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Assessment of growth and yield variability in F_4 generation of China aster cross Arka Poornima × AAC-1

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Abstract
China aster (*Callistephus chinensis*), a widely cultivated ornamental crop belonging to the Asteraceae family, is extensively grown in India for various floral applications, including loose flowers, cut flowers, and decorations. The present study assessed genetic variability, heritability, and genetic advance in fifteen F_4 lines derived from the cross Arka Poornima ×AAC-1 at Kittur Rani Channamma College of Horticulture, Arabhavi, during the Rabi season of 2023-24. The experiment followed a randomized block design (RBD). Results revealed significant genetic variability, with traits such as individual flower weight (heritability: 94.43%, genetic advance: 67.82%) and flower yield per plant (heritability: 85.13%, genetic advance: 43.47%) showing high heritability and genetic advance, indicating strong additive gene action. Traits with moderate to low heritability and genetic advance were more influenced by environmental factors, suggesting limited potential for direct selection. The findings emphasize the potential of selecting high-yielding genotypes to develop improved *China aster* cultivars with enhanced ornamental and commercial value.

Keywords: China aster, ornamental crop, genetic variability, heritability, breeding programs

Introduction
The China aster (*Callistephus chinensis* (L.) Nees), a member of the Asteraceae family, is a widely cultivated annual flowering plant grown globally for its ornamental value. In India, it is extensively cultivated for diverse applications, including loose flowers, cut flowers, floral arrangements, garlands, venis (hair adornments) and vase decorations. The crop is predominantly grown in Karnataka, Tamil Nadu, West Bengal, and Maharashtra, where it is mainly cultivated by marginal and small-scale farmers. Additionally, dwarf varieties of China aster are preferred for pot cultivation, making them well-suited for hedges, window boxes, and home gardens (Rao *et al*., 2012) [17].
The genus Callistephus is monotypic, comprising only a single species, C. chinensis, which is a diploid with a chromosome number of 2n = 18 (Huziwara, 1954) [9]. Understanding the extent and nature of genetic variability within a germplasm is crucial for enhancing desirable floral attributes. In breeding programs, the assessment of genotypic and phenotypic coefficients of variation (GCV and PCV, respectively) provides insight into the degree of variation among genotypes. These parameters help breeders evaluate the potential genetic gain and the effectiveness of different selection methods. The process of determining heritability and genetic parameters allows for an informed selection strategy, helping breeders predict the expected response to selection (Holland *et al*., 2003) [8].
Several quantitative genetic studies have been conducted on flower characteristics in China aster (Rao, 1982; Negi *et al*., 1983; Ravikumar and Patil, 2003) [16, 13, 18]. These studies highlight the importance of genotypic variability, heritability, and genetic advance in the selection and improvement of floral traits. In general, early segregating generations exhibit greater genetic variation compared to later generations.

Thus, the F_4 population plays a crucial role in facilitating the selection of superior lines with desirable traits, including high yield and unique flower colours. Given that China aster is a self-pollinated crop, developing a high-yielding variant with distinct floral characteristics is fundamental for establishing a successful and efficient breeding program aimed at improving both ornamental and commercial value.

Materials and Methods

The present study was conducted at the Department of Floriculture and Landscaping, Kittur Rani Channamma College of Horticulture, Arabhavi, during the Rabi season of 2023-24. The experiment involved fifteen F_4 lines derived from the cross Arka Poornima × AAC-1, along with their respective parental varieties, AAC-1 and Arka Poornima, which were included as checks for comparison.

The experiment was laid out in a randomized block design (RBD) to ensure proper replication and minimize experimental errors. Seedlings aged 45 days were transplanted in the field using the ridge and furrow method at a spacing of 30 × 30 cm to facilitate proper growth and development. All recommended agronomic practices, including irrigation, fertilization, and pest management, were meticulously followed to ensure optimal crop performance.

Observations were recorded on various growth, flowering, yield, and quality parameters across all F_4 populations. The variability parameters, including mean, range, phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV), were computed following the methodology described by Burton and De Vane (1953) [2]. Additionally, broad-sense heritability and genetic advance were estimated to assess the extent of genetic control over traits and the expected response to selection. These parameters provided critical insights into the potential for genetic improvement in the studied China aster population, aiding in the identification of superior breeding lines for future cultivar development.

Results and Discussion

The estimates of phenotypic coefficient of variation (PCV) were consistently higher than those of the genotypic coefficient of variation (GCV) for all the recorded traits (Table 1 and Fig. 1), highlighting the presence of significant genotype × environment interactions. Traits exhibiting high variability (PCV > 20%) included number of branches (PCV: 33.82%, GCV: 33.27%), number of flowers per plant (PCV: 29.58%, GCV: 28.05%), individual flower weight (PCV: 34.86%, GCV: 33.88%), and flower yield per plant (PCV: 24.79%, GCV: 22.87%). The narrow difference between PCV and GCV values in these traits suggests that genetic factors play a predominant role, and there exists considerable genetic variability, indicating significant potential for trait improvement through selection.

Moderate PCV and GCV values were observed for traits such as plant height (PCV: 17.71%, GCV: 16.74%), stem girth (PCV: 17.93%, GCV: 17.08%), and flower diameter (PCV: 13.84%, GCV: 10.23%). On the other hand, low PCV and GCV values were recorded for traits like days to first flowering (PCV: 6.12%, GCV: 3.21%), days to 50% flowering (PCV: 5.46%, GCV: 2.86%), duration of flowering (PCV: 9.23%, GCV: 6.93%), and vase life (PCV: 4.08%, GCV: 2.14%). These results suggest that environmental factors significantly influence the expression of these traits, as evident from the greater difference between PCV and GCV values. The findings are in line with previous research conducted by Hittalmane *et al.* (2022) [6], Kumar *et al.* (2022) [12], Ramya *et al.* (2019) [15], Rajiv *et al.* (2014) [14] and Harishkumar *et al.* (2017) [3] in China aster. The low variability observed in certain traits could be attributed to the fact that the population was derived from a bi-parental cross and was significantly influenced by environmental factors, posing a challenge for genetic improvement through selection. These observations align with earlier studies by Rajiv *et al.* (2014) [14], Harishkumar *et al.* (2017) [3], and Ramya *et al.* (2019) [15] on China aster.

In the present study, while PCV was higher than GCV for all traits, several traits showed a narrow gap between the two, indicating that the phenotypic expression of these genotypes is primarily controlled by genetic factors, with only a slight to moderate environmental influence. These results support findings reported by Hittalmane *et al.* (2022) [6], Kumar *et al.* (2022) [12], Ramya *et al.* (2019) [15], Rajiv *et al.* (2014) [14], and Harishkumar *et al.* (2017) [3] in studies on China aster.

Heritability and Genetic Advance

Traits demonstrating high heritability (>60%) coupled with high genetic advance over mean (>20%) were recorded for individual flower weight (heritability: 94.43%, genetic advance: 67.82%) and flower yield per plant (heritability: 85.13%, genetic advance: 43.47%) (Table 1 and Fig. 1). These findings suggest that these traits are primarily governed by additive gene action, making them ideal candidates for direct selection in breeding programs. Conversely, low heritability and low genetic advance were observed for days to first flowering (heritability: 27.45%, genetic advance: 3.46%) and days to 50% flowering (heritability: 27.45%, genetic advance: 3.09%), indicating strong environmental influence and limited scope for genetic improvement through selection alone.

High heritability coupled with high genetic advance is considered desirable for effective trait improvement through selection, as it indicates a strong genetic component with minimal environmental interference. These results are consistent with those reported by Hittalmane *et al.* (2022) [6], Kumar *et al.* (2022) [12], Hosalli *et al.* (2019) [7], Ramya *et al.* (2019) [15] and Khangjarakpam *et al.* (2015) [11] in China aster, as well as Henny *et al.* (2021) [5] and Hebbal *et al.* (2018) [4] in chrysanthemum.

Moderate heritability coupled with moderate genetic advance was recorded for plant height (heritability: 89.28%, genetic advance: 32.58%), number of branches (heritability: 88.83%, genetic advance: 30.93%), stem girth (heritability: 90.81%, genetic advance: 33.53%), and number of flowers per plant (heritability: 89.94%, genetic advance: 54.80%), suggesting that while selection may be effective, improvement in these traits may also benefit from hybridization approaches.

Moderate heritability with low genetic advance was observed for flower diameter (heritability: 54.69%, genetic advance: 15.59%) and duration of flowering (heritability: 56.37%, genetic advance: 10.72%), while low heritability with low genetic advance was recorded for vase life (heritability: 27.45%, genetic advance: 2.31%). This suggests that both additive and non-additive gene effects influence these traits, meaning improvement can be achieved through hybridization followed by selection in later generations. These findings corroborate previous research by Harishkumar *et al.* (2017) [3], Ramya *et al.* (2019) [15], Hittalmane *et al.* (2022) [6], and Anitha *et al.* (2021) [1]. Similar results were also reported by Ramya *et al.* (2019) [15] and Harishkumar *et al.* (2017) [3] in China aster, as well as Karuppaiah and Kumar (2011) [10] in marigold.

Table 1: Estimation of mean, range, components of variance, heritability and genetic advance of F_4 population "Arka Poornima x AAC-1" for 11 parameters

Characters	Mean	Range	PCV (%)	GCV (%)	h^2(%)	GA	GAM
Plant height(cm)	53.76	38.10 - 79.60	17.71	16.74	89.28	17.51	32.58
Number of branches	8.81	5.00 - 16.00	33.82	33.27	96.73	5.94	67.40
Stem girth (cm)	1.05	0.72 - 1.53	17.93	17.08	90.81	0.35	33.53
Days to first flowering (days)	61.53	57.22 - 70.82	6.12	3.21	27.45	2.13	3.46
Days to 50% flowering (days)	77.51	71.11 - 85.42	5.46	2.86	27.45	2.39	3.09
Duration of flowering (days)	34.51	23.72 - 37.56	9.23	6.93	56.37	3.68	10.72
Flower diameter (cm)	5.68	4.48 - 6.81	13.84	10.23	54.69	0.89	15.59
Vase life (days)	9.13	8.58 - 9.60	4.08	2.14	27.45	0.21	2.31
Number of flowers per plant	38.89	21.00 - 60.00	29.58	28.05	89.94	21.31	54.80
Individual flower weight (g)	3.71	1.57 - 6.46	34.86	33.88	94.43	2.51	67.82
Flower yield per plant (g)	155.52	98.36 - 212.47	24.79	22.87	85.13	67.60	43.47

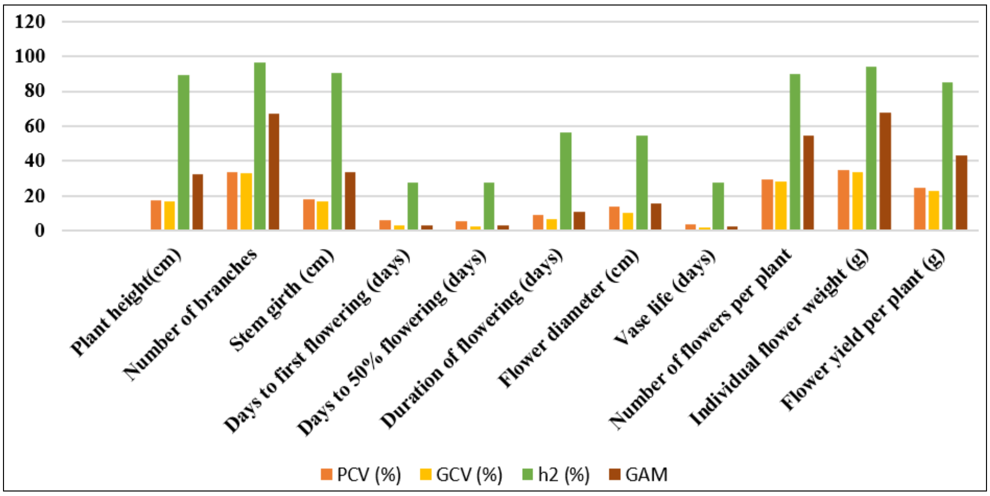

Fig 1: PCV, GCV, h^2 and GAM exhibited for various traits in cross Arka Poornima x AAC-1

Conclusion

The present study revealed a wide range of genetic variability in the F_4 population derived from the cross Arka Poornima × AAC-1 for various growth and flower yield traits. Traits such as number of branches, number of flowers per plant, individual flower weight, and flower yield per plant exhibited high heritability coupled with high genetic advance, indicating their suitability for direct selection in breeding programs. These traits can be effectively utilized for developing high-yielding China aster cultivars in future breeding efforts.

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Competing Interests

The authors declare that there are no competing interests.

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