCV (%)	h^2 bs (%)	GAM (%)
Plant height (cm)	66.44-116.69	13.30	14.28	86.76	25.52
Number of primary branches / plant	5.60-9.50	10.64	11.78	81.55	19.80
Number of leaves	100.3-282.50	31.14	31.80	95.87	62.81
Plant spread (cm)	35.35-43.93	4.84	6.22	60.49	7.75
Number of days taken to first flowering	31.40-56.40	11.40	14.25	75.70	22.22
Number of days taken to 50 per cent flowering	55.40-95.40	13.14	15.27	83.29	26.2
Duration of flowering	46.90-84.80	11.29	12.59	80.48	20.87
Length of petal (cm)	1.52-7.25	36.08	36.82	96.64	72.84
Width of petal (cm)	0.88-3.05	22.43	22.79	96.84	45.47
Number of petals per flower	19.90-104.30	37.09	38.54	92.51	73.44
Shelf life (days)	2.00.10	25.68	27.07	91.01	50.19
Stalk length (cm)	6.70-14.04	18.96	19.63	93.25	37.79
Individual flower weight (g)	2.43-15.33	36.37	37.26	95.30	77.14
Length of tuber (mm)	55.25-92.87	13.05	13.99	87.03	25.08
Width of tuber (mm)	91.75-157.06	9.31	9.88	88.68	18.06
Number of flowers per plant	15.50-67.40	44.87	45.34	97.93	91.47
Flower yield per plant	57.53-559.23	51.14	52.77	95.39	103.69
Individual tuber weight (g)	18.32-28.45	10.25	11.46	80.02	18.88
Number of tubers per plant	5.00-12.90	22.68	23.81	90.77	44.52
Total tuber weight per plant	11.83-314.7	24.01	24.84	93.44	47.80

GCV- Genotypic Co-efficient of Variation, PCV- Phenotypic Co-efficient of Variation, h^2- Heritability in Broad sense, GAM- Genetic Advance as per cent of Mean

The estimates of genotypic coefficients of variation in the present study were found to be lower than those of phenotypic coefficient of variation indicating that the apparent variation is not only due to genotype, but also due to the influence of environment. Similar results have been reported by Telem et al. (2017) [8], Kumar et al. (2015) [9] and Pratap and Rao (2006) [10]. Narrow differences between genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were observed for all the characters except plant spread, number of days taken to first flowering, number of days taken to 50 per cent flowering and shelf life which indicated that least influence of environment on these characters.

Heritability (h^2) of a character can be relied upon as it enables the plant breeder to decide on extent of selection pressure to be applied under a particular environment, which separates out the environmental influence from the total variability. The estimation of heritability has a greater role to play in determining the effectiveness of selection of a character provided, when it is considered in conjunction with the predicted genetic advance as suggested by Panse and Sukhatme (1967) [11].

In the present study, the magnitude of heritability (Table 2) ranged from 60.49 to 97.93 and genetic advance was ranged 7.75 from to 103.69. The higher magnitude of heritability was exhibited in all the characters. High heritability associated with high genetic advance proves more useful for efficient improvement of a character through simple selection. High heritability with high genetic advance indicating the possible role of additive gene action. Whereas, moderate heritability with low genetic advance can be exploited through heterosis. This result was supported by Patil et al. (2017) [12].

Table 3. Cluster composition based on D^2 statistics in dahlia genotypes

Cluster	Number of genotypes	Genotypes included in the cluster
1	18	HUBD-8, HUBD-31, HUBD-16, HUBD-5, HUBD-7, HUBD-4, HUBD-24, HUBD-18, HUBD-9, HUBD-35, HUBD-20, HUBD-11, HUBD-13, HUBD-14, HUBD-3, HUBD-33, HUBD-2, HUBD-1
2	5	HUBD-23, HUBD-26, HUBD-17, HUBD-6, HUBD-27
3	7	HUBD-22, HUBD-29, HUBD-28, HUBD-15, HUBD-12, HUBD-34, HUBD-25, HUBD-10, HUBD-30, HUBD-21, HUBD-19
4	4	HUBD-10, HUBD-30, HUBD-21, HUBD-19
5	1	HUBD-32

HUBD: Horticulture University of Bagalkot Dahlia

Table 4. Intra cluster and inter cluster D^2 values in dahlia genotypes

	I	II	III	IV	V
I	**588.00**	1353.43	1960.62	1256.64	2279.2
II		**743.78**	2365.77	1756.8	3477.94
III			**723.37**	2997.32	6704.46
IV				**941.75**	1849.57
V					**0.00**

Table 5. The mean values of 20 characters for five clusters in dahlia genotypes

Character	Clusters				
	I	II	III	IV	V
Plant height (cm)	83.75	107.4	80.83	86.74	94.06
Number primary branches/plant	7.14	8.52	6.94	6.73	7.05
Number of leaves	144.65	269.2	124.67	164.3	145.76
Plant spread (cm)	36.79	41.82	36.26	36.11	36.78
Days to first flowering	48.62	36.4	49.27	47.66	49.00
Days to 50% flowering	75.09	76.00	69.24	77.53	94.00
Duration flowering	63.41	63.66	60.40	72.80	63.70
Length of petal (cm)	8.66	8.89	6.58	12.41	12.50
Width of petal (cm)	3.69	3.43	2.53	5.74	4.38

Character	Clusters				
	I	II	III	IV	V
Number of petals per flower	1.89	2.06	1.50	2.25	2.29
Shelf life (days)	50.72	59.16	60.23	71.10	86.5
Stalk length (cm)	3.56	4.00	4.14	3.95	2.70
Individual flower weight (g)	9.00	10.20	9.74	11.07	9.21
Length of tuber (mm)	7.05	8.17	7.02	13.77	10.29
Width of tuber (mm)	73.80	83.93	74.38	70.18	59.97
Number of flowers per plant	29.65	61.46	29.54	23.65	16.70
Flower yield per plant (g)	213.05	502.25	193.49	325.94	172.61
Individual tuber weight (g)	22.15	22.61	21.74	25.39	26.31
Number of tubers per plant	8.23	11.69	9.54	7.65	7.10
Total tuber weight per plant (g)	181.13	265.75	209.28	191.40	186.7

Table 6. Per cent contribution of different characters to the total divergence in dahlia genotypes

Character	Per cent contribution
Plant height (cm)	0
Number primary branches/plant	0
Number of leaves	0.17
Plant spread (cm)	0
Days to first flowering	0
Days to 50% flowering	0
Duration flowering	0
Length of petal	0
Width of petal	0
Number of petals per flower	0.67
Shelf life	1.51
Stalk length	0.67
Individual flower weight	1.68
Length of tuber	0
Width of tuber	2.86
Number of flowers per plant	17.48
Flower yield per plant	11.43
Individual tuber weight	5.88
Number of tubers per plant	45.38
Total tuber weight per plant	8.07

On basis of D^2 analysis (Mahalanobis 1936) [5], the thirty five genotypes were grouped into five clusters (Table 3). The cluster I was very large and comprised of 18 genotypes (HUBD-8, HUBD-31, HUBD-16, HUBD-5, HUBD-7, HUBD-4, HUBD-24, HUBD-18, HUBD-9, HUBD-35, HUBD-20, HUBD-11, HUBD-13, HUBD-14, HUBD-3, HUBD-33, HUBD-2 and HUBD-1). Cluster II included five genotypes (HUBD-23, HUBD-26, HUBD-17, HUBD-6 and HUBD-27). Cluster III included seven genotypes (HUBD-22, HUBD-29, HUBD-28, HUBD-15, HUBD-12, HUBD-34 and HUBD-25). However, Cluster IV includes four genotypes (HUBD-10, HUBD-30, HUBD-21 and HUBD-19), whereas Cluster V includes HUBD-32. The clustering pattern showed that genotypes of different geographical areas were clubbed in one group and also the genotypes of same geographical area were grouped into same cluster as well as in different cluster indicating formal relationship between geographical diversity and genetic diversity.

The maximum inter cluster distance was observed between cluster V and III (D^2=6704.46) indicate wide genetic distance between these clusters. Crossing between members of clusters having maximum inter cluster distance can generate relatively higher heterosis than having less inter cluster distance (Prasad et al, 2002) and the least inter cluster distance was observed between cluster IV and I (D^2 =1256.64). It indicates that genotypes of cluster V and III very close to each other, which indicates the close

genetic makeup of genotypes included in these clusters which suggests the lower degree of divergence in the genotypes. The genotype from individual cluster can be utilized in the selection/breeding programme for desirable economic characters in dahlia. Similar conclusions were drawn Kumar et al., (2017) [13] (Table 4).

A considerable range of variation was found in cluster mean value in respect of all 20 characters given in Table 5. The highest cluster mean for plant height was observed in cluster II (107.40 cm), number of primary branches per plant in cluster II (8.52), number of leaves per plant in cluster II (269.2), plant spread in cluster II (41.82 cm), days to first flowering in cluster III (49.27 days), days to 50 per cent flowering in cluster V (94.00 days), duration flowering in cluster IV (72.80 days). Highest cluster mean characters can be given more emphasis for the purpose of fixing priority of parents for hybridization programmes. This results were similar with the result of Kameshwari et al. (2014) [14]. Highest cluster mean for length of petal in cluster V (12.50 cm), width of petal in cluster IV (5.74 cm), shelf life of flower in cluster V (2.29 days), number of petals per flower in cluster V (86.50), stalk length in cluster III (4.14 cm), individual flower weight in cluster IV (11.07 g), length of tuber in cluster IV (13.77 mm). width of tuber in cluster II (83.93 mm), number of flowers per plant observed in cluster II (61.46), flower yield per plant in cluster II (502.25 g), individual tuber weight in cluster V (26.31 g), number of tubers per plant in cluster II (11.69 g) and total tuber weight per plant in cluster I (265.75 g). The hybridization programme may be initiated involving the genotypes belonging to diverse clusters with high mean values. Similar trend was followed by Patel et al. (2018) [15] and Bhajantri et al. (2016) [16].

The relative contribution of different characters for genetic parameters for genetic divergence (D^2) is given in the Table 6. Number of tubers per plant contributed maximum (45.38%) to the total divergence among the genotypes followed by number of flowers per plant (17.48%), flower yield per plant (11.43%), total tuber weight per plant (8.07%) and the characters which contributed to maximum divergence can be used in selecting diverse parent for hybridization programme. This findings were similar with the results of Mahanta et al. (2019) [17] and Kamble et al. (2004) [18].

4. CONCLUSION

The improvement in these characters through direct selection to develop better cultivars of dahlia can easily be done. High heritability with low genetic advance indicated the contribution of non-additive gene effects. Hybridization and asexual propagation of F_1 can be done to exploit [19,20]. The clustering pattern showed that genotypes of different geographical areas were clubbed in one group and also the genotypes of same geographical area were grouped into same cluster as well as in different cluster indicating formal relationship between geographical diversity and genetic diversity. From the investigation it was found that inter crossing genotypes from clusters V and III and cluster IV and I might result in wide array of variability for exercising effective selection.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

REFERENCES

1. Manjula BS, Nataraj SK, Hegde PP, Anitha G, Ayesha N. Evaluation of dahlia genotypes (*Dahliavariabilis* L.) for growth, yield and quality traits under hill zone of Karnataka. Journal of Environment and Ecology. 2017;35: 365-369.
2. Burton GW, Devane EM. Estimating heritability in tall fescue (*Festuaca cirunclinaceae*) from replicated clonal material. Agronomy Journal. 1953;45:378–481.
3. Hanson CH, Robinson HR, Comstock RS. Biometrical studies of yield in segregating population of Korea Lespedeza. Agronomy Journal. 1956;48:268-272.
4. Johnson HW, Robinson HF, Comstock RE. Estimates of genetic and environmental variability in soybeans. Agronomy Journal. 1955;47:314-318.
5. Mahalanobis PC. On the generalized distance in statistics. (In) Proceedings of National Academy of Science (Indian). 1936;12:49-55.
6. Rao CR. Advanced Statistical Methods in Biometrical Research, edn I. John Wiley and Sons, New York;1952.
7. Gomez KA, Gomez AA. Statistical Procedure for Agricultural Research, 2nd edn, 1983;pp 357-422. John Wiley and Sons, New York.

8. Telem RS, Sadhukhan R, Sarkar HK, Akoijam R, Haribhushan A and Wani SH. Genetic studies for flower yield and component traits in *Chrysanthemum morifolium* Ramat. Journal of Applied Natural Science. 2017;9(1):211-214.
9. Kumar S, Kumar S, Malik S, Kumar M, Malik OS, Kumar M, Singh O. Variability, heritability and genetic advance in chrysanthemum (*Dendranthema grandiflora* Tzvelev). Progressive Horticulture. 2015;47(2):272-274.
10. Pratap M, Rao AM. Assessment and variability studies in gladiolus. Journal of Ornamental Horticulture. 2006;9(2):145-147.
11. Panse VG, Sukhatme PV. 1967. *Statistical Methods for Agricultural Workers*, ICAR. New Delhi.
12. Patil S, Chawla SL, Patel AI. Genetic divergence analysis in gladiolus (*Gladiolus grandiflorus*). Indian Journal of Agriculture Scences. 2017;87(7):953-957.
13. Kumar S, Kumar M, Yadav HK, Sharma S, Kumar S. Genetic diversity and structure population analysis of Chrysanthemum (*Dendranthema grandiflora* Tzvelev) germplasm based on RAPD marker. Journal environmental biology. 2017;38:457-464.
14. Kameswari PL, Pratap M, Anuradha G, Hameedunnisabegum. Genetic divergence studies in chrysanthemum (*Dendranthema grandiflora* Tzvelev). Journal of Science Research and Technology. 2014;9:25-28.
15. Patel MA, Chawla SL, Chauhan DA, Patil S, Chhatrola HN. Character association and path analysis studies in marigold (*Tagetes* spp.) under the South Gujarat region. Journal of Pharmacognosy and Phytochemistry. 2018;7(2):3576-3580.
16. Bhajantri A, Patil VS, Rajesh M. Genetic diversity analysis in gladiolus genotypes (*Gladiolus hybridus* Hort.). Journal of Appied Natural Science. 2016;8(3):1416-1420.
17. Mahanta S, Choudhury M, Talukdar P. Genetic divergence studies in marigold (*Tagetes erecta*). International Journal of Current Microbiology and Applied Science. 2019;8(5):8-12.
18. Kamble BS, Reddy BS, Patil RT, Kulkarni BS. Performance of gladiolus (*Gladiolus hybridus* Hort.) cultivars for flowering and flower quality. Journal of Ornamental Horticulture. 2004;7:51-56.
19. Prasad VSRK, Pitchaimuthu M, Dutta OP. Adaptive responses and diversity pattern in watermelon. Indian Journal of Horticulture. 2002;59(3):298-306.
20. Vikas HM, Patil VS, Agasimani AD and Praveenkumar DA, Performance and correlation studies in dahlia (*Dahlia variabilis* L.). International Journal of Science and Nature. 2015;2(2):379-383.

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