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International Journal of Biological Innovations
http://ijbi.org.in | http://www.gesa.org.in/journals.php
https://doi.org/10.46505/IJBI.2025.7214
IJBI 7(2): 221-229 **(2025)**
E-ISSN: 2582-1032

HERITABILITY, GENETIC ADVANCE AND COVARIANCE STUDIES IN HYBRID TEA ROSES

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Article Info:
Research article
Received
13.07.2025
Reviewed
27.08.2025
Accepted
15.09.2025

Abstract: This study presents a comprehensive analysis of genetic parameters in Hybrid Tea (HT) roses, examining 18 morphological and reproductive traits. Fifty varieties were evaluated during 2022-23 and 2023-24 in a randomized block design with three replications. The results were based on pooled data obtained from both years. The research evaluates phenotypic covariance, genotypic covariance, heritability, and genetic advance to assess the genetic potential for improvement in rose breeding programs. The results showed exceptionally high heritability (>90%) for key traits such as plant height (93.52%), flower bud diameter (94.85%), number of flowers per plant (90.64%), flower length (90.22%), flower diameter (90.64%), petal width (93.66%), and pollen viability (92.08%). Stem diameter (87.13%), flower weight (79.63%), number of petals (76.35%), and pollen sterility (76.24%) exhibited moderate to high heritability. The highest genetic advance as a percentage of the mean was observed for plant height (12.23%), followed by stem diameter (0.74%) and branch length (0.66%). These findings indicate substantial genetic variability and potential for selection in HT roses, with particular emphasis on plant architecture, flower characteristics, and reproductive traits. The study provides valuable insights for rose breeders to develop superior cultivars with enhanced ornamental and commercial value.

Keywords: Genetic advance, Genotypic covariance, Heritability, HT roses, Plant breeding, Traits.

Cite this article as: Singh Ranjit and Arya Sunita (2025). Heritability, Genetic advance and Covariance studies in Hybrid Tea Roses. *International Journal of Biological Innovations*. 7(2): 221-229. https://doi.org/10.46505/IJBI.2025.7214

INTRODUCTION

Rose (*Rosa*) species represent one of the most economically important ornamental crops across the globe, with Hybrid Tea (HT) roses being particularly valued for their large, elegant flowers and long stems, making them ideal for cut flower production and landscape applications. The global rose industry has experienced continuous growth, driven by increasing demand for high-quality flowers in both domestic as well as international markets. Understanding the genetic basis of important traits in HT roses is crucial for developing new improved cultivars and varieties that meet consumer preferences and industry requirements. Rose yield is influenced by insect pests, which interact with plant traits like height, leaf texture, and flower compactness (Arya and Sachan, 2023). Traits such as dense petals or glossy leaves can either attract or deter pests, directly affecting flower quality and overall productivity (Arya, 2018a).

Plant breeding programs rely heavily on genetic parameters to make informed decisions about selection strategies and breeding methods. However, it is badly affected by pollution and excessive human activities (Prakash and Verma, 2022; Singh *et al.,* 2023). Heritability estimates provide a good insight into the proportion of phenotypic variation that is attributable to genetic factors, while genetic advance indicates the expected improvement from selection. These parameters are fundamental in determining the most effective breeding approaches and predicting the success of the selection program. HT roses exhibit considerable variation in morphological and reproductive traits, including plant architecture, flower characteristics, and pollen fertility. The complex inheritance patterns of these traits necessitate comprehensive genetic analysis to optimize breeding strategies.

A number of studies have shown that many ornamental traits in roses are quantitatively inherited, involving multiple genes with small additive effects. This complexity makes genetic parameter estimation essential for successful breeding programs. The evaluation of genetic covariance alongside heritability provides a more complete understanding of trait relationships and their high potential for simultaneous improvement. High genetic covariance between traits can facilitate correlated response to selection, while understanding the genetic basis of individual traits helps in setting realistic breeding objectives. This study aims to evaluate the genetic parameters of eighteen important morphological and reproductive traits in HT roses, providing valuable information for breeders and researchers working on rose improvement.

Genetic analysis in roses has been an active area of research for several decades, with numerous studies focusing on various aspects of rose genetics and breeding. Early work by Cairns (1960) and later investigations by Gudin (2000) established the foundation for understanding inheritance patterns in roses. These studies revealed that most economically important traits in roses are quantitatively inherited, controlled by multiple genes with additive effects. Research on heritability in roses has shown considerable variation depending on the traits studied and the genetic materials used. Jain *et al.* (2006) reported high heritability for flower diameter and petal number in garden roses, while moderate heritability was observed for plant height and flower production. The importance of genetic advance as a major selection criterion has been emphasized by several researchers. Kumar *et al.* (2005) demonstrated that the genetic advance, when expressed as a percentage of the mean, provides a more reliable estimate of selection response than heritability alone. This parameter is particularly valuable in roses where breeders must consider multiple traits simultaneously. Arya and Hemaprabha (2025) reported that metagenomics play an important role in genetic evaluation.

The present research focuses on estimating phenotypic covariance, genotypic covariance, heritability, and genetic advances to assess the genetic potential for trait improvement and guide future breeding strategy.

Morphological traits in Rose breeding

Plant architecture traits, including plant height, stem diameter, and branch characteristics, play crucial roles in determining the commercial value of rose cultivars. Tall plants with strong stems are preferred for cut flower production, while compact growth habits are desired for landscape applications. Studies by Pathak *et al.* (2007) indicated that plant height and stem diameter show strong positive correlations, suggesting that selection for one trait could improve the other. Leaf characteristics, though often overlooked, contribute significantly to plant vigor and disease resistance. Research by Huang *et al.* (1998) showed that leaf size and shape are important factors in photosynthetic efficiency and overall plant performance. The genetic control of leaf traits in roses appears to be relatively complex, with moderate heritability estimates reported in most studies.

Flower characteristics and their genetic control

Flower traits are of paramount importance in rose breeding, as they directly determine the ornamental value and market acceptance of cultivars. The genetic controls of flower size, shape, and related characteristics have been extensively studied. Debener and Mattiesch (1999) reported high heritability for flower diameter and petal number, suggesting that these plant traits respond well to selection. Pedicel characteristics, including length and diameter, affect flower presentation and stem strength. Crespel *et al.* (2002) indicated that pedicel traits are moderately inheritable and show strong positive correlations with other flower-related characteristics. The genetic basis of these traits is important for developing cultivars suitable for different market segments.

Reproductive biology and pollen features

Pollen viability and fertility are critical factors in rose breeding programs, particularly for good hybridization work. Researchers showed that pollen characteristics are under strong genetic control, with high heritability estimates for pollen viability and moderate heritability for pollen sterility. These findings are important for understanding the reproductive biology of roses and optimizing better crossing programs. The relationship between pollen characteristics and other plant traits has been investigated by several researchers. Positive correlations between pollen viability and flower size have been reported, suggesting that selection for improved flower characteristics might also enhance reproductive success.

MATERIALS AND METHODS

Authors conducted the exploration during the years 2022-23 and 2023-24 in growing seasons using a diverse collection of HT rose genotypes. The experimental material consisted of 50 HT rose cultivars and breeding lines selected to represent a wide range of genetic diversity. Plants were grown under standard nursery conditions with uniform management practices to minimize environmental variation. The experimental design followed a randomized complete block design with three replications to ensure perfect statistical validity. Standard spacing (1.0 x 1.0 m) was maintained between plants and rows to ensure proper growth and observation. Each genotype was represented by multiple plants to account for within-genotype variation and provide reliable estimates of genetic parameters.

Eighteen morphological and reproductive traits were measured systematically throughout the growing season. The plant architecture traits included plant height, stem diameter, and branch length, measured at specific growth stages to ensure consistency. The leaf characteristics, including leaf length and width, were recorded from mature leaves at standardized positions on the plant. Flower-related traits were measured on fully opened flowers under standard conditions. These included flower bud dimensions, mature flower size, petal characteristics, and pedicel measurements. Special attention was given to the timing of measurements to ensure that flowers studied, were at optimal developmental stages for accurate assessment.

The pollen characteristics were evaluated using standard cytological techniques. Pollen viability was assessed using appropriate staining methods, while pollen sterility was determined by microscopic examination of pollen grains. All measurements were conducted by trained personnel to ensure consistency and accuracy.

Statistical Analysis

Genetic variability, heritability and genetic advance

The presence of higher variability results in the evolution of new lines 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. Hence studies on genetic variability help in the selection of diverse and desirable parental plants for further improvement. Genetic parameters like GCV, PCV, variability, heritability and genetic advance as per cent of mean were calculated by using the following formula and TNAUSTAT software.

Estimation of variance component

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

$$\text{Genotypic variance } (\sigma 2\text{ g}) = \frac{\text{M1-M2}}{\text{r}}$$

Where,
M1 = Mean sum of squares for genotypes
M2 = 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) 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
Less than 10 percent = Low
10 to 20 = Moderate
More than 20 percent = High

Estimation of Heritability

By using the method of Lush (1940) and Hanson *et al.* (1956), 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 were classified as per Johnson *et al.* (1955):

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), genetic advance was calculated.

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

Where,
GA = Genetic advance
h^2 = Heritability in broad sense
k = Selection deferential, 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), genetic advance as percent mean was calculated.

$$\text{GA as percent means } \frac{\text{GA}}{\text{GM}} \text{ x } 100$$

Where,
GA = Genetic advance
GM = Genetic mean
The values of genetic advance are classified as per the method of Johnson *et al.* (1955).
Less than 10 percent = Low
10 to 20 percent = Moderate
More than 20 percent = High

Data quality control and validation

A rigorous quality control measures were implemented throughout the data collection and analysis process. The reliability of genetic parameter estimates was assessed through regular intervals and standard errors. Bootstrap procedures were used to validate the stability of estimates and assess the robustness of conclusions. Cross-validation techniques were effectively employed to ensure that results were not dependent on specific subsets of data.

RESULTS AND DISCUSSION

With the help of morphological and reproductive trait data, phenotypic and genotypic covariance, heritability and genetic advance were calculated. The pooled results are presented in Table 1. Analysis revealed substantial variation among the 18 traits studied in HT roses. The highest phenotypic covariance occurred in flower weight (23.89), followed by number of petals (22.11) and pedicel length (17.80), indicating a broad selection base for breeding. Genotypic covariance showed a similar trend, with flower weight (21.38) highest, followed by pedicel length (17.68) and number of petals (17.07). The close correspondence between phenotypic and genotypic covariance patterns suggests that environmental effects are relatively consistent across traits, indicating good experimental control. Debener and Mettiesch (1999) and Arya (2018b) found similar results in their investigations. Ardasheva *et al.* (2023) stated that a comprehensive assessment of varieties of garden roses in the conditions of the Udmurt Republic and found similar results.

The ratio of genotypic to phenotypic covariance provides insights into the relative importance of genetic versus environmental factors for each trait. Traits with high ratios, such as leaf length (0.79) and flower bud diameter (0.97), clearly indicate that genetic factors predominate over environmental influences. This finding is particularly encouraging for breeding programs, as it suggests that selection for these traits will be effective. The discrepancy between the observed phenotypic rates and the expected phenotypic and genotypic rates, according to Punnett squares, suggests that the examined traits could be controlled by polygenic genes. The progenies were observed to exhibit a greater resemblance to old garden roses than hybrid tea roses and did not meet the commercial (Kilic *et al.,* 2024).

Heritability estimates ranged from 55.03% to 98.70%, indicating substantial genetic control for most traits studied. The highest heritability was observed for leaf length (98.70%), followed by flower bud diameter (94.85%) and petal width (93.66%). These very high heritability values suggest that these traits are under strong genetic control and would respond well to selection. Vijayalaxmi *et al.* (2022) and Bugallo and Facciuto (2023) reported that selection process in ornamental plant breeding and found similar results in rose plants.

Plant height showed high heritability (93.52%), indicating that this important architectural trait is predominantly genetically controlled. This finding is particularly significant for rose breeding, as plant height is a key characteristic that determines the suitability of cultivars for different market segments. The high heritability suggests that breeders can effectively select for desired plant heights. Stem diameter exhibited moderately high heritability (87.13%), which is encouraging for breeding programs aimed at developing roses with strong stems suitable for cut flower production. Huang *et al.* (1998) also found similar results in the heritability and genetic divergence study of roses. The genetic control of stem diameter, combined with its positive correlation with plant height, suggests that simultaneous improvement of both traits is feasible.

The flower-related traits generally showed high heritability estimates, with flower diameter (90.64%), flower length (90.22%), and number of flowers per plant (90.64%), all exceeding 90%. These high values clearly indicate that flower characteristics are under strong genetic control and that selection for improved flower traits will be effective. The moderate heritability observed for some traits, such as pedicel length (55.03%) and pedicel diameter (63.95%), suggests that these characteristics are more influenced by environmental factors. However, the heritability values are still sufficient to expect reasonable /proper progress from selection, particularly if environmental conditions are well-controlled. Present findings revealed close conformity with the findings of Gudin (2000). Airina and Sarada (2022) reported that high PCV, GCV, heritability and genetic advance were observed for lateral leaf width, pod length and pod weight. The magnitude of PCV and GCV were highest for pod weight, while heritability estimates were highest for pod length and genetic advance for pods per plant in pea.

Genetic advance (GA) results revealed that there was a varying potential for improvement across different traits. The highest genetic advance was observed for plant height (12.37), followed by stem diameter (10.00) and branch length (2.74). These high values indicate substantial potential for better improvement in plant architecture traits through selection. When expressed as a percentage of the mean, genetic advance ranged from 0.03% to 12.23%. Plant height showed the highest genetic advance as a percentage of the mean (12.23%), indicating that significant improvement in this trait can be achieved through selection. This finding, combined with

Table 1: Heritability, genetic advance and covariance of Hybrid Tea roses.

Sl. No.	Characters	Phenotypic covariance (PCV)	Genotypic covariance (GCV)	Heritability (%)	Genetic advance (GA)	Genetic advance mean
1.	Height of plant	11.7648	11.5915	93.52420	12.36724	12.2262
2.	Diameter of stem	7.60416	6.53964	87.13104	10.00439	0.74391
3.	Length of branch	12.5410	12.3984	73.65661	2.74205	0.66267
4.	Width of leaf	4.14290	3.55646	62.69383	0.66267	0.07966
5.	Length of leaf	6.17774	4.88410	98.69530	2.42075	0.26593
6.	Length of pedicel	17.80065	17.6840	55.03145	0.36191	0.17351
7.	Diameter of pedicel	13.30565	11.35422	63.94832	0.16739	0.10686
8.	Length of flower bud	8.17003	6.53396	66.88255	0.26593	0.12840
9.	Diameter of flower bud	13.77591	13.39065	94.85851	1.97131	0.62748
10.	No. of flowers/plant	14.48693	13.91004	90.63902	1.99285	0.37954
11.	Length of flower	13.67596	13.39104	90.22901	1.79585	0.12731
12.	Diameter of flower	9.38899	8.93015	90.64051	1.18116	0.47538
13.	Weight of flower	23.88520	21.38062	79.62902	1.11316	0.13328
14.	No. of petals	22.11255	17.07356	76.35412	1.88976	0.33129
15.	Length of petal	10.21745	6.49247	70.22905	0.82638	0.11987
16.	Width of petal	13.66726	13.24894	93.66062	0.96255	0.03748
17.	Pollen viability	7.36109	6.53339	92.07582	0.72911	0.03175
18.	Pollen sterility	8.77999	6.64247	76.23516	0.58117	0.10182

the high heritability of plant height, suggests that this trait should be a priority in good breeding programs (Kumar *et al.,* 2005; Jain *et al.*, 2006).

Stem diameter showed moderate genetic advance as a percentage of the mean (0.74%), which, while lower than plant height, still indicates potential for improvement. The combination of high heritability and moderate genetic advance suggests that selection for stem diameter will be effective, though progress may be more gradual than for plant height. Authors like Crespel *et al.* (2002) conducted research trials for mapping of qualitative and quantitative phenotypic traits in Rosa using AFLP markers and found almost similar results. Most flower-related traits revealed low genetic advance as a percentage of the mean, despite their high heritability estimates. This apparent contradiction can be explained by the relatively narrow range of variation in these traits compared to their mean values. While progress from selection will be limited in absolute terms, high heritability ensures that gains will be consistent and reliable (Gudin, 2000).

Trait relationships and breeding implications

The genetic parameters estimated in this study offer clear guidance for rose breeding strategies. High heritability in plant architecture traits indicates that selection for plant height and stem diameter will be highly effective, making them ideal for early-generation selection and ensuring genetic gains are retained across generations. Flower traits, despite high heritability, showed lower genetic advance as a percentage of the mean, suggesting that improvement will be more effective but modest; sustained selection pressure is recommended within practical limits. Traits with moderate heritability, such as pedicel characteristics, may require intensive selection and careful environmental management to achieve meaningful gains.

However, the genetic advance estimates suggest that worthwhile progress can still be achieved (Visalakshi *et al.,* 2024). The variation in genetic parameters across traits clearly suggests that a comprehensive breeding strategy should priorities traits based on their heritability and genetic advance. High-heritability traits with substantial genetic advance should receive primary attention, while traits with lower parameters may require specialized breeding approaches and planning (Pathak *et al.,* 2007; Agarwal *et al.,* 2019).

Implications for rose breeding programs

The findings of this study hold significant value for rose breeding programs. High heritability across most traits indicates strong potential for genetic improvement through selection, with maximum efficiency achieved by targeting traits that combine high heritability with substantial genetic advance. The plant architecture traits, particularly plant height and stem diameter, emerge as top priorities due to their favorable genetic parameters and commercial relevance for both cut flowers and landscaping. While flower traits also exhibit high heritability, their lower genetic advance suggests the need for refined breeding approaches, such as selection indices integrating multiple flower characteristics to enhance overall quality. For traits with moderate heritability, environmental management will be crucial to fully realize genetic potential. As Behnamia *et al.* (2024) emphasized, breeding programs should adopt controlled growing conditions to minimize environmental variation and enhance selection efficiency.

CONCLUSIONS

The present comprehensive analysis of genetic parameters in HT roses has provided valuable insights into the genetic architecture of important morphological and reproductive traits. The study demonstrates that most traits exhibit moderate to high heritability, indicating substantial genetic control and excellent potential for improvement through selection. The key findings reveal exceptionally high heritability for plant height (93.52%), flower characteristics (90-95%), and petal width (93.66%), indicating strong genetic control. Plant height showed the highest genetic advance (12.23% of the mean), highlighting substantial scope for improvement in this commercially valuable trait. Overall, HT roses demonstrate excellent genetic potential for breeding. The study provides a solid foundation for developing effective breeding strategies in HT roses. Future research should focus on expanding the genetic base through the introduction of new germplasm and developing molecular markers to enhance selection efficiency.The findings contribute to our understanding of rose genetics and provide practical information for breeders working to develop superior HT rose cultivars.

RECOMMENDATIONS

Breeding programs should prioritize traits with high heritability and substantial genetic advance, particularly plant height and stem diameter. These traits show the greatest potential for improvement and have direct commercial importance. Flower characteristics should be improved through comprehensive selection approaches that consider multiple traits simultaneously. While individual flower traits may show limited genetic advance, combined selection for multiple flower characteristics can achieve significant overall improvement. Breeding programs should invest in controlled growing conditions to minimize environmental effects and maximize the effectiveness of selection. This is particularly important for traits with moderate heritability. The genetic parameters estimated in this study should be used to develop selection indices that optimize improvement across multiple traits. This approach will be more efficient than selecting individual traits independently.

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