International Journal of Farm Sciences **15(1):** 1-5, 2025; **doi: 10.5958/2250-0499.2025.00001.8**

Genetic variability in hibiscus (*Hibiscus rosa-sinensis* L)

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Received: 11.06.2024/Accepted: 11.08.2024

ABSTRACT

The study analyzed genetic variability, heritability and genetic advance in *Hibiscus rosa-sinensis* L. Significant treatment differences were observed across all traits, with flower number per plant ranging from 13.00 to 74.00 (mean 33.67), plant height from 52.24 to 247.68 cm and flower weight per plant from 164.96 to 4,925.24 g. Phenotypic coefficient of variation (PCV) exceeded genotypic coefficient (GCV), indicating environmental influence. High GCV and PCV were recorded for flower weight per plant (GCV 94.94, PCV 96.65), petal number (GCV 81.26, PCV 82.33) and flower weight (GCV 76.67, PCV 77.25), signifying substantial genetic diversity. Heritability ranged from 47.32 per cent (secondary branches/plant) to 99.61 per cent (flower longevity), with high values for flower weight (98.51%), flowering initiation (98.34%) and petal number (97.43%). Genetic advance was highest for flower weight per plant (2,190.86), plant height (75.67) and flowering initiation (74.72). Traits like flower weight, pedicel length and plant spread exhibited high heritability and genetic advance, suggesting additive gene action and potential for improvement through simple selection. These findings highlight significant genetic variability and inform breeding strategies for *H rosa-sinensis*.

Keywords: Hibiscus; GCV; PCV; genetic variability; heritability; genetic advance

INTRODUCTION

Hibiscus rosa-sinensis L is a perennial shrub belonging to the family Malvaceae and genus *Hibiscus*. The species of genus *Hibiscus* are native to tropical and south Asia and are widely distributed in different regions of the world. Many hibiscus species are mostly cultivated as ornamental plants (Lowry 1976). They produce vibrantly coloured showy flowers throughout the year. Various cultivars are having flowers (single or double) in shades of red, peach, white, pink and orange (Gilman 1999). Hibiscus has medicinal properties and takes part as a primary ingredient in many herbal teas. The red flowered variety is preferred in medicine (Khristi and Patel 2016).

The genus *Hibiscus* is believed to possess around more than 300 species (Braglia et al 2010). It is native of tropical Asia (Vietnam and south China). Out of 300 species, four main species of hibiscus are having ornamental value and are cultivated in tropics and sub-tropics viz are *Hibiscus rosa-sinensis* L, *H mutabilis* L, *H syriacus* L and *H schizopetalus* Hook. Among these species, *H rosa-sinensis* is with most beautiful flowers and is widely cultivated in India. It is also called the shoe flower or Chinese rose (Shandilya and Pathak 2021). *H rosa-sinensis* is a medium to tall shrub. Its leaves are oval or elliptic, dark green with pointed apex and serrated margins.

Analysis of variance for each character helps in meaningful comparison of variation of several traits of plants within population or comparison of variation of same trait as expressed by different populations of the same or different crops (Panse and Sukhatme1985). The genotypic coefficient of variance (GCV) and phenotypic coefficient of variance (PCV) measure the extent of variation present in the population in the particular character (Patel et al 2021). Heritability is a good indicator of transmission of characters from parents to the progeny. The estimates of heritability help the plant breeder in selection of genotypes from diverse genetic populations. Therefore, high heritability helps in effective selection for a particular character. The genetic advance is a useful indicator of the effective and efficient selection progress that can be expected as result of exercising selection on the base population (Terfa and Gurmu 2020). Heritability and genetic advance of the individual trait are the major factors determining the efficiency by which the genotypic variability can be utilized through selection (Bilgin et al 2010). Therefore, keeping the above points in view, present study was undertaken to find out the genetic variability in *H rosa-sinensis* L.

MATERIAL and METHODS

The experiment was conducted at the horticulture section of College of Agriculture, Pune, Maharashtra in RBD with two replications. The experimental material consisted of 20 genetically diverse genotypes of *H rosa-sinensis*. Each plot contained six plants spaced at 1.8 m × 1.0 m. All cultural practices and application of fertilizers were common for all the varieties. The recommended cultural practices like weeding, irrigation and plant protection measures were followed as and when required during the growth period of the crop. Three plants per treatment were used for recording the observations. The plant growth characters viz plant height, number of primary and secondary branches per plant, plant spread (EW and NS), stem colour, leaf shape, leaf margin type, leaf and leaf venation colour; duration attributes like days to flower bud initiation, days to anthesis and bloom period and flower characters like flower bud length, flower diameter, number of petals per flower, number of flowers per plant, flower colour, average flower weight, flower weight per plant, pedicel length and its colour, style length, number of stigma lobes and presence of eyes and their colour were recorded. The analysis of variance was done as suggested by Panse and Sukhatme (1985). The variability of each quantitative trait was estimated by simple measures such as mean, range, standard deviation, phenotypic and genotypic variances and coefficients of variation. The PCV and GCV were computed as per Burton and DeVane (1953).

RESULTS and DISCUSSION

Analysis of variance in *H rosa-sinensis* L is indicated in Table 1. Significant treatment differences indicated appreciable amount of variability for all the characters studied (Table 2).

The variability for number of flowers per plant (yield) ranged between 13.00 and 74.00 with mean of 33.67. Likewise other growth, duration, yield and flower quality attributes showed wide range of variability viz plant height (52.24-247.68 cm), East-West plant spread (27.75-143.76 cm), North-South plant spread (25.98-127.75 cm), number of primary branches per plant (3.33-19.50) and number of secondary branches per plant (2.66-15.50). The number of nodes at which first flower appeared range was from 12.93 to 43.76, days to flower bud initiation from planting from 88.00 to 194.50 and days to anthesis from flower bud initiation from 15.66 to 28.16. Pedicel length was from 12.73 to 103.20 mm, flower bud length from 2.46 to 3.57 cm, flower weight from 8.88 to 113.24 g, style length from 19.23 to 71.35 mm, flower weight per plant from 164.96 to 4,925.24 g, flower diameter from 4.45 to 15.72 cm, number of petals per flower from 5.00 to 37.00 and flower longevity from 8.13 to 16.83 h.

The estimates of PCV were magnitudinally higher than the estimates of GCV for all the characters studied indicating the influence of environmental factors on these traits. The estimates of GCV and PCV were of high magnitude for flower weight per plant (GCV = 94.94, PCV = 96.65), number of petals per flower (GCV = 81.26, PCV = 82.33) and flower weight (GCV = 76.67, PCV = 77.25), indicating good amount of variability for these characters. The selection for these traits would be effective and would have high scope for improvement.

High heritability indicates the effectiveness of selection based on phenotypic performance, but does not necessarily mean a high genetic gain for a particular trait. The characters with high genetic gain may be attributed to the additive gene effects (Panse and Sukhatme 1985) which can easily be improved by simple selection. On the other hand, high heritability and low genetic advance may be attributed to non-additive gene action and such characters may be improved by hybridization. Burton (1952) suggested that through GCV, the heritable variation cannot be estimated as GCV together with heritability would furnish most reliable information on the amount of genetic advance to be expected for selection.

In the present investigations, the heritability estimates varied between 47.32 (number of secondary

Table 1. Analysis of variance in *Hibiscus rosa-sinensis* L

Character	Mean sum of squares		
	Replication (1)	Treatments (19)	Errors (19)
Plant height (cm)	104.491	3,967.653**	496.680
Plant spread E-W (cm)	65.613	1,420.282**	117.411
Plant spread N-S (cm)	0.689	1,067.078**	120.450
Number of primary branches/plant	2.347	25.867**	3.383
Number secondary of branches/plant	0.131	22.550*	8.063
Days to flower bud initiation from planting	193.600	2,698.268**	22.547
Days to anthesis	0.025	19.642**	1.867
Flower longevity (h)	0.021	11.526**	0.023
Flower bud length (cm)	0.040	0.215**	0.066
Number of nodes at first flower appearance	47.067	132.819**	23.473
Flower diameter (cm)	0.116	12.216**	0.439
Number of petals/flower	152.100	153.179**	1.995
Number of flowers/plant	0.025	570.488**	22.078
Flower weight (g)	0.227	1,326.775**	9.98
Flower weight/plant (g)	1,657.373	2,387,037.787**	42,620.712
Pedicel length (mm)	0.529	779.123**	21.471
Style length (mm)	10.032	362.694**	9.176

Figures in parentheses indicate degrees of freedom; *Significant at 5% LoS, **Significant at 1% LoS

Table 2. Range, general mean, PCV, GCV, heritability and GA of 17 characters of *Hibiscus rosa-sinensis* L

Character	Range	Mean	GCV	PCV	Heritability (%)	GA	GA % of mean
Flower weight (g)	8.88-113.24	33.47	76.67	77.25	98.51	52.46	156.20
Pedicel length (mm)	12.73-103.20	43.12	45.14	46.40	94.64	39.01	90.47
Style length (mm)	19.23-71.35	45.42	29.27	30.02	95.06	26.70	58.79
Number of flowers/ plant	13.00-74.00	33.67	49.17	51.11	92.55	32.82	97.45
Flower weight/ plant (g)	164.96-4,925.24	1,140.34	94.94	96.65	96.49	2,190.86	192.12
Days to flower bud initiation from planting	88.00-194.50	134.65	27.16	27.39	98.34	74.72	55.49
Flower longevity (h)	8.13-16.83	10.71	22.39	22.43	99.61	4.93	46.03
Flower diameter (cm)	4.45-15.72	8.23	29.47	30.55	93.07	4.82	58.57
Days to anthesis from flower bud initiation	15.66-28.16	20.20	14.75	16.23	82.64	5.58	27.63
Flower bud length (cm)	2.46-3.57	3.02	9.023	12.42	52.73	0.41	13.50
Number of nodes at first flower appearance	12.93-43.76	21.19	34.89	41.72	69.96	12.74	60.12
Number of petals/ flower	5.00-37.00	10.70	81.26	82.33	97.43	17.68	165.22
Plant height (cm)	52.24-247.68	103.89	40.10	45.48	77.75	75.67	72.84
East-West plant spread (cm)	27.75-143.76	54.67	46.683	50.72	84.73	48.40	88.52
North-South plant spread (cm)	25.98-127.75	52.02	41.825	46.84	79.71	40.01	76.93
Number of primary branches/plant	3.33-19.50	8.44	39.735	45.32	76.870	6.06	71.76
Number of secondary branches/plant	2.66-15.50	7.12	37.791	54.93	47.32	3.81	53.55

GCV: Genotypic coefficient of variance, PCV: Phenotypic coefficient of variance branches/plant) to 99.61 (flower longevity) per cent. The flower weight, days to flower bud initiation from planting and number of petals per flower recorded heritability of 98.51, 98.34 and 97.43 per cent respectively. The flower weight per plant, style length, pedicel length, flower diameter and number of flowers per plant recorded heritability of 96.49, 95.06, 94.64, 93.07 and 92.55 per cent respectively.

The character, flower weight per plant (2,190.86) exhibited highest genetic advance followed by plant height (75.67) and days to flower bud initiation from planting (74.72). The lowest genetic gain was exhibited by characters viz flower bud length (0.41), number of secondary branches per plant (3.81) flower diameter (4.82) and flower longevity (4.93). The estimates of genetic advance as percentage of mean were higher for flower weight per plant (192.12) followed by number of petals per flower (165.22), flower weight (156.20), number of flowers per plant (97.45), pedicel length (90.47) and East-West plant spread (88.52).

The characters, flower weight, pedicle length, style length, number of flowers per plant, days to flower bud initiation from planting, plant height, East-West and North-South plant spread recorded high genetic advance coupled with high heritability. Very high heritability and high genetic advance of these characters suggested environment having additive genetic control indicating that simple selection is sufficient for selection of better genotypes.

It may, therefore, be suggested that the characteristics flower weight per plant, days to flower bud initiation from planting, E-W and N-S plant spread, plant height, flower weight, pedicle length, number of flowers per plants and style length in present study were likely to be operated by additive gene action generation and, on the other hand, characters like number of petals per flower and number of nodes at which first flower appeared, number of primary and secondary branches per plant, flower longevity, flower diameter, days to anthesis of flower from bud initiation and flower bud length were operated by non-additive gene action.

Allen et al (2019) observed high genotypic and phenotypic coefficients of variance for characters like leaf area, petal width, style length, leaf length, flower diameter and single flower weight in *H rosa-sinensis* genotypes. Flower yield was found to be positively related with floral parameters like petal length, petal width, style length and single flower weight.

Ullah (2024) evaluated five Roselle genotypes in Bangladesh and analysis of variance indicated significant differences among the five genotypes for most of the characters studied. The PCV was higher than the corresponding GCV for all the studied traits. Phenotypic as well as genotypic coefficients of variability were high for the trait branches per plant (75.92 and 77.81% respectively). High heritability estimates (>0.70) were recorded for plant height, leaves per plant, branches per plant, fruit length, calyces per fruit and fruit weight. Medium heritability coupled with a high expected genetic gain was observed for leaves per plant. The highest genetic advance as per cent of mean was also observed in branches per plant (152.59%).

Seemanthini et al (2022) evaluated thirty *H rosa-sinensis* genotypes and observed high heritability for the characters, plant height, number of primary and secondary branches per plant, leaf area, days to bud initiation, days taken to flowering, flower longevity, pedicel length, petal length, petal width and style length.

Tetteh et al (2019) investigated distribution and diversity in twenty five Roselle accessions of northern Ghana. The most variable traits, plant height and branch number, varied from 184 to 284 cm with six accessions HA-44, HA-47, HA-43, HA-38, HA-52 and HA-42 having the tallest plants and least basal branching of four. Mean flowering time was between 96 and 104 days.

Ahmed et al (2022) observed twenty five genotypes of Kenaf (*H cannabinus* L) in Bangladesh and observed significant variation for all the characters among the genotypes. High heritability (>85%) coupled with high genetic advance in per cent of mean was observed for most of the traits.

Varma et al (2022) recorded substantial amount of genetic variability in 110 Mesta (*Hibiscus* spp) genotypes for all the characters studied. The estimates of GCV and PCV were high for some characters. High heritability estimates were observed for all the traits. However, high genetic advance as per cent of mean was noted for all the characters except for days to maturity, where it was moderate.

CONCLUSION

In this study, the observed high heritability and genetic advance for flower weight per plant, days to flower bud initiation, plant spread, plant height, flower weight, pedicel length, number of flowers and style length indicate that these traits were primarily influenced by additive gene action, suggesting that simple selection methods could effectively improve these characteristics. Conversely, traits such as petal number, node number at first flowering, branching, flower longevity, flower diameter, days to anthesis and flower bud length, showing high heritability but lower genetic advance, were likely governed by non-additive gene action, necessitating more complex breeding strategies like hybridization for their enhancement.

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