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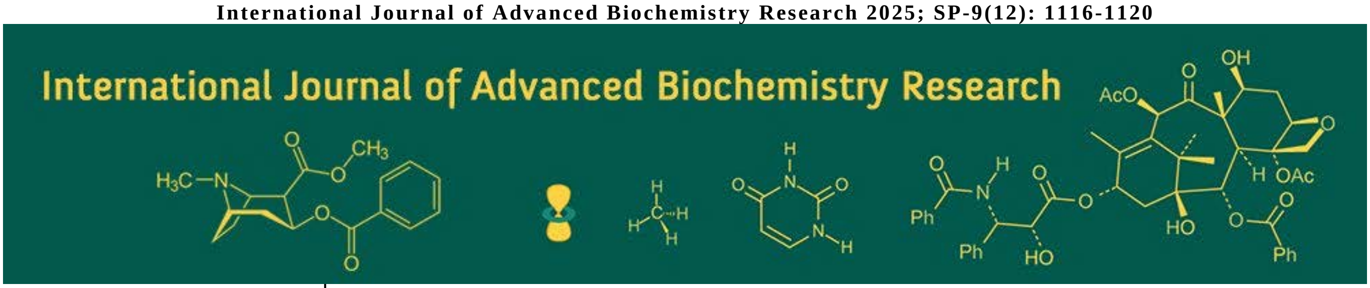

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Estimation of genetic variability in china aster (*Callistephus chinensis*) genotypes at Raipur Chhattisgarh

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Abstract

The present investigation was conducted to evaluate genotypic variability among China aster (*Callistephus chinensis* L.) genotypes for key morphological, floral and yield traits. The field experiment was carried out during 2022-23 and 2023-24 at the Horticultural Research cum Instructional Farm, Department of Floriculture and Landscape Architecture, College of Agriculture, Indira Gandhi Krishi Vishwavidyalaya, Raipur, Chhattisgarh. The experiment was laid out in a Completely Randomized Design with three replications. The current study thoroughly evaluated genetic variability among China aster genotypes over two consecutive *Rabi* seasons (2022-23 and 2023-24) using ANOVA and essential genetic parameters such as genotypic coefficient of variance, phenotypic coefficient of variance, heritability and genetic advance. The notable genotypic differences identified across all traits confirm the presence of significant genetic diversity, which is vital for effective selection and future breeding initiatives. High phenotypic coefficients of variation and genotypic coefficients of variation were observed for traits including flower yield per plant number of leaves per plant at 90 DAT, number of ray florets, number of branches and number of flowers per plant. Notably, the narrow difference between phenotypic coefficients of variation and genotypic coefficients of variation for these traits suggests minimum environmental impact and strong genetic variability, thereby increasing their appropriateness for direct phenotypic selection. Traits such as flower yield per plant and number of ray florets consistently demonstrated high heritability (>99%) along with high genetic advance as a percentage of mean (>100%), indicating a predominance of additive gene action and a favorable response to selection. Likewise, plant height, flower stalk length and number of flowers per plant exhibited high heritability with moderately high genetic advance, highlighting their breeding potential. In contrast, traits like seed germination, flower head diameter and disc diameter, while moderately heritable, showed low genetic advance, reflecting limited additive genetic variance and greater environmental influence, thus constraining their potential for direct improvement. In summary, traits with high heritability and genetic advance, particularly flower yield per plant, number of ray florets and number of leaves per plant, are optimal targets for genetic enhancement. These results establish a solid genetic basis for selection strategies aimed at developing superior China aster genotype with enhanced yield and floral quality like diameter of flower head, disc diameter, number of ray florets and number of flower and weight of flower thereby promoting sustainable advancements in floriculture.

Keywords: China aster, Genotypic coefficient of variance, Genetic advance as percent of mean, Heritability, Phenotypic coefficient of Variance

Introduction

China aster (*Callistephus chinensis*) is one of the most commonly cultivated annual flowering plants worldwide. The genus name derives from the Greek words ‘kalistos’ meaning "most beautiful" and ‘stephos’ meaning "a crown", referencing the flower’s striking appearance. It belongs to the family Asteraceae and consists of only one species, *chinensis*, which is native to China. China aster is classified as a half-hardy annual, meaning it thrives in moderate climates but is sensitive to frost. The plant exhibits an upright growth habit, with rough, hairy branches and alternate leaves that are broad, elliptical or ovate in shape, and distinctly serrated. The flowers vary in form ranging from solitary, single, semi-double, to fully double bloomsand are commonly found in shades of indigo-blue, lavender, rose and white. China aster serves both commercial and ornamental purposes, cultivated for cut and loose flowers. (Arora, 2006). Its blooms are extensively used for religious offerings, garlandmaking, home décor, and floral arrangements. (Singh, 2022) [3]. Owing to its adaptability, it grows successfully in a range of agro-climatic regions, including India, France, Germany, the Netherlands, the UK, Russia, Japan, North America, Switzerland and other parts of Europe. In India, the flower is predominantly grown by small and marginal farmers, particularly in the states of Karnataka, Tamil Nadu, Maharashtra, Andhra Pradesh and West Bengal.

In the year 2023-24, floriculture was practiced on about 2.85 lakh hectares of land in India. The total production included around 22.84 lakh tonnes of loose flowers and 9.47 lakh tonnes of cut flowers. In Chhattisgarh, flower crops are cultivated over an area of 13,638 lakh hectares, with a total production of 3,34,672 metric tonnes (MT). (Directorate of Horticulture, 2022-23). The evaluation of genetic variability is a critical initial step in any crop improvement program. Variability observed within a population result from the combined influence of genetic (G) factors, environmental (E) influences and their interaction (G × E). As emphasized by Johnson *et al.*, (1955) [14], the phenotypic variation in a segregating population arises from both inheritable and non-inheritable components, with the inheritable portion defined as genetic variance. Therefore, the estimation of genotypic variance, heritability, and genetic advance for various quantitative traits becomes essential in breeding programs designed to develop improved cultivars. Variability refers to the extent of differences among individuals in a population, which may be due to inherent genetic differences or variations in the environmental conditions under which the plants are grown. The magnitude of this variability plays a pivotal role in the selection process, as it forms the basis for identifying and selecting genetically superior genotypes. Moreover, the presence of substantial genetic variation is vital not only for enhancing tolerance to biotic and abiotic stresses but also for improving adaptability across diverse agro-climatic zones, ultimately contributing to yield stability and crop resilience. Variance, which measures the degree of deviation among individuals, was first partitioned into its components by Fisher (1935) [11], who classified phenotypic variance into genotypic and environmental variance. Additionally, he further subdivided genotypic variance into additive, dominance and epistatic components, with only the additive (genetic) portion being transmissible to the next generation. The effectiveness of selection is largely governed by the magnitude of this genetic variability, as greater diversity enhances the probability of isolating elite genotypes. Consequently, for breeders, genetic variability represents the cornerstone of any effective breeding strategy. The importance of assessing variability for formulating efficient and targeted selection approaches. In this context, the genotypic coefficient of variation emerges as a crucial parameter that allows for comparative assessment of genetic diversity across various quantitative traits, thus aiding in the identification of traits with the most promising genetic potential.

Materials and Methods

The Field experiment was carried out at Horticultural Research cum Instructional Farm, Department of Floriculture and Landscape Architecture, College of Agriculture, Indira Gandhi Krishi Vishwavidyalaya, Raipur, Chhattisgarh during 2022-23 and 2023-24. The location of experiment *i.e.,* Raipur, is situated in the central part of Chhattisgarh at 21^0 16’ N latitude, 81^0 36’ E longitude and at an altitude of 286.56 m from mean sea level. The experiment was laid out in a Completely Randomized Design with three replications. Totally 10 genotypes were collected from different sources and evaluated for growth and yield parameters. Observations were recorded on various growth parameters, plant height(cm), number of branches and plant spread(cm), floral traits days to first flower opening, flower head diameter (cm), disc diameter(cm), number of ray florets and yield parameters (number of flowers per plant, duration of flowering and flower yield per plant (g)). Analysis of variance (Fisher and Yates, 1963) [12]; Coefficient of variation and Heritability Broad Sense (Burton and De Vane, 1953) [6] and Genetic advance (Johanson *et al.*)

Results and Discussion

Analysis of variance

An analysis of variance (ANOVA) was conducted to assess the mean sum of squares for morphological and floral traits of China aster across two consecutive *Rabi* seasons (2022-23 and 2023-24), including the pooled data. ANOVA results indicated that the differences among the 10 genotypes were highly significant ($p < 0.05$) for all traits studied. This signifies the presence of considerable genetic variability within the evaluated China aster genotypes. Such variability is essential in breeding programs, as it provides a strong basis for effective selection and potential genetic enhancement of desirable traits in future cultivar development. Hence, the findings justify further genetic studies and selection efforts for crop improvement. These findings are consistent with previous research by Rai *et al.*, Natraj *et al.* and Bhargav *et al.*

Genotypic and phenotypic coefficients of variance

Genotypic and phenotypic coefficients of variance. The analysis and tabulation of genetic variability parameters for yield traits. These parameters include mean, range, genotypic and phenotypic coefficients of variance (percent), heritability in the broad sense (percent), genetic advance and genetic advance as a % of mean. The value of yield and its components for genotypic coefficients of variance and phenotypic coefficients of variance ranged low to high. For all the character genotypic coefficients of variance is smaller then phenotypic coefficients of variance, it presented the environment have masking effect on the expression on genetic variability presented in Table-1. Among the yield attributes, Flower yield per plant (g) had highest genotypic coefficients of variance (76.37) and phenotypic coefficients of variance (76.40) value followed by Number of leaves per plant [90 DAT] genotypic coefficients of variance (75.19) and phenotypic coefficients of variance (75.20) and Number of ray florets/flower head genotypic coefficients of variance (52.39) and phenotypic coefficients of variance (52.47). In contrast Seed germination (%) genotypic coefficients of variance (9.19) and phenotypic coefficients of variance (10.60) showed relatively low genotypic coefficient of vaiance and phenotypic coefficient of variation, suggesting that this trait is more strongly affected by the environment than by genetic factors, which may limit the effectiveness of selection. The comparison between genotypic coefficient of variation and phenotypic coefficient of variation for traits in China aster revealed that phenotypic coefficient of variation consistently exceeded genotypic coefficient of variation for all traits across pooled mean indicating the influence of environmental factors on the expression of these traits. These results are consistent with the findings of Mugali *et al.* in China aster, Savadi *et al.*

Heritability

Heritability estimates along with genetic advance is a useful criterion in selecting an individual, high heritability estimates along with high genetic advance as percent of mean. In case of pooled mean Heritability was attained in all characters of cultivars ranges from Number of leaves per plant [90 DAT] (99.99) followed by Plant height (cm) [90 DAT] (99.97), Flower yield per plant (g) (99.94), Weight of flower/plant (g) (97.89), Flower stalk length (cm) (99.87), Days to first flower opening (99.74), Number of branches per plant and Number of ray florets/flower head (99.72), Plant spread (cm) [E-W] (99.58), Number of flowers per plant (99.52), Plant spread (cm) [N-S] and Duration of flowering (days) (99.39), Flower head diameter (cm) (97.70), Disc diameter (cm) (97.20) and Seed germination (%) (75.03) respectively. This indicates the character were less influenced by environment. This intrinsic genetic potential is further measured through heritability, which evaluates the extent of genetic correlation between parental traits and those of their progeny and is frequently used to forecast the probability of trait transmission across generations (Bharathi *et al.*, 2023) [4].

Genetic Advance

High genetic advance (>20) was recorded for several key traits, indicating the predominance of additive gene action and the possibility of substantial improvement through selection. The highest genetic advance was observed in flower yield per plant (167.50), followed by number of leaves per plant at 90 DAT (158.61), number of ray florets per flower head (109.67), plant height at 90 DAT (38.15) and number of flowers per plant (25.89), days to first flower opening (20.48) and Flower stalk length (cm) (20.76). These traits hold significant promise for achieving genetic gains under selection pressure. Moderate genetic advance (10-20%) was noted for number of branches per plant (14.51), Seed germination (%) (13.9), duration of flowering (12.13) plant spread [E-W] (11.69) and plant spread [N-S] (10.21), suggesting reasonable potential for improvement. In contrast, low genetic advance (<10) was observed for weight of flower per plant (2.60), flower head diameter (2.30) and disc diameter (0.90). Such low values point to the predominance of non-additive gene effects and greater environmental influence, limiting the scope for improvement through direct phenotypic selection in these traits. Genetic advance gives an idea about the expected genetic changes and for efficient selection, high heritability along with high genetic advance can be used Similar results were obtained by (Johnson *et al.*, 1955) [14].

Genetic advance as % of mean

The genetic advance as a percentage of the mean for pooled mean ranged from 16.39% to 157.28%, indicating the expected improvement in trait performance through selection. High genetic advance as percent of mean (>20%) was observed for all characters except seed germination, reflecting substantial genetic variability and strong potential for genetic gain. The highest genetic advance as percent of mean was recorded for flower yield per plant (157.28%), followed by number of leaves per plant at 90 DAT (154.89), number of ray florets per flower head (107.78%), number of branches per plant (104.67%), number of flowers per plant (90.04%), flower stalk length (82.95%), weight of flower per plant (80.95%), plant height at 90 DAT (75.90%), plant spread [E-W] (48.89%), plant spread [N-S] (48.62%), duration of flowering (47.00%) and disc diameter (45.06%). These traits suggest the predominance of additive gene action and indicate that selection would be highly effective in improving these characters. Moderately high genetic advance as percent of mean (20-40%) was observed for flower head diameter (37.53%) and days to first flower opening (31.87%), which also demonstrate good potential for genetic improvement through selection. The only trait exhibiting moderate genetic advance as percent of mean (10-20%) was seed germination (16.39%), implying a relatively lower scope for genetic gain, likely due to greater environmental influence or non-additive gene effects.

Additionally, traits like plant height, number of flowers per plant, weight of flower per plant and flower stalk length showed moderately high to high genetic advance values along with high heritability, suggesting that selection based on phenotypic performance could be highly effective for these traits. Similarly, moderate genetic advance combined with high heritability was observed for traits such as days to flower opening and plant spread, indicating that although genetic control exists, environmental influence may also play a role. In contrast, traits like seed germination, flower head diameter, and disc diameter consistently exhibited low genetic advance despite moderate to high heritability, reflecting the involvement of non-additive gene action and a higher environmental influence on their expression. This reduces the efficiency of direct selection and implies that such traits may require alternate breeding strategies, such as recurrent selection or heterosis breeding, to realize genetic gains. These patterns highlight the importance of understanding genetic variability and inheritance to guide targeted improvement efforts in China aster.

Table 1: Genetic Parameters for Pooled mean of China aster genotypes studied during *Rabi*-2022-23&2023-24

Sl. No	Characters	Range	GCV (%)	PCV (%)	Heritability (%) [broad sense]	Genetic advance	Genetic advancement as percent of mean (%)
1	Plant height (cm) [90 DAT]	27.47-50.26	36.85	36.86	99.97	38.15	75.90
2	Number of leaves per plant [90 DAT]	31.12-102.40	75.19	75.20	99.99	158.61	154.89
3	Plant spread (cm) [N-S]	14.79-20.99	23.68	23.75	99.39	10.21	48.62
4	Plant spread (cm) [E-W]	16.67-33.05	23.78	23.83	99.58	11.69	48.89
5	Number of branches per plant	6.37-25.77	50.88	50.95	99.72	14.51	104.67
6	Days to first flower opening	54.03-80.20	15.49	15.51	99.74	20.48	31.87
7	Flower head diameter (cm)	4.21-7.61	18.43	18.65	97.70	2.30	37.53
8	Disc diameter (cm)	1.45-2.75	22.19	22.50	97.20	0.90	45.06
9	Flower stalk length (cm)	14.26-39.21	40.29	40.32	99.87	20.76	82.95
10	Number of ray florets/flower head	49.45-	52.39	52.47	99.72	109.67	107.78

		221.23					
11	Number of flowers per plant	15.70-45.93	43.82	43.92	99.52	25.89	90.04
12	Weight of flower/plant (g)	1.94-5.56	39.32	39.34	99.89	2.60	80.95
13	Duration of flowering (days)	17.77-36.13	22.88	22.95	99.39	12.13	47.00
14	Flower yield per plant (g)	31.58-255.73	76.37	76.40	99.94	167.50	157.28
15	Seed germination (%)	70.72-88.47	9.19	10.60	75.03	13.09	16.39

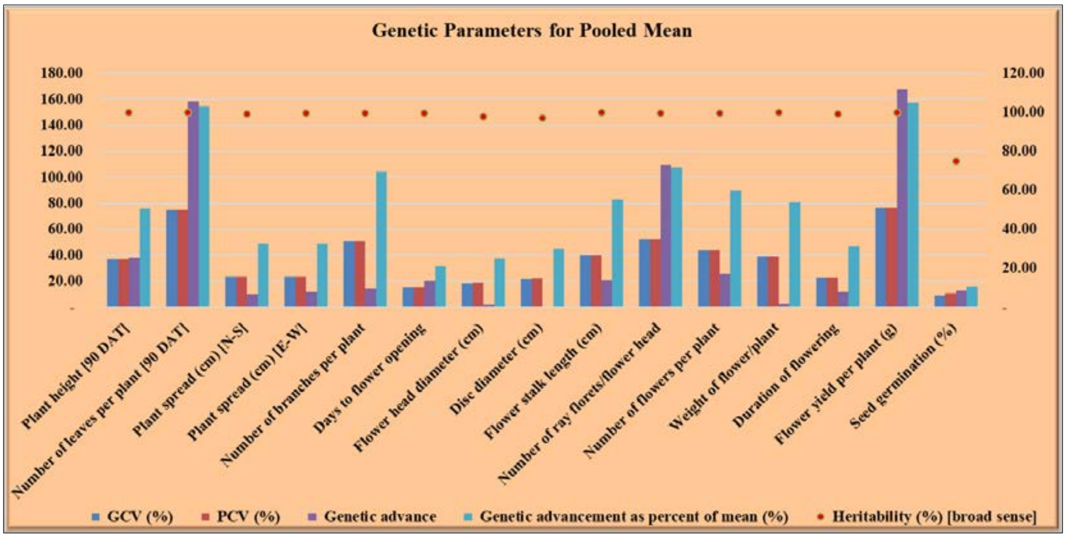

Fig 1: Variability study on different genotypes of China Aster

Conclusion

The present study comprehensively assessed genetic variability among China aster genotypes among pooled data through ANOVA and key genetic parameters, including genotypic coefficient of variation, phenotypic coefficient of variation, heritability and genetic advance. The significant genotypic differences observed across all traits reaffirm the existence of substantial genetic diversity, which is critical for effective selection and future breeding programs. High phenotypic coefficients of variation and genotypic coefficients of variation were recorded for traits such as flower yield per plant, number of leaves per plant at 90 days after transplanting, number of ray florets, number of branches, and number of flowers per plant. Importantly, the narrow gap between phenotypic coefficient of and genotypic coefficients of variation for these traits indicates minimal environmental influence and strong genetic control, thereby enhancing their suitability for direct phenotypic selection. Traits such as flower yield per plant and number of ray florets consistently exhibited high heritability (>99%) coupled with high genetic advance as percent of mean (>100%), suggesting predominant additive gene action and a promising response to selection. Similarly, plant height, flower stalk length and number of flowers per plant showed high heritability with moderately high genetic advance, underscoring their breeding potential. Conversely, traits like seed germination, flower head diameter and disc diameter, although moderately heritable, exhibited low genetic advance, indicating limited additive genetic variance and greater environmental influence, thus limiting their scope for direct improvement. Overall, traits exhibiting high heritability and genetic advance, particularly flower yield per plant, number of ray florets and number of leaves per plant, are ideal targets for

genetic enhancement. These findings provide a robust genetic foundation for selection strategies aimed at developing superior China aster cultivars with improved yield and floral quality, supporting sustainable floriculture advancement.

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Conflict of interest

The authors declare that they have no conflict of interest.

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