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Comprehensive Analysis of Genetic variability, Trait interactions and Phenotypic diversity in Marigold (*Tagetes* spp.) genotypes

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ABSTRACT

Marigold (Tagetes spp.) is a popular ornamental plant known for its vibrant flowers. This study evaluates genetic variability and correlation among key morphological traits affecting flower yield in 38 marigold genotypes. Significant differences were observed across all traits, indicating substantial variability within the genotypes while phenotypic coefficient of variation exceeded genotypic coefficient of variation for all traits, suggesting environmental influence on trait expression, though genetic factors remained dominant. Heritability estimates were high for most traits, with number of ray florets per flower exhibiting highest heritability (99.12%) coupled with highest genetic advance (121.24%), indicating that selection for this trait is likely to result in substantial genetic improvement. Correlation analysis revealed significant positive associations between flower yield per plant and traits such as plant height (0.453), fresh flower weight (0.582), and number of flowers per plant (0.414) at both genotypic and phenotypic levels. Path coefficient analysis highlighted fresh flower weight and number of flowers per plant as key determinants of yield, with direct positive effects of 1.267 and 0.988, respectively at genotypic level. Principal component analysis identified first three principal components explaining 74.61% of total variability, with days to flower initiation (PC-I), fresh flower weight and flower diameter (PC-II), and number of flowers per plant (PC-II) contributing most to observed variation. The study suggests that selection for these traits, especially fresh flower weight and number of flowers, could significantly enhance marigold productivity in future crop improvement efforts. It addresses complexity of trait interactions, offering key insights for genetic improvement.

Keywords: *Heritability, Genetic advance, Genotypic and Phenotypic coefficient of variation, Correlation, Path coefficient analysis, Principal component analysis*

INTRODUCTION

Marigold (*Tagetes* spp.), a native of Mexico, is a prominent annual flower crop, belonging to Asteraceae [9]. In India, marigold occupies the largest area (86.05 thousand hectares) and yields the highest production (954.70 thousand MT), surpassing other flower crops [3]. Among various species of *Tagetes* genus, *Tagetes erecta* L. (African marigold) and *Tagetes patula* L. (French marigold) are two main species driving marigold cultivation [7]. *Tagetes erecta* comprises of plants with tall stature, with lemon yellow to golden yellow or orange flowers, while *Tagetes patula* have dwarf genotypes with flowers varying from yellow to mahogany red [14]. Marigold has gained popularity among growers because of its easy cultivation, wider adaptability, quick growth cycle, abundant blooming, and long flowering season. It is primarily grown for loose flower production and enhancing landscapes. Marigold flowers contain carotenoids, making them valuable as colorants, while flavonoids and monoterpenoids contribute to their use in food additives and medicinal applications [20].

Lutein, a carotenoid, possesses antioxidant properties and is vital for preventing age-related macular degeneration and supporting infant brain development [11].

Genetic variability is a cornerstone of successful breeding programs. Breeders must focus on preserving genetic diversity to enhance selection and hybridization processes. Trait variation among genotypes arises from the interaction of genotype, phenotype and environment. Hence, partitioning total variability into genetic, phenotypic and environmental components is vital for effective selection and strategic breeding [15]. In marigold breeding, estimating the genetic coefficient of variation provides insight into the genetic diversity for key traits, which is essential for crop improvement. This variability helps identify suitable parental lines for breeding programs. Understanding genetic variability, heritability and genetic advances is crucial for effective breeding. The coefficient of variation reveals trait diversity within a population and enables comparisons between populations [12]. Heritability estimates indicate the proportion of variation due to genetic factors, guiding breeders in selecting traits with high heritable variability, a key for identifying superior genotypes. Correlation coefficients based on heritable variation offer a strong foundation for selection [10]. However, while correlation studies are helpful, they do not fully capture the direct and indirect effects of traits on yield. For this, Path coefficient analysis is a critical tool to disentangle these effects.

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The goal of any breeding program is to develop more efficient genotypes with higher yields, especially in economically important traits. The potential for improvement depends on the availability of usable genetic variation, which can be evaluated through genetic coefficients and heritability estimates. These estimates show how much of the observed variability is genetic in origin, helping breeders focus on traits with high heritability for efficient selection. Yield, a quantitative trait influenced by various factors and the environment, was analyzed using Principal Component Analysis (PCA) to streamline trait selection. PCA effectively reduces a large set of correlated variables to a smaller number of uncorrelated principal components, retaining the essential information. This mathematical technique simplifies complex data by identifying key traits that significantly contribute to variability [18]. The present study aims to explore the genetic variability of marigold genotypes by examining genetic parameters such as heritability and genetic advance. It also investigates the strong associations among traits, along with their direct and indirect effects through path coefficient analysis. Additionally, it is employed to reduce the dimensionality of total variation, retaining only principal components that account for most significant variation. These analytical approaches provide a deeper understanding of trait interactions and genetic control, making the research more effective in developing improved crop varieties.

MATERIALS AND METHODS

The present study is conducted at Division of Floriculture and Landscaping, ICAR, IARI, New Delhi during 2023-24. A total of 38 genotypes were studied comprising two male sterile lines (MS-5 and MS-8), three French marigold genotypes (Pusa Utsav, Pusa Parv and Pusa Deep), MGO-3 and 32 African marigold genotypes (Pusa Basanti Gainda and 31 African marigold selections). The experiment was laid out in Randomised Complete Block Design with three replications. Seeds were sown in plug trays filled with a mix of cocopeat, perlite, and vermiculite in a 3:1:1 ratio. After one month, the seedlings were transplanted to the field, spaced 45×30 cm apart. Various morphological parameters viz. Plant height (cm), Spread (cm), Number of flowers per plant, Number of ray florets per flower, Flower diameter (cm), Fresh flower weight (g), Days to bud initiation, Days to first flower initiation, Days to 50% flowering, Days to full bloom and Yield per plant (g) were recorded from three random plants per replication. Plant height and spread were measured 60 days after transplanting, and fresh flower weight was averaged from five flowers per plant. The coefficients of variation viz. Genotypic coefficient of variation (GCV) and Phenotypic coefficient of variation (PCV) were computed using the method outlined by [5]. Heritability (Broad sense) was calculated as the ratio of genotypic variance to total phenotypic variance, expressed as a percentage [2]. The expected genetic advance was derived using the approach of [8]. Both Genotypic and phenotypic correlations were determined based on the formulae by [1]. Direct and indirect effects of recorded characters on yield were assessed following the procedure of [6]. Statistical analysis was performed using R software (R.4.4.1). Mean values of all parameters were used for Principal Component Analysis (PCA), conducted using R software.

RESULTS

ANOVA analysis revealed highly significant differences among the genotypes for all traits examined, indicating substantial variability within the studied population. The degree of variability in the germplasm was assessed through several genetic measures mentioned in Table 1. Regarding mean performance, trait with the highest mean value was yield per plant (g), which had an average of 328.75, ranging from 137.13 to 561.31. This was followed by the number of ray florets per flower (139.51) and plant height (70.26 cm). On the other hand, the trait with the lowest mean value was flower diameter (cm), averaging 5.06, with a range of 4.04-7.11, followed by fresh flower weight (5.38 g). Values of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) ranged from 6.18 (Days to full bloom) to 59.11% (No. of ray florets per flower) and from 6.29 (Days to full bloom) to 59.37% (No. of ray florets per flower), respectively. Estimated PCV, for each trait was slightly higher than the corresponding GCV. A notably high heritability was observed for all the traits with the highest heritability recorded for the number of ray florets per flower (99.12%), and being lowest for plant spread (78.85%). In this study, highest heritability coupled with highest genetic advance (% mean) was found for no. of ray florets per flower (99.12% and 121.24%). Next in line were fresh flower weight (49.26%) and flower yield per plant (48.19%). High heritability with low genetic advance was observed for days to full bloom (12.50%), first flower initiation (12.85%), 50% bloom (13.72%) and bud initiation (17.35%); while moderate in case of plant height, spread and no. of flowers per plant.

Expression of yield depends on interaction of multiple traits. In present investigation (Table 2) yield per plant has highly significant ($p<0.01$) positive correlation with plant height (0.453, 0.399), fresh flower weight (0.582, 0.602) and no. of flowers per plant (0.414, 0.438) and significant ($p<0.05$) positive correlation with no. of ray florets per flower (0.336, 0.312) and flower diameter (0.356, 0.329) at genotypic and phenotypic level, respectively. On other hand, other characters showed non-significant correlation with yield. Number of flowers per plant (-0.465, -0.416) and fresh flower weight show a highly significant negative correlation with each other. Flower diameter tends to increase flower weight (0.725, 0.688) but itself decreased by rise in no. of flowers (-0.420, -0.395). Days to bud initiation, first flower initiation, 50% flowering and full bloom exhibited highly significant positive correlation among each other. Genotypic correlation was higher than phenotypic correlation for most characters, except for association of yield with plant spread, fresh flower weight and no. of flowers per plant.

It is apparent from Table 3. that dependent variable under investigation is yield per plant, on which both direct and indirect effects of ten independent variables were analyzed. Fresh flower weight exhibited most substantial positive direct effect on yield (1.267, 1.020), followed closely by no. of flowers per plant, with direct effects of 0.988 and 0.883 on genotypic and phenotypic basis, respectively. Fresh flower weight had negative indirect effect on the yield through no. of flowers per plant (-0.259, -0.368). Plant height exerted high indirect positive effect on yield via fresh flower weight (0.417, 0.299), while plant spread positively influenced yield indirectly through no. of flowers per plant (0.273, 0.237). Negative indirect effects of plant height via other traits were quite low, owing to its high positive correlation with yield. Regarding negative direct effects, days to 50% bloom (-0.475, -0.160) leads the tally, on both genotypic and phenotypic levels followed by no. of ray florets (-0.149, -0.050).

Although, days to flower initiation exhibited a slight positive and direct effect on yield but the magnitude of indirect negative effect through 50% bloom (-0.433, -0.139) was quite high.

Further, Principal component analysis revealed that first three components viz. PC-I, PC-II and PC-III were having eigen values > 1 and contributed to a cumulative variability of 74.61% (Table 4). PC-I accounted for maximum variation (33.88%), positively associated with plant height, spread, fresh flower weight, no. of ray florets/flower and flower diameter. PC-II had negative factor loading for plant spread, no. of flowers/plant and days to first flower initiation. Variation in PC-III is dominated by all the studied traits, except flower diameter and no. of ray florets/flower. Contribution of different traits was evaluated for PC-I, PC-II and PC-III (Fig. 1). Days to first flower initiation (24.28%) was found to be show max. trait contribution for PC-II followed by days to 50% flowering (22.53%) and full bloom (22.15%) indicating population comprising in terms of flowering period. PC-II is led in contribution by fresh flower weight (33.72%) and flower diameter (25.19%) reflecting significant variation in terms of flower size. No. of flowers/plant (35.10%) and yield per plant (27.51%) were found to be the most important traits explaining diversity among genotypes in PC-III.

Table 1. Genetic parameters of variability for various quantitative traits of 38 marigold genotypes

Character	Mean	Range	Coefficient of variation		Heritability (h^2)	Genetic advance	Genetic advance % mean
			GCV (%)	PCV (%)	(%)		
Plant height (cm)	70.26	46.67-103.67	13.59	15.11	80.82	17.68	25.16
Plant spread (cm)	54.62	35.67-85.33	16.44	18.51	78.85	16.42	30.07
Days to bud initiation	44.37	35.00-54.00	8.76	9.11	92.45	7.70	17.35
Days to first flower initiation	54.77	47.00-66.00	6.54	6.85	91.03	7.04	12.85
Days to 50% flowering	62.29	55.00-77.00	18.19	19.22	94.67	8.55	13.72
Days to full bloom	68.53	61.00-81.00	6.18	6.29	96.46	8.57	12.50
Number of flowers per plant	62.60	32.00-91.67	20.70	21.88	89.55	25.27	40.36
Flower diameter (cm)	5.06	4.04-7.11	13.55	13.67	98.25	1.40	27.66
Fresh flower weight (g)	5.38	2.84-9.50	25.08	26.31	90.87	2.65	49.26
Number of ray florets per flower	139.51	6.33-291.33	59.11	59.37	99.12	169.14	121.24
Yield per plant (g)	328.75	137.13-561.31	25.25	27.25	85.86	158.44	48.19

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

Table 2. Genotypic (G) and Phenotypic (P) correlations among various growth and yield related morphological traits

Characters	CV	PS	FFW	NFP	NRF	FD	DBI	DFI	DF50	DFB	YPP
PH	**G**	0.425**	0.329*	0.132	0.038	0.124	-0.209	-0.365	-0.247	-0.310	0.453**
	P	0.414**	0.293*	0.137	0.027	0.099	-0.190	-0.304**	-0.227*	-0.266*	0.399**
PS	**G**		-0.271	0.276	-0.053	-0.161	-0.230	-0.320*	-0.175	-0.295	0.032
	P		-0.218*	0.268*	-0.049	-0.139	-0.192*	-0.272*	-0.165	-0.250**	0.063
FFW	**G**			-0.465**	0.541**	0.725**	0.093	-0.090	-0.013	-0.002	0.582**
	P			-0.416**	0.514**	0.688**	0.094	-0.083	-0.033	-0.004	0.602**
NFP	**G**				-0.215	-0.420**	-0.085	0.185	0.212	0.113	0.414**
	P				-0.203*	-0.395**	-0.073	0.185*	0.195*	0.107	0.438**
NRF	**G**					0.346*	0.034	-0.126	-0.147	0.002	0.336*
	P					0.341**	0.029	-0.115	-0.143	0.002	0.312*
FD	**G**						0.217	0.012	0.028	0.006	0.356*
	P						0.206*	0.009	0.029	0.004	0.329*
DBI	**G**							0.854**	0.789**	0.763**	-0.100
	P							0.801**	0.750**	0.737**	-0.076
DFI	**G**								0.912**	0.834**	-0.052
	P								0.867**	0.800**	-0.034
DF50	**G**									0.882**	-0.018
	P									0.855**	-0.005
DFB	**G**										-0.053
	P										-0.050

*, ** *significant at 5 % and 1 % level respectively. G-Genotypic correlation, P-Phenotypic correlation. PH: Plant height (cm), PS: Plant spread (cm), FFW: Fresh flower weight (g), NFP: Number of flowers per plant, NRF: Number of ray florets per flower, FD: Flower diameter (cm), DBI: Days to bud initiation, DFI: Days to first flower initiation, DF50: Days to 50% flowering, DFB: Days to full bloom and YPP: Yield per plant (g).*

Table 3. Genotypic (G) and Phenotypic (P) path coefficient analysis of different morphological traits

Characters	CV	PH	PS	FFW	NFP	NRF	FD	DBI	DFI	DF50	DFB	Correlation coefficient with YPP
PH	G	-0.171	0.071	0.417	0.130	-0.006	-0.006	-0.010	-0.077	0.117	-0.013	0.453**
	P	-0.078	0.022	0.299	0.121	-0.001	0.001	0.003	-0.013	0.036	0.015	0.399**
PS	G	-0.073	0.168	-0.343	0.273	0.008	0.008	-0.011	-0.068	0.083	-0.012	0.032
	P	-0.032	0.054	-0.223	0.237	0.002	-0.001	-0.003	-0.012	0.026	0.014	0.063
FFW	G	-0.056	-0.045	1.267	-0.259	-0.080	-0.034	0.004	-0.019	0.006	-0.000	0.582**
	P	-0.023	-0.012	1.020	-0.368	-0.026	0.007	0.001	-0.003	0.005	0.000	0.602**
NFP	G	-0.023	0.046	-0.589	0.988	0.032	0.020	-0.004	0.039	-0.101	0.005	0.414**
	P	-0.011	0.015	-0.424	0.883	0.010	-0.004	-0.001	0.008	-0.031	-0.006	0.438**
NRF	G	-0.006	-0.009	0.685	-0.212	-0.149	-0.016	0.002	-0.027	0.070	0.000	0.336*
	P	-0.002	-0.003	0.524	-0.179	-0.050	0.003	0.000	-0.005	0.023	-0.000	0.312**
FD	G	-0.021	-0.027	0.918	-0.415	-0.051	-0.047	0.010	0.002	-0.013	0.000	0.356*
	P	-0.008	-0.008	0.701	-0.348	-0.017	0.010	0.003	0.000	-0.005	-0.000	0.329**
DBI	G	0.036	-0.039	0.118	-0.084	-0.005	-0.010	0.046	0.181	-0.375	0.032	-0.100
	P	0.015	-0.010	0.095	-0.065	-0.001	0.002	0.016	0.035	-0.120	-0.041	-0.076
DFI	G	0.062	-0.054	-0.114	0.182	0.019	-0.000	0.039	0.212	-0.433	0.035	-0.052
	P	0.024	-0.015	-0.084	0.164	0.006	0.000	0.013	0.043	-0.139	-0.045	-0.034
DF50	G	0.042	-0.029	-0.016	0.209	0.022	-0.000	0.036	0.194	-0.475	0.037	0.018
	P	0.018	-0.009	-0.034	0.172	0.007	0.000	0.012	0.038	-0.160	-0.048	-0.005
DFB	G	0.053	-0.050	-0.002	0.112	-0.000	-0.000	0.035	0.177	-0.419	0.042	-0.053
	P	0.021	-0.014	-0.004	0.094	-0.000	0.000	0.012	0.035	-0.137	-0.057	-0.050

*Genotypic residual effect = 0.0196, Phenotypic residual effect = 0.0384. *, ** significant at 5 % and 1 % level respectively. G-Genotypic effect, P-Phenotypic effect. PH: Plant height (cm), PS: Plant spread (cm), FFW: Fresh flower weight (g), NFP: Number of flowers per plant, NRF: Number of ray florets per flower, FD: Flower diameter (cm), DBI: Days to bud initiation, DFI: Days to first flower initiation, DF50: Days to 50% flowering, DFB: Days to full bloom and YPP: Yield per plant (g).*

Table 4. Loading vectors and eigen values for first three principal components of variation

Quantitative variables	Loading vectors		
	PC-I	PC-II	PC-III
Plant height (cm)	0.236	0.138	0.434
Plant spread (cm)	0.193	-0.177	0.357
Fresh flower weight (g)	0.065	0.581	0.015
No. of flowers/plant	-0.049	-0.258	0.592
No. of ray florets/flower	0.071	0.392	-0.018
Flower diameter (cm)	0.008	0.502	-0.073
Days to bud initiation	-0.444	0.148	0.022
Days to first flower initiation	-0.493	-0.022	0.103
Days to 50 % flowering	-0.475	0.013	0.183
Days to full bloom	-0.471	0.062	0.089
Yield per plant (g)	-0.092	0.338	0.524
Eigen values	3.727	2.686	1.795
Variability (%)	33.879	24.415	16.318
Cumulative (%)	33.879	58.294	74.612

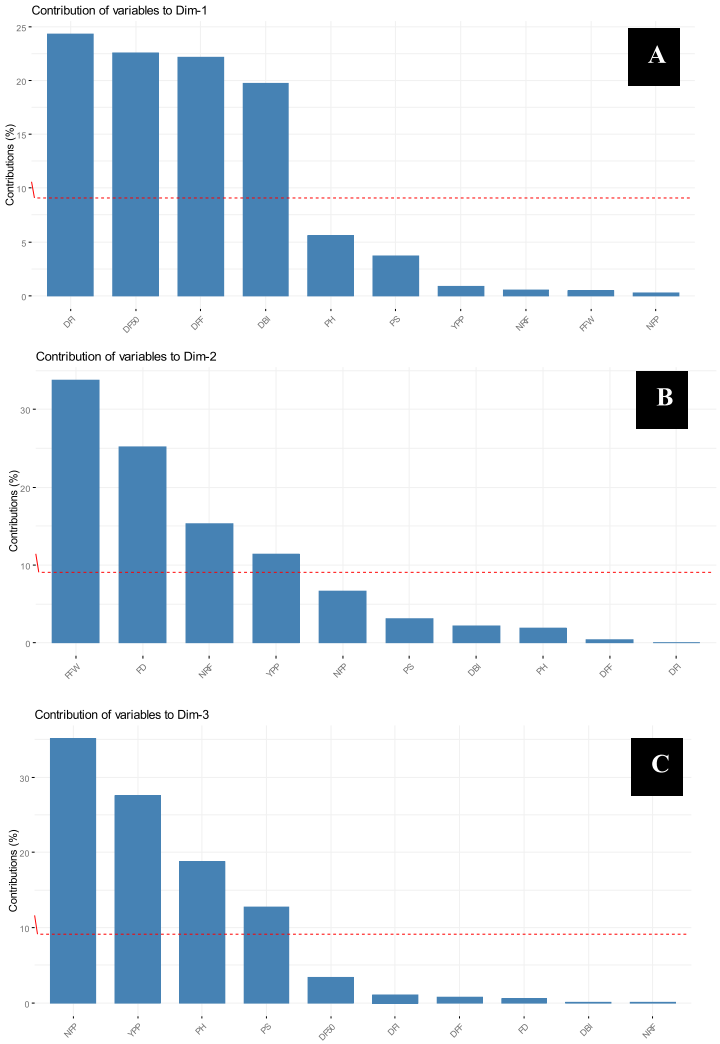

Fig. 1: *Contributions of various morphological variable to A: PC-I, B-PC-II and C: PC-III. PH: Plant height (cm), PS: Plant spread (cm), FFW: Fresh flower weight (g), NFP: Number of flowers per plant, NRF: Number of ray florets per flower, FD: Flower diameter (cm), DBI: Days to bud initiation, DFI: Days to first flower initiation, DF50: Days to 50% flowering, DFB: Days to full bloom and YPP: Yield per plant (g).*

DISCUSSION

Marigold (*Tagetes* spp.) exhibits a high degree of heterozygosity, which contributes to its genetic diversity and adaptability. Due to this genetic variability, studying traits through genetic parameters such as heritability, genetic advance, and coefficient of variation is essential for understanding the potential for improvement and selection in breeding programs. This helps in identifying traits with greater genetic control, facilitating more efficient breeding for desirable characteristics. For every trait, the PCV exceeded the corresponding GCV, suggesting the influence of environmental factors on trait expression [15]. However, the observed differences between PCV and GCV were minimal, underscoring the dominant role of genetic factors in the existing variability. Heritability measures the genetic contribution to a trait's transmission across generations. High heritability indicates that a trait can be improved through direct selection, while low heritability suggests that progeny testing is needed to select for the desired trait in offspring [14]. Heritability, combined with genetic advance, provides valuable standards for predicting the outcomes of selecting superior genotypes [8]. This study indicates that traits like no. of ray florets/flower and fresh flower weight, having high heritability along with high genetic advance are controlled by additive gene action, making selection effective. In contrast, traits with high heritability but low genetic advance involve non-additive gene action and are better suited for heterosis breeding.

Our findings are consistent with those reported by [15], [16] and [19], who have also observed similar patterns in various plant traits.

Crop improvement programs rely heavily on adequate variability and the degree of association between traits, which are crucial for effective selection. Significant correlations among traits with high heritability, minimally influenced by environmental factors, allow for more effective indirect selection. This means that selecting for related traits can simultaneously improve the desired trait. Expression of yield depends on interaction of multiple traits. In the present investigation, yield per plant showed strong association with traits like fresh flower weight, no. of flowers per plant. Negative correlation between number of flowers per plant and fresh flower weight is likely due to the partitioning of photosynthates. A strong positive correlation was observed between flower diameter and fresh flower weight, indicating that larger flowers tend to have a greater weight, which is a predictable and logical relationship. Our findings align with the works of [4], [13] and [14]. Genotypic correlation was higher than phenotypic correlation, except for association of yield with plant spread, fresh flower weight and no. of flowers per plant, which indicates that association of these traits with yield is under environmental influence. However, the difference is not substantial. Correlation analysis also revealed that plants with early bud initiation are more likely to bloom earlier.

Path coefficient analysis allows separation of correlation coefficients into direct and indirect effects of various variables on dependent variable and aids in understanding cause-and-effect relationships. Fresh flower weight and no. of flowers per plant were found to have most significant direct effect on yield. Similar findings were reported by [4] and [14]. However, a negative indirect effect of flower weight on yield via flower count indicates that as flower weight increases, the plant may produce fewer flowers, leading to a reduction in total yield, while an increase in plant spread, coupled with a higher number of flowers per plant, will enhance the overall yield. This study underscores that the higher phenotypic correlation compared to the genotypic correlation of these traits with yield per plant is attributed to the influence and interaction of other traits. Path analysis highlights that fresh flower weight and number of flowers per plant are key yield determinants, and selecting for these traits can drive significant, sustainable improvements. Thus, they should be prioritized in future crop improvement efforts to optimize flower yield. The application of PCA for understanding genetic divergence in marigold, particularly with respect to morphological traits, is relatively limited. Thus, we employed this statistical approach to explore the dimensions of variation and identify which traits contribute most to the overall variability. However, its effective use has been reported by [16] in wild rose, where six principal components explained 65.44% of the total variation. Principal components with eigenvalues greater than 1 are considered the most significant, as they account for the majority of the variation and serve as the best representatives of the system's attributes in the principal components analysis.

Thus, study highlights significant genetic variability among marigold genotypes and traits like no. of ray florets/flower show substantial potential for genetic improvement, while others, such as days to full bloom and flower initiation, are more influenced by environmental factors. Positive correlations with yield were observed for traits like plant height, fresh flower weight and number of flowers per plant, reinforcing their importance in crop improvement.

Path coefficient analysis further emphasizes that fresh flower weight and number of flowers per plant have the strongest direct effects on yield, while traits like days to 50% flowering exert negative direct effects. PCA further confirmed the genetic divergence among marigold genotypes, identifying key traits such as fresh flower weight, number of flowers/ plant and flower diameter as crucial factors for improving yield. Overall, the study underscores the importance of these morphological traits in marigold breeding, suggesting that they should be prioritized for selection to achieve sustainable improvements in floral yield in future crop improvement programs. Future research could incorporate genomic approaches to further elucidate the genetic basis of these traits and explore their potential in developing high-yielding, climate-resilient marigold cultivars.

AUTHOR'S CONTRIBUTION: Shorya Sharma (SS) and Reeta Bhatia Dey (RBD) were primarily responsible for the conceptualization of the research. Kanwar Pal Singh (KPS) and Akshay Talukdar contributed to shaping the research design. Bharti (B), Sapna Panwar (SP), and Eram Arzoo (EA) played crucial roles in designing the experiments, ensuring optimal conditions for genetic assessment. KPS, SP and AT contributed experimental materials. SS and RBD led the preparation of the manuscript, with SS drafting the primary content and RBD refining the scientific clarity.

CONFLICT OF INTEREST: The authors state that they have no conflicts of interest to disclose.

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