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Assessment of genetic parameters in periwinkle through diallel analysis

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ABSTRACT

Estimation of genetic variability assists in determining the contribution of various plant parameters in exhibiting the improvement of genotypes under a specific set of environmental factors. Genetic analysis allows us to clearly understand various morphological, physiological, and genetic traits, in addition to the type and extent of their role in the advancement of cultivars. The present investigation was carried out to evaluate six inbred lines of periwinkle (Vi-15-1, Vi-13-2, Vi-16, Vi-15-2, Vi-29, Vi-14-3), and their cross combinations in the full diallel fashion for ornamentally important characters. Analysis of variance revealed highly significant variations for all the parameters in all the inbred lines utilized in the study. The highest broad sense heritability estimates were observed for the number of seeds/follicles (H= 97.77 %) in the parents, whereas plant height had the highest heritability in the cross combinations (H= 98.73%). The high values of phenotypic and genotypic coefficient of variation in parents (PCV=34.41; GCV=34.02) and crosses (PCV=25.49; GCV=24.93) were recorded for the number of seeds/follicles. In the present study, moderate to high heritability together with a high percentage of genetic advance was recorded for seeds/follicle, follicle length, primary branches/plant, plant height, internode length and plant spread, suggesting that the additive gene action controlled these characters. Therefore, the results suggested the existence of variability for studied traits in these periwinkle inbred lines, which should be improved in future breeding.

Key words: *Catharanthus roseus*, Genetic advance, Coefficient of variation, Heritability, Vinca.

INTRODUCTION

The genus *Catharanthus* includes eight species, and all are native to Madagascar except *Catharanthus pusillus*, which originated from India and Sri Lanka. *Catharanthus roseus* belongs to the *Apocynaceae* family with chromosome number 2n = 16. It is an erect, evergreen, ever-blooming, and perennial herb with purple/green flexible branches (Kaur and Dhatt, 8). It is utilized in water-scarce gardens, butterfly gardens, and recreational playgrounds as a ground cover, bedding, and border planting, and possible to grow in pots (Krishnan *et al*., 9). It is one of the most popular garden plants in the USA because it withstands drought, stress, and pollution. Insect and disease attacks are rare, and the plant is easily perpetuated from seed. These characteristics make periwinkle an appealing plant for use in landscapes (Chen *et al*., 5). Previously it was considered a self-pollinated crop. However, natural self-pollination doesn't happen; it is accomplished by butterflies and Hawk moths (Sreevalli *et al*., 13).

Most of the research on *Catharanthus* species concentrated on chemical and pharmacological components, with very few focusing on genetic characteristics for ornamental purposes (Dovrat and Goldschmidt, 6). A plant's phenotype is governed by its genotype, the environment in which it grows, and genotype × environment (G×E) interactions. Plant breeders face the challenge of identifying and selecting the plants with favourable characteristics bestowed by their genetic constitution due to G×E interactions. Genetic variation among the genotypes allows the breeders to select superior genotypes for novel varieties development having resistance to biotic and abiotic stresses *per se* or as parents in hybridization (Terfa and Gurmu, 15). Genetic variation between two parents is required to achieve heterosis and transgressive segregants. The amount of variability present in the initial plant material determines the success of a breeding programme. Nevertheless, estimations of heritability combined with expected genetic advances would be more reliable (Johnson *et al*., 7). Hence, the present study was carried out to explore the extent of genetic variation and the level of heritability present in the periwinkle, which is useful from an ornamental perspective.

MATERIAL AND METHODS

The present investigation was undertaken from 2019-2022 at Floriculture and Landscaping Department, Punjab Agricultural University, India. The experimental material comprised six inbred lines of Vinca (Fig. 1). The parental lines were developed by four to five generations of selfing. The experiment was designed in randomized block design with three

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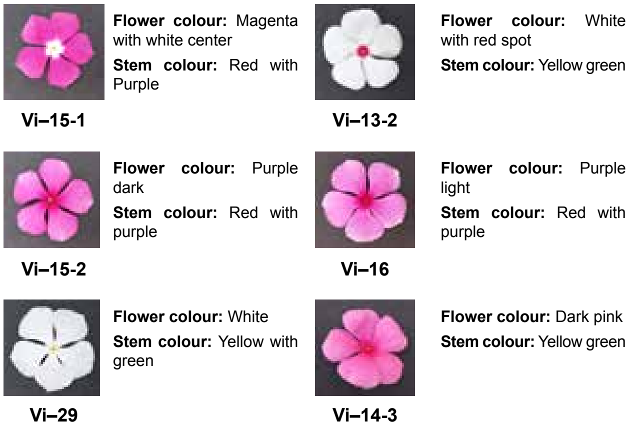

Fig. 1. Morphological characters of inbred lines

replicates. The seeds of parental lines were sown in March and transplanted in the first week of May at 60 × 40 cm spacing. The crossing was attempted amongst six inbred lines of periwinkle from August to October in full diallel fashion. The matured flower buds were emasculated in the evening and pollinated on the next morning with pollen of interest (Singh and Dhatt, 21; Bhattacharya and Mandal, 2). The observations were recorded on various morphological characters, and the data was analysed statistically using PB Tool and MS Excel-2010. The extent of genetic variability was determined by mean values, phenotypic coefficient of variation (PCV), and genotypic coefficient of variation (GCV). The PCV, GCV, and heritability in a broad sense were calculated as per Burton and DeVane (3). Genetic advance and genetic advance as per cent of mean (%) were computed utilizing the formulas reported by Johnson *et al*. (7). The coefficients of variation were categorized as high (>20 %), moderate (10-20 %), and low(<10 %). Similarly, heritability was categorized as high (>80 %), moderate (50-80 %), and low (<50 %).

RESULTS AND DISCUSSION

The results of the coefficient of variation (CV) for parental lines and cross combinations are presented in Table 1. As per results, a high CV was recorded in the number of flowers per plant (10.12 %). It was followed by plant spread (7.86 %), follicle length (7.43 %) and plant height (7.36 %). The lowest CV was reported in corolla tube length (2.54 %) among the studied characters of the parental population. The coefficient of variation varied from 2.54 to 10.12 % and 1.04 to 9.09 %, among the parents and cross combinations, respectively. Among crosses, the number of flowers per plant had a maximum percentage of CV (9.09 %). It was followed by corolla tube length (8.55 %), number of seeds per follicle (5.34 %), number of branches per plant (3.14 %), follicle length (3.12 %) and plant spread (2.95%). The phenotypic coefficient of variation (PCV) was greater than the genotypic coefficient variation (GCV) among all characters which might be due to environmental influence. These results were in conjunction with the findings of Rai *et al*. (10) studies in China aster. The phenotypic coefficient of variation (PCV) varied from 5.35 to 34.41 % in the parental population (Table 1). The highest percentage of PCV (34.41 %) was observed for seeds/follicle, followed by the length of follicle (30.85 %) and the number of branches/plant (20.10 %). It was moderate for the plant height (16.79%), internode length (14.87%), plant spread (14.27%), number of flowers per plant (13.87%), and leaf breadth (11.47%). The low PCV was observed for the duration of flowering (6.61%), corolla tube length (6.33%), and flower diameter (5.35%). Among the cross combinations, the number of seeds per follicle had the highest PCV (25.49%), followed by plant spread (21.03%) and number of branches per plant (20.86%). The low PCV was observed for days to flowering (8.45%), leaf length (7.58%), and flowering duration (4.14%). The range of PCV was recorded as 4.14 to 25.49 % among the crosses. The higher PCV and GCV values indicated a greater amount of variability among the various genotypes. Hence, it helps make the selection based on the character. Similar findings were reported by Byadwal *et al*. (4) in gaillardia, who observed higher values of PCV and GCV for different traits.

The experimental findings reported that the range of genotypic coefficient of variation (GCV) was 3.96 to 34.02 % among the parental lines (Table 1). A high GCV was observed for seeds/follicle (34.02 %) followed by the length of the follicle (29.94%). Moderate GCV was reported for the number of branches per plant (19.51 %), plant height (15.09 %), internode length (13.69 %), plant spread (11.90 %), and leaf breadth (10.38%). The range of genotypic coefficient of variation among the cross combinations was recorded as 4.01 to 24.94%. The higher GCV was observed in seeds/follicles with 24.93 %, followed by plant spread (20.82 %). It was moderate for follicle length (12.40 %), flowers/plant (11.92 %), and flower diameter (10.12 %). The lowest GCV was recorded in flowering duration (4.01%). In the present investigation, GCV exhibited slightly lower estimates than the corresponding PCV, indicating the environment's role in the trait's expression. Similar findings were also reported by Singh and Dwivedi (12) in Periwinkle. The heritability range varied from 46.74 to 97.77 % among the inbred lines. The maximum heritability was observed for number of seeds per

Table 1. Estimation of genetic characters in six inbred lines of periwinkle and their thirty cross combinations.

Characters	Mean	CV (%)	PCV (%)	GCV (%)	Heritability (%)	Genetic advance	Genetic advance as % of mean
Plant height (cm)	57.46	7.36	16.79	15.09	80.77	16.05	27.93
Plant spread (cm)	35.95	7.86	14.27	11.90	69.62	7.36	20.46
No. of primary branches/plant	8.06	4.82	20.10	19.51	94.25	3.15	39.02
Leaf length (cm)	4.63	2.84	8.79	8.32	89.57	0.75	16.22
Leaf breadth (cm)	2.30	4.87	11.47	10.38	81.96	0.45	19.36
Internode length (cm)	1.88	5.80	14.87	13.69	84.77	0.49	25.97
Corolla tube length (cm)	2.18	2.54	6.33	5.80	83.88	0.24	10.94
Days to flowering	38.80	2.61	6.66	6.13	84.70	4.51	11.63
Duration of flowering (days)	119.02	4.31	6.61	5.02	57.63	9.34	7.85
No. of flowers/plant	381.61	10.12	13.87	9.49	46.74	50.98	13.36
Flower diameter(cm)	4.55	3.60	5.35	3.96	54.76	0.27	6.03
Follicle length (cm)	2.38	7.43	30.85	29.94	94.20	1.42	59.86
No. of seeds/follicle	24.10	5.14	34.41	34.02	97.77	16.70	69.29
Range	1.88-381.61	2.54 – 10.12	5.35 – 34.41	3.96 – 34.02	46.75 – 97.77	0.24 – 16.70	6.03 – 69.29
Cross Combinations							
Plant height (cm)	67.20	1.92	17.06	16.95	98.73	23.32	34.70
Plant spread (cm)	47.03	2.95	21.03	20.82	98.03	19.97	42.47
No. of primary branches/plant	8.82	3.14	20.86	20.62	97.74	3.70	42.00
Leaf length (cm)	5.25	1.69	7.58	7.39	95.05	0.78	14.84
Leaf breadth (cm)	2.54	2.13	9.17	8.92	94.60	0.45	17.87
Internode length (cm)	2.54	2.73	15.61	15.37	96.93	0.79	31.17
Corolla tube length (cm)	2.13	8.55	12.17	8.66	50.62	0.27	12.69
Days to flowering	32.94	2.40	8.45	8.10	91.92	5.27	15.99
Duration of flowering (days)	132.28	1.04	4.14	4.01	93.69	10.58	8.00
No. of flowers/plant	492.84	9.09	14.99	11.92	63.19	96.16	19.51
Flower diameter (cm)	4.56	1.61	10.25	10.12	97.53	0.94	20.59
Follicle length (cm)	2.10	3.12	12.79	12.40	94.05	0.52	24.78
No. of seeds/follicle	22.99	5.34	25.49	24.93	95.62	11.54	50.21
Range	2.10-492.84	1.04-9.09	4.14–25.49	4.01–24.93	50.62–98.73	0.27 – 96.16	8.00 – 50.21
Overall range	1.88-492.84	1.04 – 10.12	4.14 – 34.41	3.96 – 34.02	46.75 – 98.73	0.24 – 96.16	6.0 – 69.29

Note: CV= Coefficient of Variation, PCV= Phenotypic Coefficient of Variation, GCV= Genotypic Coefficient of Variation

follicle (97.77%) followed by the number of branches/plant (94.25 %). Less heritability was reported in flowers/plants (46.74 %). These findings point to the possibility of improving the traits through direct selection. The heritability among cross combinations varied from 50.62 to 98.73%. The highest heritability was observed for plant height (98.73 %) followed by plant spread (98.03 %) and number of flowers per plant (63.18 %). The lowest heritability was recorded for corolla tube length (50.62%). These estimations agreed with the conclusions reached by Barigidad *et al*. (1) in chrysanthemums who recorded the highest heritability for the number of petals/flowers. Estimates of heritability together with genetic advance as per cent mean were helpful for determining the selection of individuals (Tamut *et al*., 14).

The range of genetic advances among the parental lines was 0.24-50.98. The maximum genetic advance (GA) was recorded for the number of flowers per plant (50.98), followed by the number of seeds per follicle (16.70), plant height (16.05), duration of flowering (9.34), and plant spread (7.36). The minimum genetic advance was observed for the corolla tube (0.24). Among the cross combinations flowers/plant had the maximum genetic advance (96.16) followed by plant height (23.32) and plant spread (19.97). The least GA was recorded for the length of corolla tube (0.27). The range of GA among cross combinations was observed as 0.27 to 96.16 %. These findings indicated the presence of differences among all traits with respect to genetic advance. Similar findings were reported by Rai *et al*., (10) in China Aster and Yuvraj and Dhatt (17) in marigold.

Genetic advance as per cent of mean (GA %) was highest in the seeds/follicle (69.29 %) followed by follicle length (59.86 %), number of primary branches per plant (39.02 %), plant height (27.93 %), internode length (25.97 %) and plant spread (20.46 %). The lowest genetic advance as per cent of the mean was recorded for flower diameter (6.03%) among the inbred lines. Likewise, the range of genetic advance as per cent of the mean was observed as 8.00 to 50.21% among the crosses (Table 1). It was high for seeds/follicle (50.21 %) followed by plant spread (42.47 %), primary branches/plant (42.00 %), plant height (34.70 %), and internode length (31.17 %). The least genetic advance among the crosses was reported for the flowering duration (8.00%).

High to moderate heritability and high genetic advance as per cent of mean were recorded for plant height, branches/plant, internode length, follicle length and number of seeds/follicles among the parents. The cross combinations of plant height, plant spread, number of branches/plants, internode length, flower diameter, follicle length and number of seeds/follicles were recorded as high to moderate heritability and genetic advance. It indicated that these characters were slightly influenced by the environment and controlled by the additive gene action, hence useful for simple selection. These results conformed with the findings of Vishnupriy *et al*. (16) in marigold. High or medium heritability and genetic gain were reported in leaf length, leaf breadth, corolla tube length, days for flowering and flowers per plant within the parental lines. Similarly, among the cross combinations, leaf length, leaf breadth, corolla tube length, days for flowering and flowers per plant reported high or medium heritability and medium genetic gain. These results suggested that both additive & non-additive genes controlled these traits. These results were closely in conformity with the findings of Singh and Dhatt (11) in periwinkle.

The high magnitude of variations of phenotypic and genotypic coefficients were observed for seeds/follicles, follicle length, and branches/plants among the parental lines. High PCV and GCV were recorded for seeds/follicles, plant spread, number of branches/plant and plant height among the crosses. Low magnitudes were recorded in flower diameter, leaf breadth, flowering days, length, and duration. As per parental results, high heritability (>80 %) was observed in most traits studied; moderate heritability was recorded in the duration of flowering and flower diameter among the parents. Likewise, among cross combinations, most traits recorded high to moderate heritability. The genetic gain as per cent was highest for seeds/follicle, follicle length, primary branches/plant, and plant height among parental lines. Among the cross combinations, a high genetic gain was observed in seeds/follicles, plant spread, branches/plant, plant height and internode length. Information on heritability is useful in selecting a strategy in a particular situation to enhance a trait. High heritability values and high genetic advance expressed as a percentage of the mean confirm the existence of additive gene action and simplify the selection process. The attribute with the highest heritability with the least genetic gain demonstrated non-additive action, and heterosis breeding is recommended here. Therefore, the present investigation was helpful for the improvement of characters among the periwinkle genotypes from a landscaping perspective.

AUTHORS' CONTRIBUTION

Conceptualization of research (BR, KKD); Designing of the experiments (BR, KKD); Contribution of experimental materials (BR, KKD); Execution of field/lab experiments and data collection (BR, KKD); Analysis of data and interpretation (BR, KKD); Preparation of the manuscript (BR, KKD).

DECLARATION

The authors declare that there is no conflict of interest.

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