

International Journal of Statistics and Applied Mathematics

ISSN: 2456-1452
Maths 2024; SP-9(2): 10-14
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<https://www.mathsjournal.com>
Received: 15-12-2023
Accepted: 18-01-2024

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Coefficient of variation (GCV & PCV), heritability and genetic advance analysis for yield contributing characters in Rose (*Rosa* spp.)

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DOI: <https://doi.org/10.22271/math.2024.v9.i2Sa.1644>

Abstract

The present study was conducted to determine the GCV and PCV, Heritability and Genetic Advance for the yield contributing characters of Rose varieties. Eleven field rose varieties (Arka parimala, Arka pride, Arka savi, Arka sinchana, Arka swadesh, Seven days rose, Scent pink, Mirabel red, Roman red, Roman yellow and Mookuthi yellow) were selected for this study. Amongst all fourteen parameters studied, High PCV and GCV was recorded for the parameter number of flowers per sprout, number of petals per flower, number of flowers per plant, number of leaves per shoot, plant spread E-W. High heritability was observed in the parameters viz. Number of flowers per sprout, Number of petals per flower, Plant spread E-W, Petal length, Shelf life, Number of leaves per shoot, Number of flower per plant, Fresh weight of flower, Fully opened flower diameter, Plant height, Number of shoots per plant, Plant spread N-S, Flower stalk length, Days taken for flower bud initiation. High GAM was observed in the parameters viz. number of flowers per sprout, number of petals per flower, number of flowers per plant, number of leaves per shoot, plant spread E-W, flower stalk length, shelf life, petal length, plant spread N-S, fresh weight of flower, fully opened flower diameter, plant height, number of shoots per plant, days taken for flower bud initiation. For the analysed parameters the varieties, Mirabel red, Seven days rose, Scent pink, Arka parimala was recorded as the superior among all the eleven varieties.

Keywords: Field rose varieties, coefficient of variation and heritability

Introduction

Rose (*Rosa species*) belongs to the family Rosaceae is the most popular commercial flower crop. The word Rose is derived from the word 'Eros' which refers the Greek's love god. Indeed, the genus has been named as *Rosa* due to its fragrant blooms, which is also derived from the Greek word, Rhedon, that means excellent fragrance. *Rosa* spp. is a woody perennial flowering plant grown all over the world especially in the sub-tropical and temperate regions of the northern hemisphere (Nybom and Werlemrk, 2017) [1]. It is an erect shrub, climbing or trailing with short prickles on the stem. It is native to the temperate regions of northern hemisphere. Historical reports showed their cultivation in China, Western Asia and Northern Africa for the last 5000 years. They are mostly diploid and tetraploid with the basic chromosome number $n=7$. Roses are universally regarded as the "Queen of Flowers" and there are around ~ 200 species and > 18,000 cultivars of roses with different shape, sizes, colour and unique fragrance (Gudin, 2000) [2].

In India the demand for the production of rose is increasing day by day due to the expansion of the international flower trade and rose alone contributes the lion's share in flower market. In recent times, many producers are interested in cultivating new cultivars with improved technologies that can withstand the biotic and abiotic limiting factors and provide greater yield to sell them for higher prices. For any breeding improvement programme, study of genetic variation among the available germplasm and incorporating that data into the breeding program would enhance the process of evolving novel cultivars. The efficiency of selection program depends on the degree of genetic variation and heritability of a trait. Since the parameters contributing the yield of the plant were found to be mostly polygenic, it is

necessary to know the heritable portion of variation as it provides a measure of transmission of characters to the next generation. With the importance of this concern, the present investigation was undertaken to assess and estimate the nature and magnitude of variation among the eleven elite rose varieties with respect to vegetative and flower parameters which can be further utilized for breeding improvement programme.

Materials and Methods

The present investigation was conducted at Department of Floriculture and Landscape Architecture, Horticultural college and Research Institute, Coimbatore during the year 2021-2022. The experimental site is geographically situated at 11°02'N latitude and 76°93' E longitude and at an altitude of 355.68 meters above the mean sea level. The experiment was carried out in Randomized Block Design with 11 treatments replicated thrice with 10 plants in each replication. The varieties are Arka parimala, Arka pride, Arka savi, Arka sinchana, Arka swadesh, Seven days rose, Scent pink, Mirabel red, Roman red, Roman yellow and Mookuthi yellow. They were planted as per the design of layout at a spacing of 100×100 cm. All the intercultural operations were carried out as per blanket recommendation equally for all the treatments. Five randomly selected plants from each replication for fourteen parameters were selected.

The parameters recorded were quantitative characters namely plant height (cm), plant spread N-S (cm), plant spread E-W (cm), number of shoots per plant, number of leaves per shoot, days taken for flower bud initiation, fully opened flower diameter (cm), fresh weight of flower (g), petal length (cm), number of petals per flower, flower stalk length (cm), shelf life (days), number of flowers per sprout and number of flowers per plant.

Genetic Variability, Heritability and Genetic Advance

The presence of higher variability results in the evolution of new line with better characteristics. The importance of genetic variability was reported earlier by Vavilov (1951) who stated that the wide range of variability is important for selecting the desirable genotype. Greater the genetic variability greater will be the probability of producing recombinants. Hence studies on genetic variability helps in the selection of diverse and desirable parents for further improvement.

Genetic parameters like variability, GCV, PCV, Heritability and Genetic advance as percent of mean were calculated by using the following formula and TNAU STAT software.

Estimation of variance component

By using the formula given by Johnson *et al.* (1955) [4], the genotypic and phenotypic variances were calculated.

$$\text{Genotypic variance } (\sigma^2 g) = \frac{M_1 - M_2}{r}$$

Where,

M_1 = Mean sum of squares for genotypes

M_2 = Mean sum of squares for error

r = Number of replications

$$\text{Phenotypic variance } (\sigma^2 p) = (\sigma^2 g + \sigma^2 e)$$

Where,

$\sigma^2 g$ = Genotypic variance

$\sigma^2 e$ = Error variance

Estimation of Co-efficient of variation

The phenotypic and genotypic coefficients of variation were calculated using the Burton and Devane (1953) [5] formula.

$$\text{PCV} = \frac{\sqrt{\sigma^2 p}}{\text{General Mean}} \times 100$$

$$\text{GCV} = \frac{\sqrt{\sigma^2 g}}{\text{General Mean}} \times 100$$

Where,

$\sigma^2 p$ = Phenotypic variance

$\sigma^2 g$ = Genotypic variance

The values of PCV and GCV were classified as per Sivasubramanian and Madhavamenon (1973) [6]

Less than 10 percent = Low

10 – 20 = Moderate

More than 20 percent = High

Estimation of Heritability

By using the method of Lush (1940) [7], Hanson *et al.* (1956) [8] heritability (h^2) was calculated and expressed as percent.

$$\text{Heritability} = \frac{\text{Genotypic variance}}{\text{Phenotypic variance}} \times 100$$

The values of heritability percent was classified as per Johnson *et al.* (1955) [4]

0 to 30 percent = Low

31 to 60 percent = Moderate

Above 60 percent = High

Estimation of Genetic Advance

By using the formula given by Johnson *et al.* (1955) [4], genetic advance was calculated.

$$\text{GA} = h^2 k \sigma p$$

Where,

GA = Genetic advance

h^2 = Heritability in broad sense

k = Selection differential which is equal to 2.06 at 5% intensity of selection (Lush, 1940)

σp = Phenotypic standard deviation

By using the method given by Johnson *et al.* (1955) [4], genetic advance as percent mean was calculated.

$$\text{Genetic advance as percent mean} = \frac{\text{GA}}{\text{GM}} \times 100$$

Where,

GA = Genetic advance

GM = Genetic mean

The values of Genetic advance are classified as per the method of Johnson *et al.* (1955) [4].

Less than 10 percent = Low

10 – 20 percent = Moderate

More than 20 percent = High

Results

Phenotypic variation

From the results detailed in the Table 1, Phenotypic variation showed the range of 0.24 to 807.52 and the greatest

phenotypic variation (807.52) was observed in number of leaves per shoot followed by number of petals per flower (398.63), plant spread E-W (148.61), plant spread N-S (123.46), number of flowers per plant (73.23).

Genotypic variation

The Genotypic variation ranged from 0.23 to 798.24 and similarly to the Phenotypic variation, the greatest Genotypic variation (798.24) was observed in number of leaves per shoot followed by number of petals per flower (396.34), plant spread E-W (147.36), plant spread N-S (116.19), number of flowers per plant (72.26)

Phenotypic and Genotypic Coefficient of Variation

Phenotypic and Genotypic Coefficient of Variation were

estimated from the corresponding variances of these parameters. The result revealed that Phenotypic Coefficient of Variation (PCV) was higher than the corresponding Genotypic Coefficient of Variation for all the fourteen parameters studied. Phenotypic Coefficient of Variation (PCV) showed the values from medium to high category (i.e., 13.81 to 66.83). High PCV was observed for the parameters viz., number of flowers per sprout (66.83%), number of petals per flower (44.46%), number of flowers per plant (40.18%), number of leaves per shoot (33.87%), plant spread E-W (31.71%), shelf life (28.84%), plant spread n-s (28.79%), petal length (27.99%) and flower stalk length (27.36%). Moderate PCV was noted for the parameters viz., fresh weight of flower (19.84%), fully opened flower diameter.

Table 1: Phenotypic Variance, Genotypic Variance, Phenotypic Coefficient of Variation (PCV), Genotypic Coefficient of Variation (GCV), Heritability and Genetic Advance as percent mean for growth and yield characters of the evaluated rose varieties.

S. No	Characters	PV	GV	PCV (%)	GCV (%)	H ² (%)	GA (%) MEAN
1	Plant height	68.24	66.65	17.61	17.40	97.67	35.43
2	Plant spread N-S	123.46	116.19	28.79	27.93	94.11	55.81
3	Plant spread E-W	148.61	147.36	31.71	31.57	99.16	64.76
4	Number of shoots per plant	0.67	0.64	15.67	15.36	96.06	31.00
5	Number of leaves per shoot	807.52	798.24	33.87	33.68	98.85	68.98
6	Days taken for flower bud initiation	3.70	2.82	13.81	12.05	76.11	21.65
7	Fully opened flower diameter	1.02	1.00	19.05	18.85	97.91	38.43
8	Fresh weight of flower	0.24	0.23	19.84	19.65	98.12	40.11
9	Petal length	0.52	0.52	27.99	27.87	99.16	57.17
10	Number of petals per flower	398.63	396.34	44.46	44.33	99.43	91.06
11	Flower stalk length	0.88	0.69	27.36	24.24	78.45	44.23
12	Shelf life	0.99	0.98	28.84	28.70	99.06	58.85
13	Number of flowers per sprout	9.20	9.18	66.83	66.77	99.80	137.40
14	Number of flowers per plant	73.23	72.26	40.18	39.91	98.68	81.67

(19.05%), plant height (17.61%), number of shoots per plant (15.67%) and days taken for flower bud initiation (13.81%).

Genotypic Coefficient of Variation (GCV) showed the values from Medium to High category (i.e., 12.05 to 66.77). High GCV was observed for the parameters viz., number of flowers per sprout (66.77%), number of petals per flower (44.33%), number of flowers per plant (39.91%), number of leaves per shoot (33.68%), plant spread E-W (31.57%), shelf life (28.70%), plant spread N-S (27.93%), petal length (27.87%), flower stalk length (24.24%). Moderate PCV was noted for the parameters fresh weight of flower (19.65%), fully opened flower diameter (18.85%), plant height (17.40%), number of shoots per plant (15.36%) and days taken for flower bud initiation (12.05%).

Amongst all fourteen parameters studied, High PCV and GCV was noted for the parameter number of flowers per sprout (66.83% and 66.77%), number of petals per flower (44.46% and 44.33%), number of flowers per plant (40.18% and 39.91%), number of leaves per shoot (33.87% and 33.68%) and plant spread E-W (31.71% and 27.93%).

Heritability and Genetic Advance

The estimated data on heritability and genetic advance as percent mean for all the fourteen parameters of the evaluated field rose varieties is given in the Table 16. From the estimated results, heritability values ranged from 76.11% to 99.80%. High heritability was observed for the parameters viz., number of flowers per sprout (99.80%), number of petals per flower (99.43%), plant spread E-W (99.16%), petal length (99.16%), shelf life (99.06%), number of leaves per shoot (98.85%), number of flower per plant (98.68%), fresh weight of flower (98.12%), fully opened flower diameter (97.91%),

plant height (97.67%), number of shoots per plant (96.06%), plant spread N-S (94.11%), flower stalk length (78.45%) and days taken for flower bud initiation (76.11%).

Genetic advance as percent mean values ranged from 21.65% to 137.40%, high GAM was observed in the parameters viz., number of flowers per sprout (137.40%), number of petals per flower (91.06%), number of flower per plant (81.67%), number of leaves per shoot (68.98%), plant spread E-W (64.76%), flower stalk length (58.85%), shelf life (58.85%), petal length (57.17%), plant spread N-S (55.81%), fresh weight of flower (40.11%), fully opened flower diameter (38.43%), plant height (35.43%), number of shoots per plant (31.00%) and days taken for flower bud initiation (21.65%).

It was revealed that high heritability combined with high genetic advance as per mean was observed for the parameters viz. number of flowers per sprout (99.80% and 137.40%), number of petals per flower (99.43% and 91.06%), plant spread E-W (99.16% and 64.76%), petal length (99.16% and 57.17%), shelf life (99.06% and 58.85%), number of leaves per shoot (98.85% and 68.98%) and number of flower per plant (98.68% and 81.67%).

Discussion

Genetic variability

The basic requirement for any crop improvement program is the information on genetic variability and divergence of the available germplasm. The presence of higher variability results in evolution of new line with better characteristics. Hence studies on genetic variability helps in the selection of diverse and desirable parents for further improvement. Analysis of variance represents significant difference for each trait among all the varieties. The extent of the variability

among the evaluated rose varieties was studied through variance, PCV, GCV, Heritability and GAM. The phenotypic and genotypic variance measures the magnitude of variation due to the differences in phenotypic and genotypic values. The phenotypic and genotypic variance are converted into Phenotypic and Genotypic coefficient of variation to compare the magnitude of variability of various growth and yield parameters as their absolute values cannot be used for comparison (Naikwad *et al.*, 2018) ^[9].

In our present study, large amount of phenotypic and genotypic variations was observed for the characters namely number of leaves per shoot, number of petals per flower, plant spread E-W, plant spread N-S, number of flowers per plant. Hence there is an ample scope for improvement program through selection of these characters. These findings agreed with Soujanya *et al.*, (2018) ^[10] who reported wide variability for plant height, plant spread, days taken to bud initiation, number of flowers per plant and number of petals per flower.

The estimates of PCV and GCV gave a clear picture of amount of variation present in the evaluated varieties. Amongst all fourteen parameters studied, High PCV and GCV was recorded for the parameter number of flowers per sprout, number of petals per flower, number of flowers per plant, number of leaves per shoot, plant spread E-W. For all the fourteen characters studied, PCV was greater in magnitude than GCV and the difference between them was also in narrow range for many parameters. Thus, it indicated that these selected traits were less influenced by environment factors. PCV and GCV values varied in magnitude for each parameter either as moderate or high range values. The results were found in accordance with the findings of Verma *et al.*, 2002 ^[11]; Zeynali *et al.*, 2009 ^[12]; Jogdande *et al.*, 2017 ^[13]; Soujanya *et al.*, 2019 ^[10] in rose.

High PCV was noted for the parameters number of flowers per sprout, number of petals per flower, number of flowers per plant, number of leaves per shoot, plant spread E-W, shelf life, plant spread N-S, petal length and flower stalk length. Moderate PCV was noted for the parameters fresh weight of flower, fully opened flower diameter, plant height, number of shoots per plant, days taken for flower bud initiation. High GCV was noted for the parameters *viz.* number of flowers per sprout, number of petals per flower, number of flowers per plant, number of leaves per shoot, plant spread E-W, shelf life, plant spread N-S, petal length, flower stalk length. Moderate PCV was noted for the parameters fresh weight of flower, fully opened flower diameter, plant height, number of shoots per plant and days taken for flower bud initiation.

Amongst all fourteen parameters studied, High PCV and GCV was noted for the parameter number of flowers per sprout, number of petals per flower, number of flowers per plant, number of leaves per shoot and plant spread E-W.

Heritability and Genetic advance

The estimate of heritability represents the measure of transmission of heritable characters from one generation to the next generation. The magnitude of heritability has a close bearing on response to selection (Panse and Sukhatme, 1957) ^[14]. It clearly defines the heritable portion of the variability thus it is very much needed for the elite selection of the breeding programs. Heritability in combination with the genetic advance increases the efficiency of the selection in breeding program by determining the influence of environment and additive gene action (Johnson *et al.*, 1955) ^[4].

In this present study, all the fourteen characters showed high heritability in the range of 76.11% to 99.80%. High

heritability was observed in the parameters *viz.* Number of flowers per sprout, Number of petals per flower, Plant spread E-W, Petal length, Shelf life, Number of leaves per shoot, Number of flowers per plant, Fresh weight of flower, fully opened flower diameter, Plant height, Number of shoots per plant, Plant spread N-S, Flower stalk length, Days taken for flower bud initiation. These findings found great similarity to the study of Sewaniya, 2009 who reported more than 77% heritability for all the characters they have studied. The obtained high heritability was strongly supported by the findings of Palai *et al.*, 2003 ^[15]; Jogdande *et al.*, 2017 ^[13]; Soujanya *et al.*, 2019 ^[10]; Suganthi, 2019 ^[16] in rose, Mohapatra *et al.*, 2000 ^[17] in chrysanthemum, Naikwad *et al.*, 2018 ^[9] in china aster.

High GAM was observed in the parameters *viz.* number of flowers per sprout, number of petals per flower, number of flowers per plant, number of leaves per shoot, plant spread E-W, flower stalk length, shelf life, petal length, plant spread N-S, fresh weight of flower, fully opened flower diameter, plant height, number of shoots per plant, days taken for flower bud initiation. These results were found in accordance to the findings of Sewaniya, 2009 ^[18], Janaki *et al.*, 2015 ^[19]; Jogdande *et al.*, 2017 ^[13]; Soujanya *et al.*, 2018 ^[10] in rose. Verma *et al.*, 2002 ^[11] reported the highest GAM of 203% for the parameter thorn density in rose strongly supported the obtained results. Vijayalaxmi *et al.* 2022 ^[20] reported that the number of flowers per bunch at 285 DAP, flower diameter at 345 DAP, flower length at 285 DAP, plant spread at 345 DAP, number of branches at 285 DAP, and plant height at 225 DAP were the genotypic factors that most positively influenced flower production per plant.

The utility of the heritability estimates is restricted as they are influenced by the environment, genetic material and other factors. Hence heritability in combination with genetic advance provides a reliable index of the selection value (Johnson *et al.*, 1955) ^[4]. In our present study all the fourteen parameters showed high heritability coupled with high genetic advance *viz.* number of flowers per sprout, number of petals per flower, number of flowers per plant, number of leaves per shoot, plant spread E-W, flower stalk length, shelf life, petal length, plant spread N-S, fresh weight of flower, fully opened flower diameter, plant height, number of shoots per plant, days taken for flower bud initiation. This finding was found in similarity to the reports of Jogdande *et al.*, 2017 ^[13]; Soujanya, 2018 ^[10]; Suganthi, 2019 ^[16]; Philip *et al.*, 2020 ^[21] in rose and Naikwad *et al.*, 2018 ^[9] in china aster. The high heritability along with high GAM indicated that the heritability is due to additive gene effect and hence the selection based on these characters will be more effective. This result was found in agreement with the results of Verma *et al.*, 2002 ^[11]; Gogoi *et al.*, 2016 ^[22]; Philip *et al.*, 2020 ^[21] in rose.

Conclusion

From the various aspects of the genetic parameters PCV, GCV, heritability and GAM, it could be concluded that all the parameters of the evaluated field rose varieties *viz.*, number of flowers per sprout, number of petals per flower, number of flowers per plant, number of leaves per shoot, plant spread E-W, flower stalk length, shelf life, petal length, plant spread N-S, fresh weight of flower, fully opened flower diameter, plant height, number of shoots per plant, days taken for flower bud initiation provides a wide scope for the selection program. The high heritability coupled with high GAM offers a wide selection to improve the next generation (Philip *et al.*, 2020) ^[21]. It was concluded that the selection of genotypes based on

the parameters viz. number of flowers per sprout, number of petals per flower, plant spread E-W, petal length, shelf life, number of leaves per shoot and number of flowers per plant. For these parameters the varieties, Mirabel red, Seven days rose, Scent pink, Arka parimala was recorded as the superior and hence these varieties can be further used for improvement and new evolution breeding programs in future.

Acknowledgement

The author acknowledge the Department of Floriculture and Landscape Architecture, TNAU, Coimbatore for providing adequate research facilities.

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