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Tejal Patel
Assistant Professor, Kishorbhai Institute of Agriculture Sciences and Research Centre, Uka Tarsadia University, Bardoli-Surat, Gujarat, India

Sudha Patil
Assistant Professor, Department of Floriculture and Landscape Architecture, ASPEE College of Horticulture, Navsari Agricultural University, Navsari, Gujarat, India

PB Patel
Associate Research Scientist, Main Rice Research Centre, Navsari Agricultural University, Navsari, Gujarat, India

Alok Shrivastava
Professor and Head, Department of Agricultural Statistics N. M. College of Agriculture Navsari Agricultural University, Navsari, Gujarat, India

Corresponding Author:
Tejal Patel
Assistant Professor, Kishorbhai Institute of Agriculture Sciences and Research Centre, Uka Tarsadia University, Bardoli-Surat, Gujarat, India

Genetic variability, character association and path analysis studies in periwinkle genotypes under the South Gujarat region

Tejal Patel, Sudha Patil, PB Patel and Alok Shrivastava

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Abstract
Eleven periwinkle genotypes were evaluated for qualitative and quantitative characters to assess the genetic variability, association of characters and their direct and indirect effects on secondary branches per plant. Correlation and path coefficient analysis indicated that the characters viz., plant height, plant spread (N-S), plant spread (E-W), number of primary branches per plant, leaf area, survival percentage, fresh weight of shoot, fresh weight of root, fresh weight of whole plant, dry weight of shoot, dry weight of root and dry weight of whole plant exhibited positive significant correlation (genotypic and phenotypic) with secondary branches per plant. The highest positive direct effect towards secondary branches per plant was exerted via dry weight of whole plant and was followed by fresh weight of whole plant, survival percentage, number of primary branches per plant, days to 50% flowering, shoot length, flower diameter, internodal distance and flower length. The present investigation indicated that these characters are important in deciding the secondary branches per plant. Hence these characters may be considered as selection indices for deciding secondary branches per plant and might be considered as selection indices in periwinkle improvement programme.

Keywords: Periwinkle, genotype, qualitative, quantitative, correlation, coefficient

Introduction

Catharanthus roseus is a perennial plant from Apocynaceae family and is generally identified as a Madagascar periwinkle. It was originally classified as *Catharanthus rosea* by Linnaeus, and later renamed as *Catharanthus roseus* built on their morphological features (Van Der Heijden *et al.*, 2004) [18]. The genus *Catharanthus* has 8 known species of which 7 are endemic to Madagascar. It is one of the most interesting groups of ornamental plants in the world with a very high medicinal value (Papon *et al.*, 2005) [9]. It is an important floral species in horticulture and is one of the few pharmacological plants that have a long history. It is cultivated as ornamental plant almost throughout the tropical and subtropical world. It grows like weeds in many parts of the country.

In recent years, crop improvement played an important role in producing new types in any crops and for that the knowledge of genetic base of crop is must. Hence, characterization of accessions provides description of the material which is essential for their identification, conservation, management and utilization in crop improvement programmes. Morphological characterization is the first step in description and classification. Apart from this, it is commonly known that morphological data can be dubious for taxonomic reliability because of environmental interaction and largely unknown mechanisms of genetic control of these traits. The estimates of variability, heritability and genetic advance for the yield components and their correlation with yield have been of great importance. The genetic variability would be determined with the help of certain genetical parameters such as genetic coefficient of variation (GCV), heritability estimates (h^2) and genetic advance (GA). GCV indicates the relative degree of genetic variability existing for different characters in the population of genotypes. The heritability expresses the relative amount of heritable portion of variation. However, the heritability estimates along with genetic gain is more useful in selecting the best population individual (Ranchana *et al*., 2013) [14].

The analysis of variance for different traits helps in estimation of genotypic and phenotypic coefficients of variability of various polygenic traits which are the measures of variability due to the inherent capacity of genotype and the phenotypic expression of genotype due to the environmental effect, respectively. These two coefficients allow meaningful comparison of the variation of several traits in genotypes. Selection will be effective only when the observed variability in the population is heritable in nature and hence, the heritability estimates that forms a measure of transmission of genetic characters from one generation to the other are essential to enable a plant breeder in isolation of elite selection. Heritability gives the idea of additive and non-additive components of which additive components respond to selection. However, in selecting the best population individual, the heritability estimates along with genetic gain is more useful as they together indicate the possibility and degree of improvement through effective gene transfer.

The parameters like correlation coefficient measures the mutual relationships between various plant characters and determines the component characters on which selection can be based for improvement in various characters. Path analysis reveals whether the association of these characters with yield is due to their direct effects or indirect effects for one or other traits. Such a study may be useful and effective in selection for simultaneous improvement of the component characters that contribute towards yield.

Materials and Methods

The present investigation was carried out for two successive years 2022-23 and 2023-24 at Floriculture Research Farm, ASPEE College of Horticulture, Navsari Agricultural University, Navsari (Gujarat). Rooted cuttings of eleven different genotypes of periwinkle with uniform length (15 cm - 16 cm) were obtained from the local nursery for experimentation and were grown in a randomized block design (RBD) with three replications. The genotypes were planted in a double row of 24 plants under each replication with a spacing of 45 cm x 30 cm with all the agronomical practices and plant protection measures. The observations were recorded on five randomly tagged plants from each genotype of each replication. The mean values of five randomly selected plants were calculated for each observation under individual years for all the characters under study. The pooled data of both the years were analysed for genetic variability, phenotypic and genotypic correlations as well as path coefficient analysis.

Results and Discussion

Genetic variability

The parameters of genetic variability viz., mean, range, genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability (broad sense), genetic advance and genetic advance expressed as percent mean are presented in (Table 1).

The genotypic and phenotypic coefficients of variation are thus needed to understand the effect of environment on various polygenic traits (Allard, 1960) [1]. The phenotypic and genotypic coefficients of variation were estimated from the corresponding variances and were used for the assessment of variability among the characters studied. GCV and PCV were high for all the parameters, except survival percentage, plant spread in E-W direction at 3 months, flower diameter and internodal distance. GCV for plant spread at 3 months and PCV for leaf area which recorded the moderate values whereas, low values for GCV and PCV were estimated by flower length and GCV for leaf area. Among all the characters studied, the highest GCV and PCV were recorded for fresh weight of shoot (74.26 and 75.80, respectively) and were followed by fresh weight of whole plant (70.75 and 71.73, respectively) whereas, the lowest values for GCV and PCV were observed for flower length (5.98 and 7.97, respectively). The highest difference between GCV and PCV values was recorded for leaf area (4.4) whereas, the lowest difference (0.42) was observed for plant height at 6 months after transplanting.

It is revealed that environmental factors have played a major role with respect to leaf area while, their influence was negligible in the plant height at 6 months. The estimates of genotypic coefficient of variation were lower than the phenotypic coefficient of variation for all the characters under consideration. It is due to the fact that phenotypic coefficient of variation includes environmental component also and indicates that the apparent variation is not only due to genotype but also due to the influence of environment. The present observation is in agreement with the interpretations of the research outputs of Kameswari *et al.* (2015) [6], Telem *et al.* (2017) [17], Kumar and Dewan (2017) [7], Prakash *et al.* (2017) [12], Kumar *et al.* (2018) [8], Verma and Shukla (2018), Patil *et al.* (2019) [10] and Gaikwad *et al.* (2020) [4] on the estimates of coefficient of variation in chrysanthemum who found higher phenotypic coefficient of variation than genotypic coefficient of variation.

However, the differences between the GCV and PCV were relatively very small which indicates that large amount of variability was contributed by their inherent genetic component and was under less influence of environmental factors. It indicates that these genotypes had a stable performance at this site. A similar trend of low environmental influence has also been reported in the previous findings by Punetha *et al.* (2012) [13], Kameswari *et al.* (2015) [6], Telem *et al.* (2017) [17], Kumar and Dewan (2017) [7], Prakash *et al.* (2017) [12], Kumar *et al.* (2018) [8], Patil *et al.* (2019) [10] and Gaikwad *et al.* (2020) [4] in chrysanthemum.

Heritability

The estimate of heritability ranged between leaf area (46.08%) to dry weight of whole plant (98.13%). High estimate of heritability (98.13%) was recorded for dry weight of whole plant; followed by fresh weight of root (98.07%). Lowest value of heritability (46.08%) was reported for leaf area. Heritability estimate provide the information regarding the amount of transmissible genetic variation to total variation and determine genetic improvement and response to selection. High heritability portion of variability is in confirmation with the findings of Punetha *et al.* (2012) [13], Sahu and Sharma (2014) [15], Kameswari *et al.* (2015) [6], Telem *et al.* (2017) [17], Kumar and Dewan (2017) [7], Verma and Shukla (2018), Patil *et al.* (2019) [10] and Gaikwad *et al.* (2020) [4] in chrysanthemum.

Genetic advance

All the characters under study recorded high values for genetic advance as *percent* of mean which was the highest for fresh weight of shoot (152.97%) followed by fresh weight of whole plant (145.12%), dry weight of shoot (144.26%) and rest others, except for the flower length (12.32%) and leaf area (19.14%) which recorded the value in the moderate range of estimates of genetic advance. High genetic advance (>20%) coupled with high heritability noticed for all the traits, except flower length and leaf area indicates that these characters are controlled by genes with additive gene action and that there is a wide scope for improvement for these traits simply through selection. However, flower length and leaf area with moderate heritability and low genetic advance estimate indicated that these are governed by non-additive gene action and direct selection may not be possible due to most of the variations are attributed to environmental effects. Kameswari *et al.* (2015) [6], Telem *et al.* (2017) [17], Kumar and Dewan (2017) [7], Verma and Shukla (2018), Patil *et al.* (2019) [10] and Gaikwad *et al.* (2020) [4] also recorded a wide variation in genetic advance as percent of mean for varying characters in chrysanthemum.

Correlation coefficient analysis

It has been found that the number of secondary branches per plant provides the association between component characters and suggests that while going for mere selection of better genotypes in periwinkle, the traits *viz.*, plant height, plant spread (N-S), plant spread (E-W), number of primary branches per plant, leaf area, survival percentage, fresh weight of shoot, fresh weight of root, fresh weight of whole plant, dry weight of shoot, dry weight of root and dry weight of whole plant which recorded significant positive association at both genotypic and phenotypic levels should be taken into consideration (Table 2 & 3). Simultaneous improvement on these traits will be helpful in improving number of secondary branches per plant in periwinkle which ultimately improve structure of plant and flowers both terminally hence, more branches resulted into more proliferous flowering. This finding indicates that genotypic and phenotypic correlation values were close to each other and the phenotypic expression is lessened under the influence of environment. Similar trend was noticed in chrysanthemum earlier by Punetha *et al.* (2012) [13], Sahu and Sharma (2014) [15], Kameswari *et al.* (2015) [6], Suvija *et al.* (2016) [16], Telem *et al.* (2017), Kumar and Dewan (2017) [7], Kumar *et al.* (2018) [8], Jaslam *et al.* (2018) [5], Beeralingappa *et al.* (2019) [2], Bindhushree *et al.* (2019) [3] and Pawar (2021) [11].

Path coefficient analysis

In the present study, path coefficient analysis was computed at genotypic level for all the characters and depicted in Table 4. Path coefficient analysis was carried out by taking secondary branches per plant as dependent variable to partition correlation coefficient into direct and indirect effects in order to determine the contribution of different characters towards the secondary branches per plant. Direct and indirect effects of various characters on secondary branches per plant indicated that there is an agreement between direction and magnitude of direct effect of various characters and correlation with secondary branches per plant. Thus, a significant improvement in secondary branches per plant can be expected through selection in the component traits with high positive direct effects. As the genotypic path coefficients are devoid of environmental effect hence should be considered more reliable selection criteria than phenotypic coefficients. It is clear from the Table 4 that maximum positive direct effect towards secondary branches per plant was exerted via dry weight of whole plant and was followed by fresh weight of whole plant, survival percentage, number of primary branches per plant, days to 50% flowering, shoot length, flower diameter, internodal distance and flower length. Similarly, the positive direct effect on flower yield per plant was also observed by plant spread in N-S direction by Kameswari *et al.* (2015) [6], Bindhushree *et al.* (2019) [3] and Pawar (2021) [11]; days for 50% flowering by Kameswari *et al.* (2015) [6], Telem *et al.* (2017), Bindhushree *et al.* (2019) [3] and Pawar (2021); plant height by Pawar (2021) [11]; flower diameter by Suvija *et al.* (2016) [16], Beeralingappa *et al.* (2019) [2] and Pawar (2021) [11]. The magnitude of residual effect was negligible and negative, which indicated that major portion of contribution towards number of secondary branches per plant might be explained based on characters included in the present study. Based on present research, it may be concluded that the characters like number of primary branches per plant, shoot length, flower diameter, flower length, internodal distance, survival percentage, days to 50% flowering, fresh weight of whole plant and dry weight of whole plant are the important characters affecting number of secondary branches per plant since they had positive direct effect.

Table 1: Range, mean, components of variance, genotypic and phenotypic coefficient of variation, heritability in broad sense and genetic advance as percent of mean for various traits in periwinkle

Characters	Genetic parameters									
	Range		Mean	Components of variance			GCV%	PCV%	h^2 bs (%)	GAM (% of mean)
	Min.	Max.		σ^2_g	σ^2_p	σ^2_e				
Survival percentage	58.33	97.92	85.73	239.94	287.15	47.21	18.07	19.77	83.56	37.22
Plant height (cm) at 3 months	36.31	69.59	52.19	120.95	138.19	17.23	21.07	22.52	87.53	43.41
Plant height (cm) at 6 months	39.44	105.34	77.55	810.75	828.75	18.73	36.70	37.12	97.74	75.61
Plant height (cm) at 9 months	48.51	117.10	84.57	760.52	785.27	24.74	32.61	33.14	96.85	67.18
Plant spread (E-W) (cm) at 3 months	40.97	61.02	50.97	42.25	49.95	7.70	12.75	13.87	84.58	26.27
Plant spread (E-W) (cm) at 6 months	44.32	95.03	74.05	449.91	466.14	16.23	28.64	29.16	96.52	59.00
Plant spread (E-W) (cm) at 9 months	47.88	102.07	80.48	530.22	549.86	19.63	28.61	29.14	96.43	58.94
Plant spread (N-S) (cm) at 3 months	37.13	60.57	48.85	88.63	98.64	10.01	19.27	20.33	89.85	39.70
Plant spread (N-S) (cm) at 6 months	39.78	95.16	71.64	494.76	509.30	14.54	31.05	31.50	97.15	63.96
Plant spread (N-S) (cm) at 9 months	41.98	100.25	76.14	517.85	538.79	20.94	29.89	30.49	96.11	61.57
Number of primary branches per plant	2.30	4.40	3.39	0.66	0.70	0.04	23.98	24.72	94.09	49.40
Number of secondary branches per plant	14.10	36.20	26.68	88.52	94.93	6.41	35.26	36.51	93.24	72.63

σ^2g = Genotypic variance GCV = Genotypic coefficient of variation h^2 = Heritability (broad sense) GA = Genetic advance
σ^2p = Phenotypic variance PCV = phenotypic coefficient of variation GAM = Genetic advance as percentage of mean

Characters	Genetic parameters									
	Range		Mean	Components of variance			GCV%	PCV%	h^2 bs (%)	GAM (% of mean)
	Min.	Max.		σ_g^2	σ_p^2	σ_e^2				
Shoot length (cm)	29.64	89.71	62.33	654.17	669.78	15.61	41.03	41.52	97.67	84.53
Leaf area (cm^2)	5.82	8.75	7.23	0.45	0.98	0.53	9.29	13.69	46.08	19.14
Internodal distance (cm)	1.94	2.74	2.29	0.11	0.12	0.02	14.22	15.33	85.97	29.29
Fresh weight of shoot (g)	38.60	563.43	91.83	39510.44	41175.26	1664.82	74.26	75.80	95.96	152.97
Fresh weight of root (g)	9.20	91.83	54.58	1230.57	1254.74	24.17	64.27	64.89	98.07	132.39
Fresh weight of whole plant (g)	43.92	649.87	322.36	51569.73	53460.39	1890.66	70.75	71.73	96.46	145.12
Dry weight of shoot (g)	7.60	130.42	64.30	2027.52	2072.68	45.16	70.03	70.80	97.82	144.26
Dry weight of root (g)	2.19	21.71	12.60	71.46	73.92	2.47	67.11	68.25	96.66	138.24
Dry weight of whole plant (g)	10.07	149.19	76.86	2717.52	2769.23	51.71	67.83	68.47	98.13	139.72
Days to 50% flowering	15.50	37.00	23.45	46.76	51.62	4.86	29.15	30.63	90.58	60.06
Flower diameter (cm)	3.75	5.13	4.35	0.26	0.33	0.07	11.74	13.15	79.71	24.19
Flower length (cm)	2.26	2.90	2.60	0.02	0.04	0.02	5.98	7.97	56.34	12.32

σ^2g = Genotypic variance GCV = Genotypic coefficient of variation h^2 = Heritability (broad sense) GA = Genetic advance
σ^2p = Phenotypic variance PCV = phenotypic coefficient of variation GAM = Genetic advance as percentage of mean

Table 2: Genotypic correlation coefficients among different traits of periwinkle

Traits	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18
1	1																	
2	0.850**	1																
3	0.758**	0.989**	1															
4	0.466	0.796**	0.748**	1														
5	0.345	0.610*	0.647*	0.856**	1													
6	1.002**	0.889**	0.810**	0.532	0.378	1												
7	-0.032	0.471	0.489	0.926**	1.099**	0.054	1											
8	-0.131	-0.095	0.024	-0.221	0.052	-0.112	0.399	1										
9	-0.364	-0.364	-0.319	-0.522	-0.724*	-0.306	-0.663*	0.249	1									
10	0.467	0.409	0.444	0.035	0.117	0.468	-0.344	-0.211	0.010	1								
11	0.451	0.608*	0.551	0.853**	0.812**	0.464	0.642*	-0.502	-0.634*	0.145	1							
12	0.456	0.409	0.443	0.007	-0.023	0.494	0.124	0.666*	0.193	0.292	-0.396	1						
13	0.743**	0.916**	0.939**	0.716*	0.692*	0.768**	0.448	-0.065	-0.708*	0.349	0.653*	0.253	1					
14	0.674*	0.806**	0.743**	0.919**	0.854**	0.696*	0.735**	-0.150	-0.732*	0.098	0.845**	0.042	0.792**	1				
15	0.754**	0.924**	0.936**	0.768**	0.737**	0.779**	0.505	-0.080	-0.731*	0.321	0.704*	0.226	0.996**	0.847**	1			
16	0.798**	0.932**	0.931**	0.739**	0.707*	0.818**	0.405	-0.165	-0.650*	0.379	0.720*	0.195	0.985**	0.846**	0.992**	1		
17	0.717*	0.822**	0.722*	0.891**	0.715*	0.748**	0.622*	-0.165	-0.594	0.010	0.758**	0.100	0.735*	0.972**	0.792**	0.797**	1	
18	0.807**	0.941**	0.922**	0.786**	0.729*	0.829**	0.453	-0.168	-0.659*	0.329	0.746**	0.186	0.972**	0.890**	0.987**	0.995**	0.853**	1

**; Significant at $p<0.01$, *; Significant at $p<0.05$

Table 3: Phenotypic correlation coefficients among different traits of periwinkle

Traits	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18
1	1																	
2	0.811**	1																
3	0.738**	0.946**	1															
4	0.438*	0.732**	0.686**	1														
5	0.313	0.592**	0.615**	0.790**	1													
6	0.974**	0.869**	0.787**	0.494**	0.350*	1												
7	0.011	0.210	0.278	0.536**	0.531**	0.060	1											
8	-0.128	-0.088	0.004	-0.181	0.045	-0.103	0.208	1										
9	-0.214	-0.236	-0.249	-0.310	-0.509**	-0.183	-0.051	0.065	1									
10	0.430*	0.390*	0.442*	0.041	0.114	0.437*	-0.212	-0.197	-0.105	1								
11	0.413*	0.551**	0.520**	0.755**	0.748**	0.430*	0.334	-0.503**	-0.363*	0.159	1							
12	0.427*	0.394*	0.404*	-0.005	-0.011	0.463**	0.110	0.606**	0.146	0.253	-0.375*	1						
13	0.719**	0.877**	0.890**	0.648**	0.641**	0.724**	0.238	-0.052	-0.391*	0.294	0.539**	0.259	1					
14	0.659**	0.790**	0.711**	0.861**	0.831**	0.678**	0.404*	-0.137	-0.490**	0.090	0.784**	0.046	0.759**	1				
15	0.731**	0.891**	0.889**	0.699**	0.688**	0.739**	0.270	-0.069	-0.418*	0.271	0.588**	0.236	0.995**	0.818**	1			
16	0.785**	0.907**	0.901**	0.696**	0.680**	0.789**	0.214	-0.148	-0.433*	0.358*	0.650**	0.170	0.953**	0.825**	0.962**	1		
17	0.705**	0.791**	0.689**	0.823**	0.675**	0.713**	0.320	-0.142	-0.375*	-0.001	0.684**	0.088	0.705**	0.950**	0.763**	0.775**	1	
18	0.796**	0.917**	0.895**	0.740**	0.701**	0.801**	0.239	-0.152	-0.436*	0.311	0.676**	0.163	0.943**	0.872**	0.959**	0.995**	0.836**	1

**; Significant at $p<0.01$, *; Significant at $p<0.05$

Table 4: Direct and indirect genotypic effects of different characters on number of secondary branches per plant in periwinkle genotypes

Traits	1	2	3	4	6	7	8	9	10	11	12	13	14	15	16	17	18
1	-0.967	-0.475	-0.628	0.298	0.551	0.003	-0.039	-0.023	0.055	0.372	0.274	-3.692	-0.268	4.240	-17.644	-3.497	21.786
2	-0.821	-0.559	-0.819	0.509	0.489	-0.047	-0.028	-0.023	0.049	0.501	0.246	-4.550	-0.321	5.201	-20.608	-4.013	25.406
3	-0.733	-0.553	-0.829	0.478	0.445	-0.049	0.007	-0.020	0.053	0.454	0.266	-4.666	-0.296	5.264	-20.552	-3.523	24.899
4	-0.450	-0.445	-0.620	0.639	0.293	-0.092	-0.066	-0.033	0.004	0.703	0.004	-3.556	-0.366	4.322	-16.346	-4.350	21.216
6	-0.969	-0.497	-0.671	0.340	0.550	-0.005	-0.034	-0.020	0.056	0.383	0.297	-3.816	-0.277	4.381	-18.087	-3.649	22.397
7	0.031	-0.263	-0.405	0.592	0.030	-0.100	0.119	-0.042	-0.041	0.530	0.074	-2.226	-0.293	2.839	-8.953	-3.033	12.240
8	0.127	0.053	-0.020	-0.141	-0.062	-0.040	0.299	0.016	-0.025	-0.414	0.400	0.324	0.059	-0.448	3.650	0.807	-4.534
9	0.352	0.203	0.264	-0.334	-0.168	0.066	0.075	0.064	0.001	-0.522	0.116	3.515	0.291	-4.114	14.360	2.897	-17.791
10	-0.452	-0.229	-0.368	0.022	0.257	0.034	-0.063	0.001	0.119	0.119	0.176	-1.735	-0.039	1.804	-8.370	-0.046	8.886
11	-0.436	-0.340	-0.457	0.545	0.255	-0.064	-0.150	-0.041	0.017	0.824	-0.238	-3.242	-0.336	3.958	-15.923	-3.699	20.138
12	-0.440	-0.229	-0.367	0.004	0.271	-0.012	0.199	0.012	0.035	-0.326	0.601	-1.257	-0.017	1.271	-4.301	-0.486	5.020
13	-0.718	-0.512	-0.778	0.458	0.422	-0.045	-0.020	-0.045	0.041	0.538	0.152	-4.968	-0.315	5.601	-21.766	-3.586	26.233
14	-0.652	-0.451	-0.616	0.588	0.383	-0.073	-0.045	-0.047	0.012	0.696	0.025	-3.937	-0.398	4.765	-18.695	-4.745	24.044
15	-0.729	-0.517	-0.775	0.491	0.428	-0.050	-0.024	-0.047	0.038	0.580	0.136	-4.946	-0.337	5.626	-21.920	-3.867	26.651
16	-0.772	-0.521	-0.770	0.473	0.450	-0.040	-0.049	-0.042	0.045	0.594	0.117	-4.891	-0.336	5.578	-22.107	-3.892	26.872
17	-0.693	-0.460	-0.598	0.570	0.411	-0.062	-0.050	-0.038	0.001	0.625	0.060	-3.650	-0.387	4.457	-17.628	-4.881	23.036
18	-0.780	-0.526	-0.764	0.502	0.456	-0.045	-0.050	-0.042	0.039	0.615	0.112	-4.826	-0.354	5.552	-21.999	-4.164	27.004
Geno. Corr.	0.345	0.610*	0.647*	0.856**	0.378	1.099**	0.052	-0.724*	0.117	0.812**	-0.023	0.692*	0.854**	0.737**	0.707*	0.715*	0.729*

(Residual effect = -0.0064)

Notes: Indicating traits for Table 2, 3 and 4

1	Plant height (cm)
2	Plant spread (E-W) (cm)
3	Plant spread (N-S) (cm)
4	Number of primary branches per plant
5	Number of secondary branches per plant
6	Shoot length (cm)
7	Leaf area (cm^2)
8	Flower diameter (cm)
9	Flower length (cm)
10	Internodal distance (cm)
11	Survival percentage (%)
12	Days to 50% flowering
13	Fresh weight of shoot (g)
14	Fresh weight of root (g)
15	Fresh weight of whole plant (g)
16	Dry weight of shoot (g)
17	Dry weight of root (g)
18	Dry weight of whole plant (g)

Conclusion

The analysis of variance for eighteen characters with all the eleven genotypes showed wide differences among the genotypes, indicating sufficient amount of variability present in the material. The study for number of secondary branches per plant provides the association between component characters and suggests that while going for mere selection for number of secondary branches per plant improvement in periwinkle, the traits *viz.*, plant height, plant spread (N-S), plant spread (E-W), number of primary branches per plant, leaf area, survival percentage, fresh weight of shoot, fresh weight of root, fresh weight of whole plant, dry weight of shoot, dry weight of root and dry weight of whole plant recorded significant positive association at both genotypic and phenotypic levels should be taken into consideration. The maximum positive direct effect towards number of secondary branches per plant was exerted by dry weight of whole plant and was followed by fresh weight of whole plant, survival percentage, number of primary branches per plant, days to 50% flowering, shoot length, flower diameter, internodal distance and flower length. The magnitude of residual effect was negligible, which indicated that major portion of contribution towards number of secondary branches per plant might be explained on the basis of characters included in the present study

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