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STUDIES ON VARIABILTY, HERITABILTY AND GENETIC ADVANCE IN DAHLIA (DAHLIA VARIABILIS L.) GENOTYPES UNDER HILL ZONE OF KARNATAKA

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ABSTRACT

Twenty five genotypes of dahlia were used to study the genetic variability, heritability, genetic advance and correlation for growth and yield contributing characters under Mudigere condition. Significant variations were observed for all twenty different characters studied. The study indicated that the moderate to high genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were observed for all the characters (more than 20 % value for both GCV and PCV). High heritability (more than 60 %) with high genetic advance as per cent mean was observed for most of the characters.

INTRODUCTION

Dahlia (*Dahlia variabilis* L.) is one of the most popular tuberous rooted perennial herbaceous flowering plant, valued its their gorgeous attractive spectacular flowers. This tuberous rooted, half-hardy herbaceous perennial belonging to the family asteraceae. Dahlia originated in Mexico and received its name by Cavanilles in the year 1791, to commemorate the work of a Swedish Botanist Dr. Andreas Dahl, a pupil of Linneaus (Smith, 1971). Flower yield as well as quality improvement efforts continue to be the major objective of dahlia improvement programme. Flower yield is a complex inherited character influenced by several attributes of the plant. Productivity of any crop can be increased by cultivating new genotypes. So area based screening for improving the productivity of dahlia is an important step to increase the production. A wide range of variability is available in dahlia genotypes which provide great scope for improving flower yield through systematic breeding. A critical estimate and study of genetic variability is pre-requisite for initiating appropriate breeding procedure for effective selection of superior genotypes.

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However, utilization of this variability requires its systematic evaluation to understand and to estimate the genetic variability, heritability and genetic advance of various yield components. So, there is an urgent need of information on the nature and magnitude of variation available in the material and part played by environment in expression of different characters.

MATERIAL AND METHODS

The present investigation was carried out in the Department of Floriculture and Landscape Architecture, College of Horticulture, Mudigere, University of Agricultural and Horticultural Sciences, Shivamogga during 2014-15. Twenty five genotypes were taken for the study. Experiment was laid out in randomized block design with two replications. Thirty days old rooted cuttings were transplanted in 60 x 40 cm spacing and all the recommended agronomic package of practices were followed. In each genotype, 5 plants were randomly selected for recording the observations. Observations were recorded on various growth, flowering, yield and quality parameters. The parameters of variability like grand mean, range, phenotypic and genotypic coefficient of variation (As per the Burton, 1952), broad sense heritability (Burton and Dewane, 1953) and genetic advance were calculated.

RESULTS AND DISCUSSION

Analysis of variance revealed significant differences among the genotypes for all the traits indicating the presence of sufficient genetic variability in the genotypes and considerable scope for their improvement. Sufficient genetic variability for many of the horticultural traits studied in dahlia had also been reported by earlier workers (Basavaraj 2006, Mishra *et al*., 1997 and Vikas *et al.* 2011). The extent of variability with respect to twenty characters in different genotypes measured in terms of range, genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), along with the amount of heritability (h), expected genetic advance and genetic advance as per cent of mean (GAM) are given in Table 1 and 2. The considerable amount of variation was observed for all the characters. The phenotypic coefficient of variability (PCV) was higher than the genotypic coefficient of variability in all the characters (Table 1 and 2).

The estimates of PCV and GCV were high for number of branches per plant at 30 DAT (26.19 and 30.69), internodal length at 30 DAT (19.71 and 25.51), leaf width (22.15 and 26.25), number of flowers per plant (20.37 and 20.90), number of flowers per hectare (20.73 and 20.90) and number of petals per flower (21.06 and 21.39) reveals the presence of high variability (Table 1 and 2). From this, it can be confirmed that the expression depends more on the non-genetical factors which are governed by additive genes. Moderate variability noticed for plant height at 30, 60 and 90 DAT (10.86,16.74, 13.14 and 12.88, 17.07, 13.39), number of branches per plant at 60 (17.47 and 19.88) and 90 DAT (13.55 and 14.06), Stem diameter at 30 DAT (13.23 and 13.66), leaf length (17.30 and 19.24), stalk length (10.89 and 11.44), number of days taken to first flowering (17.09 and 17.33), number of days taken to 50 per cent flowering (13.51 and 13.71), number of days taken for complete flowering (10.50 and 10.74), duration of flowering (11.28 and 11.86), number of tubers per plant (18.39 and

Table 1. Estimates of mean, range and genetic parameters for growth parameters in dahlia genotypes

Character	Mean	Range	GV	PV	GCV (%)	PCV (%)	h^2bs (%)	GA	GAM (%)
Plant height at 30 DAT (cm)	20.72	15.75-27.75	5.07	7.12	10.86	12.88	71.00	3.91	18.89
Plant height at 60 DAT (cm)	62.24	41.50-83.91	108.61	113	16.74	17.07	96.00	21.04	26.97
Plant height at 90 DAT (cm)	88.89	67.50-113.50	136.58	140.58	13.14	13.39	97.00	23.73	26.69
Plant height at 120 DAT (cm)	108.96	97.75-129.50	54.91	58.29	6.80	7.00	92.00	14.18	13.59
Number of branches / plant at 30 DAT	1.54	1.00-2.70	0.16	0.22	26.19	30.69	72.00	0.71	46.04
Number of branches / plant at 60 DAT	4.21	3.00-6.10	0.54	0.70	17.47	19.88	77.00	1.33	31.65
Number of branches / plant at 90 DAT	7.27	5.15-9.65	0.97	1.04	13.55	14.06	92.00	1.95	26.91
Number of branches / plant at 120 DAT	11.33	9.30-14.05	1.14	1.34	9.43	10.23	84.00	2.02	17.90
Stem diameter at 30 DAT (cm)	0.43	0.36-0.55	0.003	0.004	13.23	13.66	92.00	0.11	25.96
Stem diameter at 60 DAT (cm)	0.78	0.69-0.89	0.003	0.003	6.41	7.23	78.00	0.09	11.73
Stem diameter at 90 DAT (cm)	1.13	1.05-1.23	0.002	0.003	4.36	5.02	75.00	0.08	7.81
Stem diameter at 120 DAT (cm)	1.36	1.28-1.46	0.003	0.003	3.96	4.20	88.00	0.10	7.70
Internodal length at 30 DAT (cm)	3.16	2.10-5.00	0.38	0.65	19.71	25.51	59.00	0.99	31.76
Internodal length at 60 DAT (cm)	7.20	6.15-8.90	0.29	0.54	7.51	10.19	54.00	0.82	11.42
Internodal length at 90 DAT (cm)	11.52	10.60-13.00	0.24	0.45	4.30	5.86	53.00	0.74	6.49
Internodal length at 120 DAT (cm)	16.07	14.95-18.25	0.55	0.84	4.63	5.72	65.00	1.24	7.74
Duration of the crop (days)	141.63	123.16-160.75	82.72	86.17	6.42	6.55	96.00	18.35	12.96
Leaf length (cm)	6.54	5.31-9.55	1.28	1.58	17.30	19.24	80.00	2.09	32.05
Leaf width (cm)	4.50	3.05-7.45	0.99	1.40	22.15	26.25	71.00	1.73	38.51
Stalk length (cm)	12.60	10.10-15.73	1.88	2.08	10.89	11.44	90.00	2.69	21.34

DAT- Days After Transplanting
GV- Genotypic Variance
PV- Phenotypic Variance
GCV- Genotypic Co-efficient of Variation
PCV- Phenotypic Co-efficient of Variation
h^2- Heritability in Broad sense
GA-Genetic Advance
GAM- Genetic Advance as per cent of Mean

Table 2. Estimates of mean, range and genetic parameters for flowering, yield and quality parameters in dahlia genotypes

Character	Mean	Range	GV	PV	GCV (%)	PCV (%)	h^2bs (%)	GA	GAM (%)
Flowering parameters									
Number of days taken to first flowering	69.36	2.92-102.90	140.58	144.54	17.09	17.33	97.00	24.08	34.73
Number of days taken to 50 per cent flowering	86.32	69.80-120.75	136.11	140.25	13.51	13.71	97.00	23.67	27.42
Number of days taken for complete flowering	101.99	87.80-133.10	114.83	120.13	10.50	10.74	95.00	21.58	21.16
Duration of flowering (days)	53.73	40.90-67.10	36.77	40.62	11.28	11.86	90.00	11.88	2.12
Yield parameters									
Number of flowers per plant	27.53	19.60-44.00	31.41	33.11	20.37	20.90	95.00	11.26	40.89
Number of flowers per hectare	203969	145185.00-325925.50	122686 9000	48185 85000	20.73	20.90	95.00	83418	40.89
Number of tubers per plant	7.06	4.65-10.75	1.68	1.99	18.39	19.98	84.00	2.46	34.90
Quality parameters									
Flower weight	23.13 40.71	8.5-29.75			18.36	20.35	81.00	7.89	34.11
Tuber weight	12.59	26.25-51.75	18.03	22.16	14.99	18.03	69.00	10.44	25.66
Flower diameter	110.55 5.24	7.26-17.16	37.25	53.95	16.32	17.98	82.00	3.84	30.52
Number of petals per flower		51.75-150.50	4.22	5.13	21.06	21.39	97.00	47.24	42.73
Vase life		3.25-6.60	542.46 0.57	559.37 0.60	14.39	14.88	93.00	1.50	28.67

PCV- Phenotypic Co-efficient of Variation
GV- Genotypic Variance
PV- Phenotypic Variance
GAM- Genetic advance as per cent of mean
GCV- Genotypic Co-efficient of Variation
h^2- Heritability in broad sense
GA-Genetic Advance

19.98), flower weight (18.36 and 20.35), tuber weight (14.99 and 18.03), flower diameter (16.32 and 17.98) and Vase life (14.39 and 14.88), are in line with the previous reports by Mishra *et al*. (1997), Singh (2003), Janakiram and Rao (1991) and Vikas *et al.* (2011).

The high heritability with high genetic advance was noticed for plant height at 60 DAT (96) and 90 DAT (97), number of branches per plant at 30 DAT (72), 60 DAT (77) and 90 DAT (92), stem diameter at 30 DAT (92), leaf length (80), leaf width (71), stalk length (90), number of days taken to first flowering (97), number of days taken to 50 per cent flowering (97), number of days taken for complete flowering (95), number of flowers per plant (95), number of flowers per hectare (95), number of tubers per plant (84), flower weight (81), tuber weight (69), flower diameter (82), number of petals per flower (97) and vase life (93) in Table 1 and 2.

High heritability coupled with high genetic advance is indicative of greater proportion of additive genetic variance and consequently a high genetic gain is expected from selection under situation (Basavaraj 2006, Beura *et al.*, 1995, Mishra 2001, Vikas *et al.* 2011). The characters which exhibited high variability with moderate or low genetic advance can be improved by intermating the superior genotypes in the segregating population developed from multiple crosses and the desirable genes can be accumulated (Negi 1988 and Singh 2003).

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