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Studies on Variability and Heritability for yield contributing traits in Ornamental Sunflower (*Helianthus annuus* L)

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ABSTRACT

An investigation entitled "Genetic Variability and Heritability Studies in Ornamental Sunflower (Helianthus annuus L.)" was conducted at the Department of Floriculture and Landscape Architecture, College of Horticulture, Bengaluru. Twenty-three ornamental sunflower genotypes were evaluated with three replications using a Randomized Complete Block Design (RCBD). The study revealed considerable variability among the 23 genotypes with respect to vegetative, floral, and flower yield parameters. Flower stalk girth recorded the highest genotypic coefficient of variation (GCV) at 39.03%, followed by leaf area at 60 days after sowing (37.54%), total flower heads per plant (30.88%), and vase life (28.89%). The highest phenotypic coefficient of variation (PCV) was observed for flower stalk girth (39.06%), followed by leaf area (37.54%), plant height (29.49%), and vase life (29.38%). The presence of high GCV and PCV values indicated substantial variability within the germplasm, providing a strong base for effective selection. High heritability estimates (>60%) were recorded for all studied parameters. Furthermore, the expected genetic advance as a percentage of the mean (>20%) was high for flower stalk girth, plant height at 60 DAS, total flower heads per plant, vase life, and flower stalk length, the research highlighted significant variability among ornamental sunflower genotypes, with clear indications of both heritable and non-heritable components. These findings suggest that the identified traits can be effectively utilized for selecting superior parents in future sunflower breeding programmes.

Keywords: *Heritability, genetic advance, variability, Helianthus, ornamental sunflower.*

Introduction

Sunflower (*Helianthus annuus* L.) was primarily cultivated as an important oilseed crop, valued for its edible oil rich in unsaturated fatty acids, particularly linoleic acid. The genus name *Helianthus* is derived from the Greek words *helios* (sun) and *anthos* (flower), reflecting both the plant's characteristic appearance and its heliotropic behavior [1]. Belonging to the family Compositae (Asteraceae)—the largest family of flowering plants—the sunflower is distinguished by its unique composite inflorescence, known as a capitulum or head. The capitulum consists of a central receptacle surrounded by an involucre of protective bracts, giving rise to the iconic floral structure that defines the species. It contains two distinct types of florets: ray florets and disc florets. The ray florets, arranged along the periphery, are sterile and serve the primary function of attracting pollinators with their large, showy ligules, which are fused petals pointing outward. At the center lie the disc florets, which are hermaphroditic and fertile, producing pollen and ovules essential for seed development. This intricate floral architecture contributes to efficient pollination, often aided by bees and other insects and its role as an oilseed crop, sunflower has gained importance as a multipurpose plant. Its seeds are used for direct consumption as snacks, in confectionery, and as bird feed [2]. Sunflower oil is also valued for culinary use, biodiesel production, and pharmaceutical formulations, sunflower serves ecological and environmental functions, such as phytoremediation of heavy metals from contaminated soils and as a rotation crop to improve soil structure [3].

Its bright and ornamental flower heads make it a popular choice in landscaping and cut-flower industries, sunflower represents a remarkable plant that combines economic, nutritional, environmental, and ornamental significance, making it one of the most versatile crops worldwide. Sunflower is an annual erect plant with a long stem and one or more flower heads [12]. Sunflower is recently being grown as an ornamental crop and Indian farmers can definitely fetch benefit from the revival of this flower, as well as the lengthy, warm growing season in the south by taking up sunflower cultivation as an ornamental cut flower with broad seasonal habit and soil type adaptability [4]. Sunflower is a short-duration crop that has gained importance for its early maturity, photo-insensitivity, wide adaptability to diverse cropping systems, and tolerance to drought. It blooms 55 to 75 days after sowing. Thus breeding programme in sunflower aims to develop cultivars that have varying durations and good ornamental characteristicsmore number of branches, attractive colours, proportionate plant height and spread, maximum flowering time, maximum flower longevity [5] *etc*. A fundamental understanding of the level of diversity contained in the available germplasm is essential for such a crop development effort. A planned breeding programme must give careful consideration to the selection of eligible parents. Therefore, it is essential to select the finest parents with significant genetic variance for traits that are economically significant in order to use them in breeding programmes [6], non-heritable variation frequently obscures the heritable variance, making selection programmes challenging.

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With this as major objective a research was conducted to use the heterogeneity found in sunflower genotypes for future crop development programmes.

Material and methods

The experiment was conducted at the College of Horticulture, Mysuru, during 2023. A total of 23 germplasm lines of ornamental sunflower, exhibiting variation in growth, flowering, yield, and quality traits, were evaluated for their suitability as cut flowers. The crop was established using the ridge and furrow method with a spacing of 60 cm × 40 cm. Observations on yield-contributing and quality traits were recorded from five plants per replication, and uniform cultural practices were followed throughout the growing season to ensure proper crop growth.

The recorded data were subjected to statistical analysis using Inquest data analytics software. Genetic parameters such as genotypic and phenotypic coefficients of variation (GCV and PCV) were estimated following the method of [7]. The coefficients of variation were classified as low (<10%), moderate (10–20%), and high (>20%). Broad-sense heritability (h^2) was estimated according to [8] and categorized as low (<30%), moderate (31–60%), and high (≥61%). Genetic advance as a percentage of the mean was calculated following [9] and similarly grouped into low (0–30%), moderate (31–60%), and high (≥61%).

For recording flower yield parameters, flower heads were harvested with secateurs at the stage when one to two ray florets had opened, preferably during early morning or late evening to minimize postharvest stress. Observations were taken on five randomly selected plants under each treatment and replication. Heritability in the broad sense was computed using the formula suggested by [10] providing insights into the proportion of phenotypic variance attributable to genetic causes. This facilitated the assessment of genetic control over traits, thereby aiding in the selection of superior ornamental sunflower lines for cut flower production.

$$H^2 = \frac{Vg}{Vp} \times 100$$

Where,

H^2 = Heritability in the broad sense, V_g = Genotypic variance, V_p = Phenotypic variance

Heritability was classified following Robinson et al. (1949):

- Low: 0–30%
- Moderate: 31–60%
- High: ≥61%

Genetic Advance (GA):

Genetic advance was estimated using the formula given by [11]:

$GA = H^2 \times K \times \sigma_p$

Where,

H^2: Heritability,

K: Standard selection differential (2.06 at 5% probability level)

σ_p: Phenotypic standard deviation of the trait

Genetic Advance as Percent of Mean (GAM): The expected genetic advance as a percent of the mean was computed as:

$$\text{GA as per cent of mean} = \frac{\text{GA}}{\text{Grand mean}} \times 100$$

Where:

- GAGAGA = Genetic advance
- Grand Mean = Mean of the trait

Classification of GAM (Johnson et al., 1955):

- Low: 0–10%
- Moderate: 10–20%
- High: >20%

Results and Discussion

The genetic parameters of ornamental sunflower genotypes, including range, mean, genotypic variance, phenotypic variance, genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), genetic advance (GA), broad-sense heritability (H^2), and genetic advance as percent of mean (GAM), are summarized in Table 1. The magnitude of GCV and PCV provides insight into the extent of genetic and environmental variability present in the population for different traits. For the improvement of flower yield, it is essential to have a precise understanding of the genetic architecture of yield and its contributing components. In this study, considerable variation was observed among the ornamental sunflower genotypes, and estimates of genetic parameters were used to assess the potential of different traits for selection and breeding. The combined evaluation of GCV, PCV, heritability, and GAM offers valuable information for identifying traits that are largely governed by genetic factors and thus hold promise for effective selection in future breeding programmes.

Genotypic and Phenotypic Variation

Genotypic variance and overall phenotypic variance were estimated to determine the extent of genetic contribution to yield and quality traits in ornamental sunflower (Table 1). The highest genotypic coefficient of variation (GCV) was observed for flower stalk girth (39.03%), followed by leaf area at 60 days after sowing (36.83%), total flower heads per plant (30.88%), and vase life (28.89%). Similar trends were earlier reported by Nair and Shiva (2003) and Magar (2008) in gerbera. The lowest GCV (10.85%) was recorded for the number of ray florets per flower head, indicating limited genetic variability for this trait. Overall, the GCV ranged from 10.85% (ray florets per head) to 39.03% (flower stalk girth). Comparable results have been documented in tuberose by [12–13], where phenotypic coefficients of variation (PCV) consistently exceeded GCV, suggesting an appreciable influence of the environment. Likewise, [14] reported high GCV and PCV for plant spread, plant height, disc diameter, number of flowers per plant, individual flower weight, flower stalk length, and head diameter in ornamental crops. In the present study, PCV values followed a similar trend, with the highest PCV recorded for flower stalk girth (39.06%), followed by leaf area (37.54%), plant height (29.49%), and vase life (29.38%). The lowest PCV was noted for ray florets per flower head (11.31%), followed by plant spread in the north–south direction (12.47%) and east–west direction (12.73%), in line with earlier reports by [15].

In all traits studied, PCV values were slightly higher than their corresponding GCV values, reflecting the predominance of genetic factors with relatively limited environmental influence. The high estimates of both GCV and PCV for traits such as flower stalk girth, leaf area, vase life, total flower heads per plant, and plant height suggest the presence of substantial variability. These traits, therefore, represent promising targets for improvement through direct selection.

Comparable findings have also been reported by [16–17] in other ornamental crops.

The traits evaluated included flower stalk length (cm), flower disc diameter (cm), duration of flowering (days), days from flower bud initiation to flower opening, and number of branches [4] recorded medium PCV and GCV, indicating scope for their improvement through selection. However, low variability measurements were observed for the ray florets number per flower head, diameter of flower head (cm), number of days for flower bud initiation, duration of crop, plant spread at N-S direction at 60 days after sowing, and plant spread at E-W direction at 60 days after sowing.The coefficient of variation does not show the heritable portion; it only indicates the degree of variability prevalent for various characters. Efficacy of selection can be improved by the heritability estimate as quoted by [10] which reflects the impact of the environment on total variability and showing the importance of phenotypic effect on a genotype, thus increasing the efficacy of selection. As a result,heritability in a general sense is the ratio of genotypic variability to overall variability [18]

The estimates of broad-sense heritability (H^2) ranged from 60.86% to 99.84%, while genetic advance as percent of mean (GAM) varied from 20.86% to 80.34% (Table 2). Among the traits studied, flower stalk girth (H^2 = 99.84%, GAM = 80.34%), leaf area at 60 DAS (H^2 = 96.28%, GAM = 75.43%), total flower heads per plant (H^2 = 97.03%, GAM = 62.66%), and vase life (H^2 = 96.66%, GAM = 58.51%) exhibited high heritability coupled with high genetic advance. This combination indicates that these traits are largely governed by additive gene action and, therefore, direct selection would be highly effective in improving them. Similar results have been reported by [19–20], who also observed high heritability for vase life, yield, and plant height in sunflower.

Traits such as flower stalk length (H^2 = 99.01%, GAM = 45.71%), days from bud initiation to flower opening (H^2 = 99.18%, GAM = 37.89%), and flower disc diameter (H^2 = 80.56%, GAM = 32.65%) displayed high heritability along with moderate genetic advance, suggesting the combined influence of both additive and non-additive gene actions. Comparable findings were documented by [13], who noted that some traits with high heritability but low GAM may reflect limited genetic variability within the genotypes evaluated.

As emphasized by [13] in sunflower, high heritability alone does not guarantee high genetic gain, as the extent of genetic variability also determines the response to selection. In the present study, the highest GAM was recorded for flower stalk girth (80.34%), followed by leaf area (75.43%), confirming their potential for genetic improvement, flower head diameter recorded the lowest GAM (20.86%), indicating a relatively limited scope for selection-based progress. It is important to note that heritable variation cannot be estimated solely through genotypic coefficient of variation. When GCV is interpreted alongside heritability estimates, it provides more reliable insights into the expected genetic advance from selection. This has also been highlighted by Burton [12–18] in marigold and by [6] in other ornamentals. Overall, the combination of high heritability and high genetic advance in key traits proves to be a valuable tool for effective selection and future improvement of ornamental sunflower.

Summary and Conclusion

High heritability does not necessarily correspond to high genetic advance for a given trait. Traits exhibiting high genetic advance are generally governed by additive gene effects [12] making them amenable to improvement through simple phenotypic selection. Conversely, high heritability coupled with low genetic advance often indicates the predominance of non-additive gene action, where hybridization may be a more effective breeding strategy [2-5]. In the present study, all evaluated traits recorded heritability (H^2) values greater than 60% and genetic advance as a percentage of the mean (GAM) above 20%, indicating that the observed variability is largely genetically determined and primarily controlled by additive gene action, with minimal environmental influence. While heritability estimates provide insight into the genetic contribution to trait expression and the potential effectiveness of selection, they can be affected by environmental conditions and experimental material. Therefore, combining heritability with genetic advance offers a more reliable basis for selection than heritability alone. From a breeder's perspective, traits with both high heritability and high GAM allow for the direct selection of superior genotypes based on phenotypic performance, thereby accelerating genetic improvement in ornamental sunflower.

Table 1: Estimates of genetic parameters for different characters inornamental sunflower (Helianthus annuus L.) genotypes

Sl. No.	Parameters	Range	Mean	GCV %	PCV %	Heritability %	GAM %
1	Plant height at 60DAS (cm)	27.27-137.36	93.17	24.14	29.49	67.10	40.72
2	Plant spread NS at 60 DAS (cm^2)	52.97-92.29	73.44	11.54	12.47	85.73	22.02
3	Plant spread EW at 60 DAS (cm^2)	52.94 - 91.06	72.38	11.85	12.73	86.69	22.74
4	Number of leaves at 60DAS	25.10 – 44.68	29.80	15.06	19.31	60.86	24.21
5	Leaf area at 60 DAS (cm^2)	1899.69-7461.90	4087.77	36.83	37.54	96.28	74.45
6	Number of branches at 60 DAS	9.74-23.68	19.72	15.82	17.35	83.19	29.74
7	Duration of crop	47.01-76.67	59.25	11.57	12.32	88.29	22.40
8	Days taken for flower bud initiation	34.03-50.14	40.01	11.60	12.34	88.40	22.47
9	Days taken for flower bud initiation to flower opening	11.84-20.95	16.27	18.47	18.54	99.18	37.89
10	Duration of flowering	15.44- 45.02	29.42	18.43	22.11	69.45	31.64
11	Flower Stalk length (cm)	13.70-50.30	33.25	22.30	22.41	99.01	45.71
12	Flower Stalk girth (cm)	0.36-6.70	4.33	39.03	39.06	99.84	80.34
13	Flower Head diameter (cm)	5.83-9.40	7.87	11.48	13.01	77.81	20.86
14	Flower disc diameter (cm)	1.79-4.83	3.40	17.66	19.67	80.56	32.65
15	Number of ray florets per flower head	22.22-34.61	28.32	10.85	11.31	92.07	21.45
16	Total flower heads per plant	3.53-28.30	17.34	30.88	31.34	97.03	62.66
17	Vase life (days)	5.59-13.01	7.28	28.89	29.38	96.66	58.51

GCV: Genotypic coefficient of variation,
PCV: Phenotypic coefficient of variation,
H^2: Broad sense heritability
GA as % mean: Genetic advance as percent mean

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