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Genetic diversity studies among marigold hybrids (*Tagetes erecta* L.)

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Abstract
The present investigation was carried out at Jarvi Seeds Private Limited, Bharadia, Bharuch, Gujarat, during the winter season of 2024-2025 using 34 exotic African marigold hybrids, procured from Thailand and China. The analysis of variance revealed highly significant differences among the hybrids for all yield and yield-contributing traits. It was observed that, for all the traits studied, the PCV values exceeded their corresponding GCV values, but differences were less in majority of cases indicated that environmental factors had played less influence on the expression of these characters. The traits *viz.*, plant height, average flower weight, branches per plant, flowers per plant flower yield per plant, days to first bud initiation, and flower diameter exhibited high heritability coupled with high/moderate genetic advance as a per cent of mean. Flower yield per plant was significantly and positively correlated with flower diameter, average flower weight, number of branches per plant and number of flowers per plant. This indicated that flower yield in marigold can be improved by direct selection of these characters. Maximum positive direct effect towards flower yield per plant was contributed by days to first bud initiation followed by number of flowers per plant, average flower weight of flower. Principal Component Analysis (PCA) indicated that among the nine characteristics examined, only two demonstrated principal components eigenvalues (PCs) exceeding 1 collectively accounting for approximately 68.62% of the cumulative variability among the studied traits.

Keywords: Marigold, *Tagetes erecta*, genetic diversity, hybrids, variability parameters

1. Introduction
Marigold (*Tagetes spp.*, 2n=2x=24) belongs to the family *asteraceae* and native of South and Central America. It is one of the most popular ornamental crops cultivated worldwide. It stands as a globally significant and commercially exploited flowering plant with a diverse array of applications extending far beyond its ornamental appeal (Cicevan *et al.*, 2022; Nikolić *et al.*, 2023) [11, 29]. The genus *Tagetes* contains over 50 cultivated and wild species (Cicevan *et al.*, 2022) [11]. Out of different species, two species *viz.*, *Tagetes erecta* (African marigold) and *Tagetes patula* (French marigold) are commonly grow species for loose flower production which are either single, semi double or double types. The word 'Marigold' is derived from the Greek word 'Mary' meaning 'Mother of Jesus' and 'Gold' meaning 'flower colour'. Marigold is extensively cultivated for its aesthetic qualities, serving as a popular cut flower, loose flower, and pot plant. Its widespread adoption is particularly evident in India, where it ranks as the third most important flower crop, after roses and chrysanthemums, and is integral to religious and social ceremonies, frequently used in garlands and Gajra arrangements (Khayum *et al.*, 2023) [23]. The crop is also valued in the cut-flower industry for its shelf life and attractive colors, particularly shades of yellow, orange and red (Rime *et al.*, 2025) [34].
Beyond its ornamental value, marigold holds significant industrial importance. Its flowers are a rich source of carotenoids, notably lutein, which are commercially extracted for use in pharmaceuticals, as natural food colorants, and in various dairy products. Lutein, a xanthophyll pigment, is essential for human health, particularly for maintaining eye health by helping to prevent conditions such as cataracts and macular degeneration (Gupta, 2014; Chitichotpanya *et al.*, 2022) [16, 7]. *Tagetes erecta* and *Tagetes patula*, exhibit nematicidal, insecticidal and antimicrobial properties, making them effective components of integrated pest management

(IPM) systems (Cristina e Santos *et al.*, 2022) [12]. In addition, marigold extracts are employed in traditional medicine for their anti-inflammatory, antioxidant and hepatoprotective activities (Venkatesh *et al.*, 2023) [45]. The increasing demand for natural colorants, biopesticides and ornamental flowers has expanded the scope of marigold cultivation, both in domestic and export markets (Singh *et al.*, 2020) [41].

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 (Santosh *et al.* 2018) [12]. 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 (Namita *et al.* 2008) [27]. 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 (Karuppaiah and Kumar, 2010) [19]. 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.

The Mahalanobis (1936) [25] D^2 statistic is used for measuring genetic diversity which provide the magnitude of divergence among the groups under consideration. On the basis of D^2 values one can group genotypes in to different clusters. This information is useful to formulate efficient crossing programme among the genotypes of diverse origin.

Yield, a quantitative trait influenced by various factors and the environment, was analysed 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 (Sinha *et al.* 2021) [42].

In recent year's addition to open-pollinated varieties, hybrid marigolds have gained prominence due to their superior performance in yield, uniformity and floral quality. Hybrids generally exhibit heterosis for key traits such as larger and firmer blooms, extended vase life, early flowering and enhanced tolerance to biotic and abiotic stresses. These advantages make hybrids particularly valuable for both ornamental purposes and industrial applications, including pigment extraction and essential oil production. The use of hybrids also enables the combination of desirable traits from diverse parental lines, ensuring better adaptability across environments and catering to the dynamic preferences of consumers and the floriculture industry. Furthermore, hybrids often show greater stability and resilience compared to traditional varieties, making them a reliable choice for commercial cultivation

(Sharma *et al.*, 2025b) [40]. Therefore, this study aims to evaluate the field performance of different African marigold (*Tagetes erecta*) exotic hybrids, identify superior ones for commercial and industrial use and study trait interrelationships to support the breeding of strong, high-yielding and good-quality.

2. Materials and Methods

2.1 The Treatments

The present investigation was carried out at Jarvi Seeds Private Limited, Bharadia, Bharuch, Gujarat, during the winter season of 2024-2025. A total of 34 exotic African marigold hybrids, procured from Thailand and China were evaluated, with their detailed descriptions presented in Table 1. Seeds of the hybrids were first raised in a nursery seedbed for 30 days, after which the seedlings were transplanted into the main experimental plots. The trial was laid out in a randomized complete block design (RCBD) with three replications. Each plot consisted of ridges measuring 10.00 m in length and 1.00 m in width, with a plant spacing of 30 cm and a row spacing of 1.00 m. Pinching was carried out 45 days after transplanting. Nutrient management involved a basal application of 150:100:100 kg ha^{-1} NPK, applied 8 days after transplanting, followed by a top dressing of 45 kg N ha^{-1} at 45 days after transplanting. The first irrigation was provided immediately after transplanting, and subsequent irrigations were scheduled weekly. All recommended cultural practices were carried out as required. The observations were recorded on five randomly tagged five plants from each cultivar of each replication. For all the characters were taken under grand growth stage (60 days), the mean values of randomly selected plants were calculated for each observation.

2.2 Statistical Analysis

The coefficients of variation *viz.* genotypic coefficient of variation (GCV) and Phenotypic coefficient of variation (PCV) were computed using the method outlined by Burton and Devane, 1953 [6]. Heritability (Broad sense) was calculated as the ratio of genotypic variance to total phenotypic variance, expressed as a percentage (Allard, 1960) [1]. The expected genetic advance was derived using the approach of (Johnson *et al.* 1995) [17]. Both genotypic and phenotypic correlations were determined based on the formulae by Al-Jabouri (1958) [2]. Direct and indirect effects of recorded characters on yield were assessed following the procedure of Dewey and Lu (1959) [13]. The software's OPSTAT and Indostat 9.1 versions were used for the statistical analysis. Mean values of all parameters were used for Principal Component Analysis (PCA), conducted using R software.

3. Results and Discussion

The analysis of variance revealed highly significant differences among the hybrids for yield and yield-contributing traits *viz.*, days to first bud initiation, days to 50% flowering, duration of flowering, plant height, flower diameter, average flower weight, branches per plant, flowers per plant, and flower yield per plant (Table 2). No parameter exhibited non-significant differences. The wide range of diversity amongst the cultivars allows for the crop to be significantly improved.

3.1 Estimation of Genetic Parameters for Growth and Flowering

The estimates of genetic parameters, including phenotypic variance (σ^2_p), genotypic variance (σ^2_g), genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), broad-sense heritability (h^2_{bs}), genetic advance (GA) and genetic advance as per cent of mean (GAM) for yield and yield attributing traits of marigold are showcases in Table 3. It was observed that, for all the traits studied, the PCV values exceeded their corresponding GCV values, but differences were less in

majority of cases. It indicated that environmental factors had played less influence on the expression of these characters. Similar results were also reported by Savadi *et al.* (2024) [38] and Kumari *et al.* (2025) [24]. The consideration of genetic factors is crucial when implementing selection programs. High GCV and PCV exhibited by flowers per plant and flower yield per plant, indicating the presence of high amount of genetic variability for these traits and effective for selection because the response to selection is directly proportional to the variability present in the experimental material. This finding are in conformity with the previous result as reported by Gangwar *et al.* (2025) [14]. However, low values of PCV and GCV were observed for days to first bud initiation, days to 50% flowering and duration of flowering. These findings have previously been reported by Thirumalmurugan *et al.* (2020) [44] and Sharma *et al.* (2025b) [40]. Plant height, flower diameter, average flower weight and branches per plant recorded moderate phenotypic and genotypic coefficient of variation (PCV and GCV) indicated that selection would be difficult for these characters, as the genotypic effect would be modified by the environmental effect. Similar results were also reported by Gobade *et al.* (2017) [15], Choudhary *et al.* (2017) [10] and Kumari *et al.* (2025) [24].

Solely relying on the genotypic coefficient of variation provides limited insight into the heritable component of the observed variation, underscoring the importance of estimating heritability for a thorough assessment. High heritability was recorded for plant height, average flower weight, branches per plant, flowers per plant and flower yield per plant indicates good correspondence between genotypic and phenotypic values and thereby low environmental effect on the expression of these characters. Heritability estimates alone do not provide reliable information about the gene action governing the expression of a particular character. The heritability estimates along with expected genetic advance is more useful than heritability alone for improving a particular trait (Johnson *et al.* 1995) [17].

The traits *viz.*, plant height, average flower weight, branches per plant, flowers per plant flower yield per plant, days to first bud initiation, and flower diameter exhibited high heritability coupled with high/moderate genetic advance as a per cent of mean. These findings suggest that selecting for these traits based on phenotype would be highly appropriate and effective. Findings by Santhosh *et al.* (2018) [37], Kumar *et al.* (2006) [21], Gobade *et al.* (2017) [15], Gangwar *et al.* (2025) [14] and Sharma *et al.* (2025b) [40] also reported similar results in Marigold. A plant breeder will be able to create criteria based on phenotypic performance only if high estimates of heredity are available. When a trait has a high heritability, selection for that trait is relatively simple since the genotype and phenotype closely coincide because the environment contributes little to the phenotype. Panse (1957) [30] suggested that the genotypic variations for such characters are probably due to high additive gene effects and least influenced by the environment. Also, moderate heritability with moderate genetic advance as a percent of mean was exhibited by days to 50% flowering and same moderate heritability but low genetic advance as a percent of mean was recorded for duration of flowering suggests that non-additive gene activities have a role in the inheritance of trait and that simple selection may not be sufficient to achieve the desired effects. According to Namita *et al.* (2008) [27], cultivar selection may not be effective for traits, so the high heritability is being displayed as a result of the environment's positive influence. Our findings were in conformity with Sahu *et al.* (2021) [36] and Sharma *et al.* (2025b) [40].

3.2 Genotypic and Phenotypic Correlation Coefficient Analysis

Yield is not an independent trait but resultant of the interactions of a number of component traits among themselves as well as with the environment in which the plant grow. Each trait is likely to be modified by action of genes present in the genotypes of plant and also by the environment so it becomes difficult to evaluate this complex trait directly. Therefore, correlation study of yield with its component traits has been executed, to find out the yield contributing traits.

Correlation analysis was done to find out association among flower yield and different yield contributing parameters both at phenotypic and genotypic levels and the data have been presented in Table 4. In general, the magnitude of correlation coefficient at genotypic level was found higher than the corresponding correlation at phenotypic level, thereby indicating a strong inherent association between various characters under study. Flower yield per plant was significantly and positively correlated with flower diameter, average flower weight, number of branches per plant and number of flowers per plant. This indicates that flower yield in marigold can be improved by direct selection of these characters. The results was consistent with previously reported by Savadi *et al.* (2024) [38]. Also, number of flowers per plant exhibited positive and significant relation with duration of flowering, flower diameter, average flower weight and number of branches per plant at both genotypic and phenotypic level. Similar result was obtained by Savadi *et al.* (2024) [38] for average flower weight and number of branches per plant; by Thakur and Kaur (2023) [43] for duration of flowering and flower weight at phenotypic level. While number of branches per plant showed was significantly and positively correlated with duration of flowering, flower diameter, average flower weight at both genotypic and phenotypic level. Similar relationship observed between average flower weight and flower diameter at both genotypic and phenotypic level [Poulose *et al.* (2021)] [33]. Also, days to first bud initiation at both genotypic and phenotypic exhibited significant and positive relation with days to 50% flowering [Poulose *et al.* (2021) [33]. Plant height with days to first bud initiation and flower yield per plant with duration of flowering showed significant and positive association at phenotypic level only. While positive and significant association at phenotypic level exhibited by average flower weight with days to first bud initiation, days to 50% flowering and plant height. For plant height similar result observed by Poulose *et al.* (2021) [33] previously.

Negative and significant association exhibited by duration of flowering with days to first bud initiation and days to 50% flowering at both genotypic and phenotypic level [Poulose *et al.* (2021) [33]. Also, number of branches per plant showed similar association with days to first bud initiation. There are some traits which showed significant and negative at phenotypic level (flower diameter and days to 50% flowering, number of flowers per plant and days to first bud initiation, number of flowers per plant and days to 50% flowering) and at genotypic level (number of branches per plant and days to 50% flowering). At phenotypic level for number of flowers per plant and days to first bud initiation and genotypic level for number of branches per plant and days to 50% flowering [Poulose *et al.* (2021) [33]. While all trait interrelationships other than above are either nonsignificant and positive or nonsignificant and negative.

Environmental factors can affect the relationships between characters. Selection is often based on the association of quantitatively significant and economically significant yield characteristics. It is impossible to assess the population for every

quantitative attribute since breeders must manage a very large population to meet their goals. Thus, estimations of the yield correlation with other traits for which genotypes could be readily quantified or evaluated visually are required. When a breeding program for crop genetic improvement is implemented, this correlation study helps in investigating the prospect of increasing yield through indirect selection of its highly correlated component characteristics. Acquiring knowledge about the relationships between various plant characteristics and yield is essential, as it enables the selection procedure to assign high-yielding genotypes more quickly. Only through genotypic correlation, which removes the influence of the environment, can true or actual link be determined Choudhary *et al.* (2015) [9].
The results stated a strong association between morphological traits and yield, suggesting that positive relationships among desirable characters can facilitate simultaneous improvement. Notably, flower diameter, average flower weight, number of branches per plant and number of flowers per plant emerged as key traits that should be prioritized in selection for higher flower yield.

3.3 Path Coefficient Analysis

In present study, path coefficient analysis was carried out by taking flower yield per plant as dependent variable to partition correlation coefficients into direct and indirect effects in order to determine the contribution of different characters towards the flower yield per plant. Direct and indirect effects of various characters on flower yield per plant indicated that there is an agreement between direction and magnitude of direct effect of various character and correlation with flower yield per plant. Thus, a significant improvement in flower yield per plant can be expected through selection in the component traits with high positive direct effects. The estimates of path coefficient for different attributes on flower yield were presented in Table 5.
Perusal of data indicated that maximum positive direct effect towards flower yield per plant was contributed by days to first bud initiation followed by number of flowers per plant, average flower weight of flower. The other traits which showed positive direct effect with flower yield per plant were duration of flowering and number of branches per plant indicating that more number of branches per plant the more will be the number of flowers through better vegetative growth, thus, ultimately increasing the flower yield. These findings are in agreement with the findings of Mathad *et al.* (2005) [26], Karuppaiah and Kumar (2011) [20], kumar *et al.* (2014) [22] and Poulose *et al.* (2021) [33] in marigold. However, days to 50% flowering, plant height and flower diameter exerted a direct negative effect on flower yield per plant. This suggests that emphasis must be given on such traits while selection to improve the flower yield. For flower diameter this findings are conformity with result obtained by Poulose *et al.* (2021) [33].
The magnitude of residual effect was low, which indicated that major portion of contribution towards flower yield per plant might be explained on the basis of characters included in the present study. However, some more characters not included in the present study may contribute to account for the residual effect. Similar findings were also reported by the finding of Panwar *et al.* (2013) [31], Namita *et al.* (2009) [28] in marigold, Anuja and Jahnavi (2012) [3] and Ushabharti *et al.* (2014) [46] in African marigold.
Path analysis highlighted flowers per plant and average flower weight as the most decisive yield-contributing traits, supported by early bud initiation and higher branching as secondary determinants. In contrast, delayed flowering (days to 50% flowering) consistently exerted a negative effect, underscoring the need to avoid late-flowering hybrids. These insights suggest a focused breeding roadmap: prioritize flowers per plant and average flower weight as primary selection indices, reinforce yield gains through early bud initiation and branching and exclude late-flowering types.

3.4 Genetic Divergence

Creation of variability and selection within, leading to diverse genotype is the common protocol that a conventional plant breeder follows. Genetic relationship among genotypes thus generated can be measured by similarity or dissimilarity of any number of quantitative characters, assuming that the differences between characters of genotypes ultimately reflect in the divergence of the genotypes. In heterosis breeding programmes, the diversity of parent is always emphasized upon. More the diverse parents within a reasonable range, better is the chance of improving economic traits under consideration in the resulting offspring. However, it is a difficult task for the breeder to select the most suitable and genetically divergent parents, unless one is provided with necessary information about genetic variability and genetic diversity present in the available germplasm.
Generally, geographical diversity is considered and taken as a measure of genetic diversity when no scientific tool is available. However, inferential criterion may not be used for discrimination among the populations occupying ecologically marginal habits. The multivariate analysis, using Mahalanobis's D^2 statistic, provide useful statistical tool for measuring the genetic diversity in a given population with respect to the characters considered together. Further, the problem of selecting diverse parents for hybridization programme can be narrowed, if one can identify the characters, responsible for discrimination between populations.
The multivariate analysis applying D^2 statistics is one among the best techniques available to compute genetic divergence in a population (Rao,1952) [35]. In any plant breeding research, for the identification of specific parents with useful recombination, it is essential to have an idea of the nature and degree of genetic diversity.
The study on the contribution of individual characters towards divergence (Table 6) revealed that flowers per plant contributed the maximum (65.95%), followed by average flower weight (10.87%), plant height (9.98%) and days to first bud initiation (8.73%). A comparatively lower contribution was observed from days to 50% flowering (1.96%), followed by duration of flowering (1.43%), flower diameter (0.71%) and flower yield per plant (0.36%). Interestingly, branches per plant recorded no contribution towards divergence. Since more than 95 per cent of the total divergence was accounted for by flowers per plant, average flower weight, plant height and days to first bud initiation, these traits may be considered as the most influential for genetic divergence and should be given due emphasis while selecting parents for hybridization and improvement programs in marigold. Similar results were reported by Choudhary *et al.* (2017) [10] and Gangwar *et al.* (2025) [14].
All the genotypes of the present investigation were subjected to multivariate analysis (D^2analysis) on the basis of all the selected 9 characters. Using Tocher's method of clustering, ten clusters were obtained by the grouping of 34 genotypes (Table 7). Among these, cluster IV had the highest number of genotypes (11), cluster I with nine genotypes, Cluster II and III with four genotypes each, and clusters V, VI, VII, VIII, IX and X were independent clusters. In a parallel investigation, Choudhary *et al.* (2017) [10] grouped 30 genotypes into six clusters. Similarly,

Gangwar *et al.* (2025) [14] categorized 16 genotypes into five clusters. The presence of several monogenotypic clusters (V to X) reflects the existence of unique and diverse genotypes that are genetically distinct from others. Meanwhile, the large size of Cluster IV indicates close genetic resemblance among those members. Overall, the clustering pattern highlights the availability of both genetically similar and highly diverse genotypes, which can be strategically exploited in breeding programs. Genotypes from distant clusters are expected to yield higher heterosis and greater variability when used in hybridization.

D^2 analysis also gives the intra and inter-cluster distances, which estimate the extent of diversification. Clusters III and IV (23.12) recorded the highest inter-cluster distance, followed by clusters III and VII (21.33), which implies that the divergence between these clusters is maximum, while, the lowest inter-cluster distance was recorded between clusters V and IX. Cluster IV (7.71) exhibited maximum intra-cluster distance followed by Cluster III (5.33), cluster I (5.27) and cluster II (5.25) indicating its variability to be significant in the genotypes within these clusters (Table 8). Hence, selection within a cluster may be practiced on the basis of the highest mean value of the genotype for advantageous traits.

Table 9 presents the variation in cluster means for nine traits across all 34 marigold hybrids. The analysis of cluster means revealed considerable variation across different traits. Cluster VII noted minimum values for days to first bud initiation (41.33 days), days to 50% flowering (51.67 days) while maximum value for duration of flowering (62.67). Cluster III noted maximum values for flower diameter (5.51 cm), branches per plant (21.72), flowers per plant (94.42) and flower yield per plant (569.30 g). Cluster II recorded higher plant height (110.18 cm) while cluster X recorded higher average flower weight (6.40 g).

From this character-wise analysis, it is evident that cluster III consistently outperformed other clusters in key yield-contributing traits, including flower diameter, branches per plant, flowers per plant and ultimately flower yield per plant. This highlights its potential as a superior cluster for yield improvement. In contrast, cluster VII consistently recorded the lowest values for several important traits, such as average flower weight and flower yield per plant, indicating comparatively weaker performance. Overall, the results suggest that cluster III genotypes may serve as promising candidates for selection in breeding programs targeting enhanced flower yield and associated components, while cluster VII may require considerable improvement for yield-related attributes.

3.5 Principal Component Analysis (PCA)

The results of the Principal Component Analysis (PCA) elucidated the genetic variation among the genotypes for all phenotypic traits under investigation. Principal components with eigenvalues exceeding 1 and a variation percentage greater than 4% were deemed significant (Brejda *et al.*, 2000) [5]. The outcomes of the PCA illustrated the genetic diversity among marigold genotypes concerning the studied traits. 'Eigenvalues' serve as a measure of the significance and contribution of each component to the total variance, while each coefficient of the eigenvectors indicates the extent of contribution of each original variable associated with each principal component. There are no standardized tests to ascertain the significance of eigenvalues and coefficients (Jolliffe, 2011) [18] (Table 10 and Fig.1). Appropriate values assess the importance and contribution of each component to the overall variance, while each value reflects the degree of contribution of the various principal components explaining the variability. This suggests a tendency for these components to remain correlated and should be considered during the utilization of these traits in breeding programs (Chakravorty and Ghosh, 2013) [8].

Principal Component Analysis (PCA) indicated that among the nine characteristics examined, only two demonstrated principal components eigenvalues (PCs) exceeding 1 collectively accounting for approximately 68.62% of the cumulative variability among the studied traits. The remaining components were excluded from further analysis due to their eigenvalues being less than one. Principal components with eigenvalues >1 explained more total variation in the data than individual attributes (Brejda *et al.*, 2000) [5]. Consequently, these two PCs were prioritized for additional interpretation. Among these, PC1 accounted for the highest variation, explaining 43.62% of the total variance with an eigenvalue of 3.93. The subsequent principal component PC2, elucidated variation of 25.00. Only these two components, which possessed eigenvalues greater than 1, were deemed suitable for further investigation. Principal components with eigenvalues exceeding 1 are known to elucidate a greater total variation in the dataset compared to individual attributes (Brejda *et al.*, 2000) [5].

The loading vectors of the first two principal components (PCs) provided insights into the major contributing traits toward total variability (Table 11). PC1, which explained 43.62% of the total variance, was strongly and positively associated with branches per plant (0.942), flowers per plant (0.940), flower yield per plant (0.939), flower diameter (0.707) and average flower weight (0.495). This indicates that these traits played a pivotal role in distinguishing the genotypes, with higher contributions toward productivity-related parameters. PC1 also showed a moderate positive loading for duration of flowering (0.431), while days to first bud initiation and days to 50% flowering contributed negatively, reflecting their inverse relationship with yield-attributing traits. On the other hand, PC2, which accounted for an additional 25.00% of the variance, was positively influenced by duration of flowering (0.459) but negatively associated with days to first bud initiation (-0.798), days to 50% flowering (-0.751), plant height (-0.493) and average flower weight (-0.691). This component thus primarily represented variation associated with flowering duration and earliness traits, contrasting with yield-related attributes. Together, the first two PCs cumulatively explained 68.62% of the variability, highlighting their importance in summarizing the underlying genetic divergence. In similar studies, Sharma *et al.* (2025a) [39] observed that three PCs contributed 74.61% of the variation, while Sharma *et al.* (2025b) [40] reported that four PCs accounted for 83.57% of the total variation. The results suggest that selection for branches per plant, flowers per plant, and flower yield per plant could be effective in identifying high-yielding genotypes, while PC2 emphasized the role of earliness and flowering behaviour in genotype differentiation.

The PCA biplot (Fig. 2) displayed the distribution of 34 genotypes along the first two principal components, which together explained 68.62% of the total variation (PC1: 43.62%, PC2: 25.00%). The vectors representing traits revealed distinct associations. Branches per plant (BPP), flowers per plant (FPP), flower yield per plant (FYPP) and flower diameter (FD) were strongly aligned with PC1, suggesting that this axis mainly captured yield-related variation. Average flower weight (AFW) also showed a positive association with PC1 but was positioned at an angle, indicating moderate influence. Days to first bud initiation (DFB) and days to 50% flowering (DTFF) projected in the opposite direction of yield traits, highlighting their negative association with productivity parameters. Duration of flowering

(DF) loaded positively on PC2, whereas plant height (PH) had a negative association with this axis. The placement of genotypes in the biplot reflected these relationships. For instance, genotypes positioned closer to BPP, FPP and FYPP vectors (such as G-10, G-11, G-23, and G-24) are characterized by superior yield attributes. Conversely, genotypes located in the direction of DFB and DTFF vectors (e.g., G-2, G-3, G-7) tended to exhibit late flowering, thereby contrasting with high-yielding genotypes. Overall, the biplot clearly separated yield-contributing traits from earliness traits, enabling the identification of genotypes that combined favorable characteristics for breeding programs.

Table 1: Detailed descriptions of 34 exotic African marigold hybrids

Sr. No.	Name of Hybrid/ Advanced Breeding Hybrids	Name of Company	Procured Country	Code	Flower colour
1.	264 Plus	AGA Agro Marigold Seeds	Thailand	MAR264SK	Yellow
2.	Chandra Yellow	AGA Agro Marigold Seeds	Thailand	MAR289SK	Yellow
3.	Vang Ving Orange	AGA Agro Marigold Seeds	Thailand	MAR005SS	Orange
4.	White Star	AGA Agro Marigold Seeds	Thailand	MAR055SS	White
5.	Bengal Orange	AGA Agro Marigold Seeds	Thailand	MAR070SS	Orange
6.	Supernova Deep Orange	AGA Agro Marigold Seeds	Thailand	MAR343SS	Orange
7.	Tall Orange#P01	Home Seeds Co. Ltd.	Thailand	P01	Orange
8.	Tall Orange#P09	Home Seeds Co. Ltd.	Thailand	P09	Orange
9.	Tall Orange#P10	Home Seeds Co. Ltd.	Thailand	P10	Orange
10.	Marigold#074	Home Seeds Co. Ltd.	Thailand	MAR074	Orange
11.	Marigold#078	Home Seeds Co. Ltd.	Thailand	MAR078	Yellow
12.	Narangi	Home Seeds Co. Ltd.	Thailand	MAR089	Orange
13.	Marigold#102	Home Seeds Co. Ltd.	Thailand	MAR102	Yellow
14.	Marigold#103	Home Seeds Co. Ltd.	Thailand	MAR103	Yellow
15.	Yellow#003	Target Genetics Pvt. Ltd.	Thailand	TGE003	Yellow
16.	Yellow#009	Target Genetics Pvt. Ltd.	Thailand	TGE009	Yellow
17.	Yellow#018	Target Genetics Pvt. Ltd.	Thailand	TGE018	Yellow
18.	Orange#002	Target Genetics Pvt. Ltd.	Thailand	TGE002	Orange
19.	Orange#003	Target Genetics Pvt. Ltd.	Thailand	TGE003	Orange
20.	Tall Orange#004	Target Genetics Pvt. Ltd.	Thailand	TGE004	Orange
21.	Yellow#071	Target Genetics Pvt. Ltd.	Thailand	TGE22SR-STY- 71YL	Yellow
22.	Yellow#023	Target Genetics Pvt. Ltd.	Thailand	TGE23SR-Y-23YL	Yellow
23.	Yellow#0068	Target Genetics Pvt. Ltd.	Thailand	TGE24WT-0068	Yellow
24.	Yellow#0065	Target Genetics Pvt. Ltd.	Thailand	TGE24WT-0065	Yellow
25.	Kolkata Orange	JYK Seed Co. Ltd.	China	1504H30-24-001	Orange
26.	Kolkata Primrose	JYK Seed Co. Ltd.	China	1504H30-24-002	Yellow
27.	Marvel yellow	JYK Seed Co. Ltd.	China	1504H30-24-003	Yellow
28.	Marvel Orange	JYK Seed Co. Ltd.	China	1504H30-24-004	Orange
29.	Marvel Gold	JYK Seed Co. Ltd.	China	1504H30-24-005	Yellow
30.	P8 Orange	JYK Seed Co. Ltd.	China	1504H30-24-006	Orange
31.	Sonata Yellow	JYK Seed Co. Ltd.	China	1504H30-24-007	Yellow
32.	Sonata Orange	JYK Seed Co. Ltd.	China	1504H30-24-008	Orange
33.	JYK24 Orange	JYK Seed Co. Ltd.	China	1504H30-24-009	Orange
34.	JYK25 Orange	JYK Seed Co. Ltd.	China	1504H30-24-010	Orange

Table 2: Analysis of variance (mean sum of squares) for different characters under study in marigold

Sr. No.	Characters	Mean Sum of Squares		
		Replications (df: 02)	Genotypes (df: 33)	Error (df: 66)
1.	Days to first bud initiation	3.19	33.99**	2.27
2.	Days to 50% flowering	12.36	58.14**	11.19
3.	Duration of flowering	20.72	51.27**	11.91
4.	Plant height	72.19	389.90**	25.55
5.	Flower diameter	0.21	0.85**	0.14
6.	Average flower weight	0.26	1.85**	0.10
7.	Branches per plant	0.69	21.32**	3.05
8.	Flowers per plant	2.02	911.33**	15.17
9.	Flower yield per plant	1551.63	45922.55**	829.04

Table 3: Estimation of genetic parameters of nine different yield and yield contributing traits

Sr. No.	Characters	Variance		GCV (%)	PCV (%)	h^2_{bs} (%)	GA	GAM (%)
		σ^2_g	σ^2_p					
1.	Days to first bud initiation	10.57	12.84	7.15	7.88	82.34	6.08	13.36
2.	Days to 50% flowering	15.65	26.84	6.72	8.81	58.31	6.22	10.58
3.	Duration of flowering	13.12	25.03	6.37	8.80	52.43	5.40	9.50
4.	Plant height	121.45	147.00	12.30	13.54	82.62	20.63	23.04
5.	Flower diameter	0.24	0.37	10.39	13.03	63.53	0.80	17.06
6.	Average flower weight	0.58	0.68	13.97	15.08	85.80	1.46	26.66
7.	Branches per plant	6.09	9.14	15.14	18.55	66.60	4.15	25.46
8.	Flowers per plant	319.28	326.56	30.76	31.11	97.77	36.40	62.65
9.	Flower yield per plant	15031.17	15860.21	37.90	38.93	94.77	245.87	76.00

Table 4: Coefficients of phenotypic and genotypic correlation among different yield components of marigold hybrids

Characters	Correlation	DTF	DF	PH	FD	AFW	BPP	FPP	FYPP
DFB	r_p	0.635**	-0.315**	0.244*	-0.099	0.201*	-0.230*	-0.258**	-0.140
	r_g	0.973**	-0.465**	0.286	-0.179	0.254	-0.358*	-0.286	-0.164
DTF	r_p		-0.284**	0.181	-0.227*	0.210*	-0.162	-0.219*	-0.121
	r_g		-0.347*	0.230	-0.255	0.231	-0.377*	-0.295	-0.196
DF	r_p			-0.092	0.155	-0.105	0.265**	0.282**	0.202*
	r_g			-0.135	0.171	-0.183	0.481**	0.389*	0.289
PH	r_p				0.048	0.243*	-0.022	-0.056	0.039
	r_g				0.112	0.253	-0.016	-0.066	0.028
FD	r_p					0.372**	0.495**	0.462**	0.518**
	r_g					0.550**	0.632**	0.592**	0.673**
AFW	r_p						0.287**	0.390**	0.647**
	r_g						0.440**	0.432*	0.666**
BPP	r_p							0.842**	0.788**
	r_g							1.028**	0.993**
FPP	r_p								0.935**
	r_g								0.961**

Note: ** Significant at 1% level, * Significant at 5% level

r_p = Phenotypic correlation coefficient, r_g = Genotypic correlation coefficient, DFB = Days to first bud initiation, DTF = Days to 50% flowering, DF = Duration of flowering, PH = Plant height, FD = Flower diameter, AFW = Average flower weight, BPP = Branches per plant, FPP = Flowers per plant, FYPP = Flower yield per plant

Table 5: Genotypic path coefficient analysis showing direct and indirect effects of different characters on flower yield per plant of marigold hybrids

Characters	DFB	DTF	DF	PH	FD	AFW	BPP	FPP	r_g with FYPP
DFB	0.82404	-0.78711	-0.07591	-0.01411	0.01598	0.10265	-0.05265	-0.17648	-0.1636
DTF	0.8019	-0.80884	-0.05663	-0.01133	0.02285	0.09345	-0.0554	-0.18243	-0.1964
DF	-0.38344	0.28081	0.16313	0.00664	-0.01529	-0.07375	0.07071	0.2402	0.289
PH	0.23565	-0.18581	-0.02196	-0.04933	-0.01003	0.10238	-0.00238	-0.04054	0.028
FD	-0.14714	0.20647	0.02787	-0.00553	-0.0895	0.2223	0.09285	0.36565	0.673**
AFW	0.20935	-0.18707	-0.02978	-0.0125	-0.04924	0.40407	0.06473	0.26661	0.6662**
BPP	-0.29512	0.30482	0.07846	0.0008	-0.05653	0.17793	0.14701	0.63538	0.9927**
FPP	-0.23537	0.23881	0.06342	0.00324	-0.05296	0.17435	0.15117	0.61787	0.9605**

Residual effect = 0.0303, Bold values = Direct effect, DFB = Days to first bud initiation, DTF = Days to 50% flowering, DF = Duration of flowering, PH = Plant height, FD = Flower diameter, AFW = Average flower weight, BPP = Branches per plant, FPP = Flowers per plant, FYPP = Flower yield per plant

Table 6: Contribution of each character to the divergence in marigold

Characters	No. of times ranked 1st	% contribution
Days to first bud initiation	49	8.73
Days to 50% flowering	11	1.96
Duration of flowering	8	1.43
Plant height	56	9.98
Flower diameter	4	0.71
Average flower weight	61	10.87
Branches per plant	0	0
Flowers per plant	370	65.95
Flower yield per plant	2	0.36

Table 7: Distribution of 34 marigold hybrids into 10 different clusters

Cluster	No. of hybrids	Name of hybrids
I	9	Marigold#103, Yellow#023, Kolkata Orange, Marigold#102, Bengal Orange, Marvel Gold, Kolkata Primrose, Yellow#071, Narangi
II	4	Tall Orange#P01, Tall Orange#P09, Tall Orange#004, Tall Orange#P10
III	4	Marigold#078, Yellow#0065, Yellow#0068, Marigold#074
IV	11	Sonata Yellow, Sonata Orange, JYK24 Orange, Chandra Yellow, Yellow#003, Vang Ving Orange, 264 Plus, Supernova Deep Orange, JYK25 Orange, P8 Orange, Yellow#009
V	1	Yellow#018
VI	1	Orange#002
VII	1	Orange#003
VIII	1	Marvel Orange
IX	1	White Star
X	1	Marvel Yellow

Table 8: Average intra (diagonal) and inter cluster distance among ten clusters

	Group 1	Group 2	Group 3	Group 4	Group 5	Group 6	Group 7	Group 8	Group 9	Group 10
Group 1	5.27	8.21	16.28	9.35	6.8	6.93	9.38	7.02	10.03	10.48
Group 2		5.25	17.68	10.98	8.37	9.1	13.76	8.99	12.3	12.27
Group 3			5.33	23.12	13.06	14.38	21.33	15.1	8.28	10.75
Group 4				7.71	12.72	11.53	9.68	12.35	16.64	16.77
Group 5					0	6.35	11.61	8.07	6.15	10.32
Group 6						0	10.4	9.76	7.94	10.81
Group 7							0	13.49	15.04	17.29
Group 8								0	10.45	6.44
Group 9									0	8.76
Group 10										0

Table 9: Cluster mean of yield and yield components of 34 marigold hybrids

Cha. →	DFB	DTF	DF	PH	FD	AFW	BPP	FPP	FYPP
I	45.04	59.74	57.52	85.07	4.58	5.38	15.94	57.94	313.68
II	50.00	62.42	56.08	110.18	5.26	6.13	16.37	56.95	352.79
III	41.75	54.17	61.58	86.40	5.51	6.10	21.72	94.42	569.30
IV	45.70	59.42	55.18	89.22	4.35	5.19	13.99	40.49	212.13
V	46.00	60.67	62.33	99.87	4.04	5.28	17.67	70.67	361.36
VI	43.33	52.33	48.33	99.00	4.36	5.02	17.20	64.33	326.95
VII	41.33	51.67	62.67	78.73	4.56	3.30	14.53	50.00	162.06
VIII	50.67	62.67	54.33	72.07	4.96	5.75	17.33	64.13	362.14
IX	42.67	55.33	61.33	93.13	4.10	5.82	19.27	79.20	468.76
X	47.67	59.00	49.33	68.93	5.34	6.40	18.40	74.47	472.36

Cha. - Characters, DFB = Days to first bud initiation, DTF = Days to 50% flowering,
DF = Duration of flowering, PH = Plant height, FD = Flower diameter, AFW = Average flower weight, BPP = Branches per plant, FPP = Flowers per plant, FYPP = Flower yield per plant

Table 10: Eigen value, % variance and cumulative total variance (%) of nine principal components

Principal Components	Eigen value	Variance (%)	Cumulative total Variance (%)
Principal Component 1	3.925	43.617	43.617
Principal Component 2	2.250	25.004	68.620
Principal Component 3	0.886	9.845	78.465
Principal Component 4	0.814	9.043	87.508
Principal Component 5	0.539	5.993	93.501
Principal Component 6	0.388	4.309	97.810
Principal Component 7	0.153	1.704	99.514
Principal Component 8	0.040	0.441	99.955
Principal Component 9	0.004	0.045	100.000

Table 11: Loading vectors and eigen values for first two principal components of variation

Quantitative variables	Principal Component 1	Principal Component 2
Days to first bud initiation	-0.408	-0.798
Days to 50% flowering	-0.416	-0.751
Duration of flowering	0.431	0.459
Plant height	-0.030	-0.493
Flower diameter	0.707	-0.188
Average flower weight	0.495	-0.691
Branches per plant	0.942	-0.047
Flowers per plant	0.940	-0.079
Flower yield per plant	0.939	-0.275
Eigen value	3.925	2.250
% Variance	43.617	25.004
Cumulative total Variance (%)	43.617	68.620

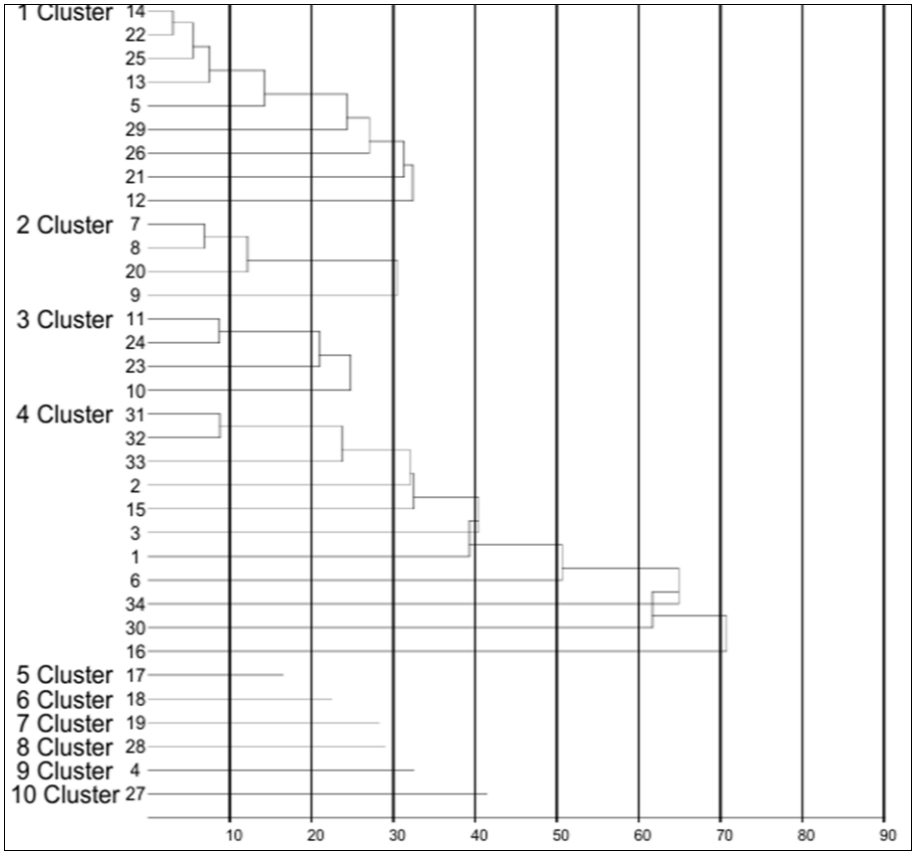

Fig 1: Dendrogram based on summarized data on differentiation among 34 hybrids according to Tocher's method

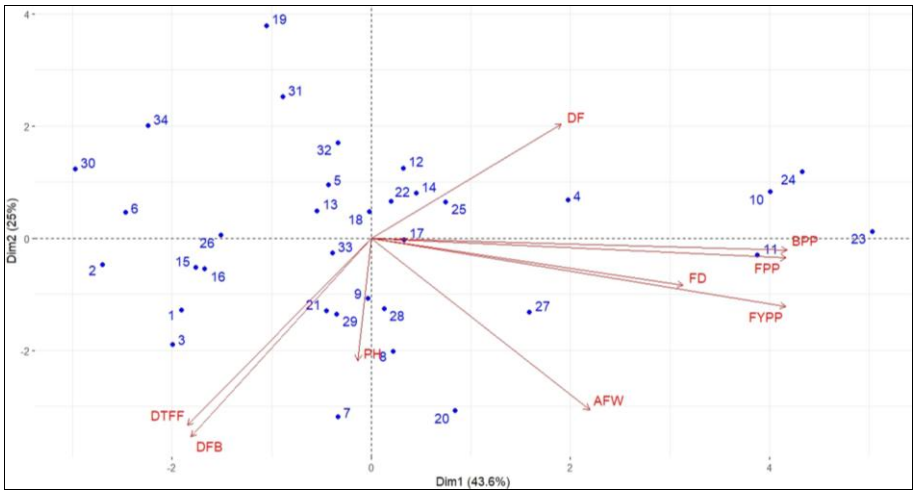

Fig 2: PCA biplot showing the relationship among 34 genotypes and nine traits based on the first two principal components

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