International Journal of Advanced Biochemistry Research

ISSN Print: 2617-4693
ISSN Online: 2617-4707
IJABR 2025; 9(1): 519-522
www.biochemjournal.com
Received: 08-10-2024
Accepted: 12-11-2024

Shorya Sharma
Division of Floriculture and Landscaping, ICAR-IARI, New Delhi, India

Reeta Bhatia Dey
Division of Floriculture and Landscaping, ICAR-IARI, New Delhi, India

Bharti
Division of Sample Surveys, ICAR-IASRI, New Delhi, India

Kanwar Pal Singh
Division of Floriculture and Landscaping, ICAR-IARI, New Delhi, India

Sapna Panwar
Division of Floriculture and Landscaping, ICAR-IARI, New Delhi, India

Akshay Talukdar
Division of Genetics and Plant Breeding, ICAR-IARI, New Delhi, India

Corresponding Author:
Reeta Bhatia Dey
Division of Floriculture and Landscaping, ICAR-IARI, New Delhi, India

Genetic assessment and trait profiling of marigold (*Tagetes* spp.) hybrids

Shorya Sharma, Reeta Bhatia Dey, Bharti, Kanwar Pal Singh, Sapna Panwar and Akshay Talukdar

DOI: https://doi.org/10.33545/26174693.2025.v9.i1g.3549

Abstract
Marigold (*Tagetes* spp.) is a highly valued loose flower crop of the floriculture industry, prized for its versatility, colourful blooms and ease of cultivation. Its resilience, low maintenance and adaptability make it an ideal choice for farmers, offering an excellent opportunity for profitable farming. Additionally, marigolds are rich in carotenoid content and have several pharmaceutical uses. This study evaluates genetic variability among key morphological traits including flower yield in 20 marigold hybrids. ANOVA analysis revealed significant variations across all traits, indicating considerable diversity within the genotypes. The phenotypic coefficient of variation was higher than the genotypic coefficient of variation for all traits, suggesting a notable environmental influence on trait expression, although genetic factors still played a dominant role due to very small differences. Heritability estimates were very high, ranging from 79.55% (plant spread) to 99.35% (flower weight). High heritability along with high genetic advance was observed for ray florets per flower, flower weight and yield per plant, indicating that selection for these traits is likely to result in substantial genetic improvement. Principal component analysis (PCA) identified four principal components, which together accounted for 83.57% of the total variability. Flower size, ray florets per flower, plant height and flower count per plant were the primary contributors to the four principal components, respectively.

Keywords: GCV, PCV, heritability, genetic advance, principal component analysis

Introduction
Marigold (*Tagetes* spp.), a prominent annual flower crop in the Asteraceae family, originated in Central and South America, particularly Mexico [7]. The main cultivars are *Tagetes erecta* L. (African marigold) and *Tagetes patula* L. (French marigold) [4]. Marigolds are valued for their ease of cultivation, adaptability, fast growth, abundant blooms, and extended flowering period. They are primarily grown for loose flowers and ornamental use. Their popularity stems from their ability to thrive in various soil and climate conditions, along with their long blooming season. Today, marigolds are also used in bedding plants, hanging baskets, rock gardens, and interior decoration [17]. Additionally, marigold essential oil is highly valued in the perfumery industry, and marigold intercropping has been shown to control nematode populations. Lutein, a carotenoid found in marigolds, boasts antioxidant properties that help prevent age-related macular degeneration and support infant brain development [8].

Genetic variability is essential for breeding success, enabling effective selection and hybridization by partitioning trait variation into genetic, phenotypic, and environmental components [11]. Coefficients of variation enable meaningful comparisons of trait variation within a population or across different populations of the same or different crops (Yuvraj and Dhatt, 2014). Heritability estimates, combined with genetic advance, guide selection, while the use of open-pollinated crops, especially in heterozygous species like marigold, gains growing importance [12]. Yield is a complex trait shaped by multiple factors, and understanding its genetic basis through variability parameters is vital for crop improvement [1]. Principal Component Analysis (PCA) was used to simplify yield data by reducing correlated variables into key uncorrelated components, highlighting the traits driving variation [15]. This study examines marigold hybrids using PCA, hence reducing dimensionality to retain the most significant components.

As a cross-pollinated crop, marigold requires high-yielding varieties along with some specific characters like robust plant stature to prevent lodging [2], early flowering types or genotypes varying in flowering time to meet varying market demands, especially during festive seasons, double flowered types, flowers with increased size etc. Hence, our study provides valuable insights into the existing variability by estimating the genetic parameters, with PCA helping in identifying the key components contributing to diversity.

Materials and Methods

The present investigation was carried out at the Division of Floriculture and Landscaping, ICAR-IARI, New Delhi, during the 2023-24 period. A total of 20 marigold hybrids were evaluated, which included two male sterile lines (MS-5 and MS-8), along with Pusa Deep and African marigold selections as their parental lines. The experimental design followed a Randomized Complete Block Design (RCBD) with three replications. Seeds were initially sown in plug trays containing a substrate mix of cocopeat, perlite, and vermiculite in a 3:1:1 ratio. After 30 days, the seedlings were transplanted into the field at a spacing of 45×30 cm. A total of 11 morphological traits were measured, viz. plant height (cm), plant spread (cm), flower count per plant, ray florets per flower, flower size (cm), flower weight (g), days to bud initiation, days to first flower appearance, days to 50% flowering, days to full bloom, and yield per plant (g), with data being recorded from three randomly selected plants per replication. The genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV), were calculated following the methodology of Burton and Devane [3]. Broad-sense heritability was computed as the ratio of genotypic variance to total phenotypic variance, expressed in percentage [5]. The expected genetic advance was estimated using the approach of Johnson *et al*. [6]. Statistical analysis was performed using R software, and principal component analysis (PCA) was conducted based on the average values of all traits using the same software.

Results and Discussion

Studying variability in a breeding program is crucial for identifying genetic potential and selecting superior traits. It helps in understanding the extent of genetic diversity, guiding the selection of parent plants with desirable traits, and improving overall breeding efficiency for better crop performance. The analysis of variance (ANOVA) revealed highly significant differences among the genotypes for all the traits examined, highlighting considerable variability within the studied population. This variability in the germplasm was further quantified using various statistical measures, as detailed in Table 1. In case of each morphological trait, the phenotypic coefficient of variation (PCV) exceeded corresponding genotypic coefficient of variation (GCV). However, very slight differences observed between PCV and GCV values suggests that genetic factors predominantly contribute to the observed variability and there is nearly negligible influence of environmental factors on the expression of studied traits [16]. GCV was found to be maximum for number of ray florets per flower (65.33%) and minimum for days to full bloom (5.93%) while the corresponding PCV values ranged from 6.11% (days to full bloom) to 66.33% (ray florets per flower). Our findings were in conformity with Poulose *et al*. [10] and Namita *et al*. [9].

Heritability reflects the proportion of genetic makeup contributing for a trait's variability. In this study, all traits exhibited high heritability i.e. > 60% [5], ranging from 79.55-99.35%. It was highest for maximum in case of flower weight followed by flower size (98.50%), ray florets per flower (96.94%) and yield (96.48). But, the estimate of broad-sense heritability alone does not offer a comprehensive understanding of the type of gene action responsible for the expression of a particular trait. The interplay of high heritability and genetic advance provides a robust framework for forecasting the effectiveness of selecting superior genotypes [6]. Ray florets per flower exhibited greatest genetic advance (132.46%) coupled with high heritability. Flower weight (73.94%) and yield per plant (61.98%) remained second and third on the list, respectively [10, 14]. Days to first flower initiation had least genetic advance irrespective of high heritability (10.39%) and is accompanied by traits such as days to bud initiation (11.61%), full bloom (11.84%) and 50% bloom (12.68%), In contrast, genetic advance as percentage of mean were observed for characters like flower size, flower count, plant height and spread [11, 16]. These findings suggest that traits exhibiting both high heritability and high genetic advance are having additive genetic action, making them more amenable to selection based on phenotype. In contrast, traits with lower genetic advance likely involve non-additive genetic effects and need progeny testing for better evaluation.

Principal Component Analysis (PCA) is a straightforward, nonparametric technique aimed at extracting a reduced set of factors that capture the maximum variance from the overall data. PCA for 11 examined traits revealed four principal components that were contributing to 83.57% of total variability. These principal components were having Eigen values >1 and were the key contributors to variation. PC-I showed positive factor loadings for most traits, except for flower count per plant (-0.216), days to bud initiation (-0.374), 50% flowering (-0.348), and full bloom (-0.363). PC-II has maximum positive loadings from ray florets/flower (0.454) and highest negative loadings from plant spread (-0.398). Flower count (0.234) and ray florets/flower (0.109) showed positive loadings for PC-III while other traits exhibited negative loading vectors. In PC-IV, plant height (-0.007), ray florets count and days to bud initiation had negative loading vectors. Contribution of different variables to principal components were shown in Table 2. The use of PCA to assess genetic divergence in marigold, especially concerning morphological traits, is still limited. However, Singh *et al*. [13] effectively applied PCA in wild rose, where six principal components accounted for 65.44% of total variability.

Table 1: Parameters of Genetic variability for morphological characters of 20 marigold hybrids

Character	Mean	Range	Coefficient of variation		Heritability (h^2)	Genetic advance	Genetic advance % mean
			GCV (%)	PCV (%)	(%)		
Plant height (cm)	85.55	58.50-109.67	16.29	16.79	94.13	27.85	32.55
Plant spread (cm)	65.99	48.50-82.00	12.06	13.52	79.55	14.62	22.15
Days to bud initiation	43.98	34.00-48.00	6.10	6.60	85.36	5.10	11.61
Days to first flower initiation	52.43	41.00-58.00	5.58	6.18	81.64	5.45	10.39
Days to 50% flowering	58.93	52.00-72.00	14.36	15.66	91.69	7.47	12.68
Days to full bloom	64.10	58.00-75.00	5.93	6.11	94.01	7.59	11.84
Flower count per plant	63.86	39.67-79.33	14.72	15.35	91.99	18.57	29.08
Flower size (cm)	5.52	3.12-8.27	19.28	19.43	98.50	2.18	39.42
Flower weight (g)	5.86	3.10-10.44	36.01	36.12	99.35	4.33	73.94
Ray florets per flower	126.57	132.46-167.65	65.33	66.33	96.94	167.65	132.46
Yield per plant (g)	365.05	196.32-605.52	30.63	31.17	96.48	226.27	61.98

GCV: Genetic coefficient of variation, PCV: Phenotypic coefficient of variation, Heritability (Broad sense)

Table 2: Loading vectors and eigen values for first three principal components of variation

Quantitative variables	Variable contribution to PCs (%)			
	PC-I	PC-II	PC-III	PC-IV
Plant height (cm)	2.13	0.75	41.93	0.00
Plant spread (cm)	1.16	15.82	19.87	2.21
Flower weight (g)	12.96	12.80	4.01	0.39
Flowers count/plant	4.65	0.15	5.46	59.42
Ray florets/flower	1.81	20.59	1.18	11.81
Flower size (cm)	15.94	5.43	0.69	0.90
Days to bud initiation	13.95	0.39	14.44	0.02
Days to first flower initiation	13.77	3.42	9.87	0.09
Days to 50 % flowering	12.15	15.02	0.89	0.17
Days to full bloom	13.16	10.84	0.44	0.15
Yield per plant (g)	8.30	14.79	1.22	24.83
Eigen values	4.31	2.15	1.68	1.05
Variability (%)	39.21	19.54	15.30	9.51
Cumulative (%)	39.21	58.75	74.06	83.57

Conclusion

This study was conducted with the aim of highlighting substantial genetic variability within the marigold genotypes which can be utilized in breeding programmes. High heritability coupled with high genetic advance for traits like ray florets per flower, flower weight and yield, revealed them ideal for phenotypic selection. Principal Component Analysis is a non-parametric approach and provided valuable insights into the genetic divergence among the genotypes, with most traits contributing positively to the first principal component. Current findings suggest that PCA can be a powerful tool for future marigold breeding programs, offering a comprehensive understanding of trait variability and aiding in the selection of superior genotypes for enhanced crop performance.

Author's Contribution

The research was conceptualized by SS, RBD, and KPS, who established the study framework. B and SP designed the experiments, while KPS, SP, and AT contributed the necessary materials. SS and RBD prepared and refined the manuscript for publication.

Declaration

The authors declare that they have no conflicts of interest to report.

Acknowledgements

The authors wish to acknowledge and extend their sincere gratitude to the Division of Floriculture and Landscaping, ICAR-IARI, New Delhi, for providing the necessary research facilities and suppo

References

1. Angadi AP, Archana B. Genetic variability and correlation studies in bird of Paradise genotypes for flower and yield parameters during 2011. Bioscan. 2014;9(1):385-388.
2. Bharathi UT, Jawaharlal M. Correlation and path analysis in African marigold (*Tagetes erecta* L.). Bioscan. 2014;9(4):1673-1676.
3. Burton GW, Devane DE. Estimating heritability in tall fescue (*Festuca arundinacea*) from replicated clonal material. Agronomy Journal. 1953;45:478-481.
4. Dhube A, Rawat V, Lakshmi V, Devi RK, Kumar R, Sah S. Post harvesting and value addition in marigold. The Pharma Innovation Journal. 2022;11:1295-1299.
5. Hanson CH, Robinson HF, Comstock RE. Biometrical studies of yield in segregating populations of Korean lespedeza. Agronomy Journal. 1956;48:268-272.
6. Johnson HW, Robinson HF, Comstock RL. Estimates of genetic and environmental variability in soybean. Agronomy Journal. 1995;47:314-328.
7. Kaplan L. Historical and ethno-botanical aspects of domestication in *Tagetes*. Economic Botany. 1960;14:200-202. https://doi.org/10.1007/BF02907950
8. Mario OB, Luis MC, Ming HL, Juan MD, Gustavo CH. Lutein as a functional food ingredient: stability and bioavailability. Journal of Functional Foods. 2020;66:1-12. https://doi.org/10.1016/j.jff.2019.103771
9. Namita, Kanwar PS, Raju DVS, Prasad KV. Studies on genetic variability, heritability and genetic advance in French marigold (*Tagetes patula* L.) genotypes. Journal of Ornamental Horticulture. 2008;12:30-34.
10. Poulose B, Paliwal A, Bohra M, Punetha P, Bahuguna P, Namita. Character association and path analysis of quantitative traits among marigold (*Tagetes* spp.) genotypes. Indian Journal of Agricultural Sciences. 2020;90(12):2362-2368. https://doi.org/10.56093/ijas.v90i12.110342
11. Santhosh N, Tejaswini, Shivashankar KS, Seetharamu GK, Archana G. Genetic diversity for morphological characters and biochemical components in African marigold. International Journal of Chemical Studies. 2018;6(6):624-627.
12. Singh D, Misra KK. Genetic variability in quantitative characters of marigold. Indian Journal of Horticulture. 2008;65(2):187-192.

13. Singh K, Sharma YP, Gairola S. Morphological characterization of wild *Rosa* L. germplasm from the Western Himalaya, India. Euphytica. 2020;216(41). https://doi.org/10.1007/s10681-020-2567-2
14. Singh KP, Raju DVS, Namita N, Janakiram T. Determination of genetic variation for vegetative and floral traits in African marigold (*Tagetes erecta* L.). Indian Journal of Agricultural Sciences. 2014;84(9):1057-1062. https://doi.org/10.56093/ijas.v84i9.43438
15. Sinha A, Singh P, Bhardwaj A, Verma RB. Principal component analysis approach for comprehensive screening of tomato germplasm for polyhouse condition. Journal of Experimental Agriculture International. 2021;43(9):67-72. https://doi.org/10.9734/JEAI/2021/v43i930739
16. Thirumalmurugan V, Manivannan K, Nanthakumar S. Genetic diversity in African marigold (*Tagetes erecta* L.) under Vellore conditions. Plant Archives. 2020;20(2):3896-3899.
17. Yuvraj, Dhatt KK. Studies on genetic variability, heritability and genetic advance in marigold. Indian Journal of Horticulture. 2014;71(4):592-594.