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Genetic variability studies in F_5 population of China aster [*Callistephus chinensis* (L.) Nees]

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Abstract
An experiment entitled "Genetic variability studies in F_5 population of China aster (*Callistephus chinensis* (L.) Nees.)" was conducted during 2024-2025 at the Department of Floriculture and Landscape Architecture, College of Horticulture, Bagalkot. The material consisted of thirty-two F_5 progenies developed from four crosses along with five parental genotypes, evaluated in a randomized complete block design with two replications. The investigation aimed to estimate genetic variability and assess heritability and genetic advance for growth, flowering, yield and postharvest traits to aid selection of superior lines. Considerable variation was observed among the genotypes for all characters studied, reflecting the presence of substantial genetic diversity. For all traits, phenotypic coefficients of variation exceeded genotypic coefficients of variation, though the magnitude of difference was small for most traits, indicating limited environmental influence. Higher variability was recorded for number of branches and shelf life. Traits such as plant height, number of branches, stem girth, shelf life, length of ray florets, disc diameter, flower yield per plant and total yield per hectare exhibited high heritability along with high genetic advance as per cent of mean, suggesting the predominance of additive gene action and greater response to selection.

Keywords: China aster, genetic variability, heritability, genetic advance, F_5 population

Introduction

China aster (*Callistephus chinensis* (L.) Nees.) is an important ornamental flowering crop belonging to the family Asteraceae and is widely cultivated for loose flowers, cut flowers and ornamental purposes. It is valued for its wide range of flower colours and forms and is extensively used for interior decoration, floral arrangements and garden display (Munikrishnappa *et al.*, 2013, Bhargav *et al.*, 2016) [10, 3]. Among traditional ornamental flowers, China aster occupies a prominent position next only to marigold and chrysanthemum. The crop is cultivated commercially in several countries across the world. In India, China aster is grown extensively in states such as Karnataka, Tamil Nadu, Telangana, Andhra Pradesh, Maharashtra and West Bengal, covering an estimated area of about 3,500 ha. Karnataka is one of the major producing states, with approximately 207 ha under cultivation and a production of about 1,448 metric tonnes, recording a productivity of 7.01 t ha^{-1} (Anonymous, 2020) [1]. Favourable climatic conditions in regions like Bengaluru support year-round cultivation, thereby enhancing its commercial importance.

Despite its economic significance, considerable variation exists in yield and flower quality among China aster genotypes. Genetic improvement of the crop largely depends on the availability and effective utilization of genetic variability for yield and its component traits. The magnitude of genetic variability present among genotypes determines the efficiency of selection and the scope for developing superior cultivars. Genetic variability is generally higher in early generations due to diverse genetic combinations but tends to decline in later generations due to selection and stabilization of desirable traits.

Phenotypic expression of quantitative traits is influenced by both genetic and environmental factors. Therefore, estimation of phenotypic and genotypic coefficients of variation, heritability and genetic advance is essential for assessing heritable variability and predicting the response to selection, thereby providing a scientific basis for genetic improvement in China aster.

Materials and Methods

The present investigation was carried out in the Department of Floriculture and Landscape Architecture, College of Horticulture, Bagalkot, Karnataka during *rabi* season of 2024-25 period. The plant material comprised F_5 progenies derived from four hybrid combinations: Miraj Local × AAC-1, Namdhari White × Arka Kamini, AAC-1 × Arka Poornima and Arka Poornima × AAC-1. The respective parental lines, AAC-1, Miraj Local, Namdhari White, Arka Poornima and Arka Kamini, were included as checks. These F_5 populations were developed through selfing of F_4 hybrid lines, resulting in a total of 37 genotypes, including 32 F_5 lines and five parental lines. The experiment was laid out in a randomized complete block design with two replications. Seedlings were transplanted at 30 × 30 cm spacing using the raised bed method and recommended agronomic practices were followed. Observations were recorded for growth, flowering, yield and quality traits. Genetic variability was assessed using mean, range, phenotypic and genotypic coefficients of variation (PCV and GCV), while broad-sense heritability and genetic advance were calculated to determine the heritable component of variation and potential for selection of superior genotypes (Burton and DeVane, 1953) [4].

Results and Discussion

The estimates of phenotypic coefficient of variation (PCV) were consistently higher than the corresponding genotypic coefficient of variation (GCV) for all the characters studied (Table 2), indicating the influence of environmental factors on the expression of these traits. High PCV and GCV values were recorded for number of branches (23.30% and 21.19%, respectively) and shelf life (26.93% and 25.23%, respectively). These findings are in agreement with Sagar *et al.* (2024) [13] in China aster and Gurung *et al.* (2023) [6] in chrysanthemum. This suggests the presence of substantial genetic variability and greater scope for improvement through selection. Moderate PCV and GCV values were observed for plant height (16.03% and 12.56), stem girth (17.61% and 14.16%), days to first flowering (15.33% and 11.04%), days to 50% flowering (12.90% and 11.04%), length of ray florets (16.48% and 12.91%), disc diameter (16.35% and 13.86), flower yield per plant (16.50% and 14.08%) and total yield per hectare (16.30% and 14.21%). Comparable observations were reported by Bhargav *et al.* (2019) [2] and Tanzeela *et al.* in China aster. This indicates moderate variability with a reasonable contribution of genetic factors. Moderate PCV and low GCV were observed for flowering duration (10.68% and 8.27%) and no. of flowers / plant (12.45% and 9.58%) suggesting that these traits are strongly influenced by environmental factors, thereby reducing the efficiency of direct phenotypic selection. Results comparable to the present study have been documented by Sagar *et al.* (2024) [13] and Tanzeela *et al.* (2023) in China aster. Conversely, greater variability for number of flowers per plant has been reported by Bhargav *et al.* (2019) [2] and Ramya *et al.* (2019) [12] in China aster which could be due to differences in genetic material and prevailing environmental conditions. Low PCV and GCV was observed for flower diameter (9.07% and 6.05%) and vase life (7.84% and 5.71%) suggesting limited variability for these traits. In contrast, higher PCV and GCV values for these traits have been reported by Ramya *et al.* (2019) [12] in China aster and Devi *et al.* (2020) [5] in dahlia, possibly due to differences in genetic material and environmental conditions.

High heritability coupled with high genetic advance as per cent of mean for number of branches (82.68% and 39.69%), stem girth (61.66% and 23.45%), shelf life (87.78% and 48.70%), length of ray florets (61.33% and 20.82%), disc diameter (71.92% and 24.22%), flower yield per plant (72.77% and 24.33%) and total yield per hectare (76.08% and 25.54%) indicates the predominance of additive gene action, suggesting that direct selection would be effective for improving these traits. Similar associations have been reported earlier in China aster by Bhargav *et al.* (2019) [2] and Ramya *et al.* (2019) [12], in marigold by Tamut and Singh (2019) [14] and Thirulmurugan *et al*. High heritability coupled with moderate genetic advance for days to 50% flowering (73.26% and 19.47%) and individual flower weight (61.78% and 16.52%) indicates good genetic control, though the expected response to selection would be moderate, as also observed by Nandana (2022) [11] in China aster. Moderate heritability and genetic advance for days to first flowering (57.99% and 18.31%), duration of flowering (59.93% and 13.19%) and no. of flowers / plant (59.18% and 15.18%) indicate the combined influence of genetic and environmental factors. Higher estimates for these traits have been reported earlier in China aster by Bhargav *et al.* (2019) [2], in dahlia by Devi *et al.* (2020) [5] and in chrysanthemum by Kavana *et al.* (2024) [7] possibly due to differences in genetic material and growing conditions. Vase life (53.12% and 8.58%) and flower diameter (44.42% and 8.30%) exhibited moderate heritability with low genetic advance, indicating limited scope for improvement through direct selection due to environmental influence. Hence, improvement of these traits may require hybridization or improved crop management practices. Similar traits showing higher heritability and genetic advance have been reported earlier in China aster by Khangjarakpam *et al.* (2014) [8] and Ramya *et al.* (2019) [12] and in chrysanthemum by Vandana *et al.* (2024) [17] which may be attributed to differences in genetic material and experimental conditions.

Table 1: Analysis of variance for growth, yield, flowering, quality and yield parameters for advanced lines of China aster

Sl. No.	Character	Genotypes	Replication	Error	S.Em±	CD@5%
A	Degrees of Freedom	36	1	36		
1.	Plant Height (cm)	103.30**	77.20	24.71	3.51	10.08
2.	No. of branches / plant	18.79**	5.49	1.78	0.94	2.71
3.	Stem girth (cm)	0.06**	0.02	0.02	0.08	0.22
4.	Days to first flowering	149.03**	5.25	39.63	4.45	12.77
5.	Days to 50% flowering	147.65**	5.90	22.78	3.38	9.68
6.	Duration of flowering (days)	18.83**	5.97	4.72	1.54	4.40
7.	Flower Diameter (cm)	0.38**	0.35	0.14	0.27	0.77
8.	Length of ray florets (cm)	0.27**	0.02	0.07	0.18	0.52
9.	Disc diameter(cm)	0.17**	0.10	0.03	0.12	0.34
10.	Vase life (days)	0.56**	2.27	0.18	0.29	0.84
11.	Shelf life (days)	0.87**	0.02	0.06	0.17	0.48
12.	No. of flowers / plant	33.30**	0.26	8.49	2.06	5.91
13.	Individual flower weight (g)	0.41**	0.01	0.1	0.22	0.63
14.	Flower Yield (g/plant)	954.73**	287.84	150.48	8.67	24.88
15.	Total yield per hectare (t/ha)	11.68**	0.99	1.59	0.89	2.55

Table 2: Genetic variability estimates for growth, flowering, quality and yield characters for advanced lines of China aster

Sl. No.	Character	Mean	Range	PCV (%)	GCV (%)	h2 (%) BS	GA	GAM (%)
1.	Plant height (cm)	49.92	35.10-62.18	16.03	12.56	61.39	10.12	20.27
2.	Number of branches	13.77	9.00-24.32	23.30	21.19	82.68	5.46	39.69
3.	Stem girth (cm)	1.06	0.65-1.32	17.61	14.16	64.66	0.25	23.45
4.	Days to first flowering	63.35	45.40-83.81	15.33	11.67	57.99	11.60	18.31
5.	Days to 50 percent flowering	71.55	58.65-89.85	12.90	11.04	73.26	13.93	19.47
6.	Duration of flowering (days)	32.12	24.25-38.51	10.68	8.27	59.93	4.24	13.19
7.	Flower Diameter(cm)	5.63	4.87-6.75	9.07	6.05	44.42	0.47	8.30
8.	Length of ray florets(cm)	2.49	1.98-3.37	16.48	12.91	61.33	0.52	20.82
9.	Disc diameter(cm)	1.92	1.44-2.64	16.35	13.86	71.92	0.46	24.22
10.	Vase life (days)	7.71	6.50-8.56	7.84	5.71	53.12	0.66	8.58
11.	Shelf life (days)	2.53	1.55-3.70	26.93	25.23	87.78	1.23	48.70
12.	Number of flowers per plant	36.61	26.20-44.15	12.45	9.58	59.18	5.56	15.18
13.	Individual flower weight (g)	3.90	2.78-5.13	12.98	10.20	61.78	0.64	16.52
14.	Flower yield (g/plant)	142.47	98.96-200.53	16.50	14.08	72.77	35.24	24.73
15.	Total yield per hectare(t)	15.81	11-22.26	16.30	14.21	76.08	4.04	25.54

PCV- Phenotypic Co-efficient of Variation, GCV- Genotypic Co-efficient of Variation, h^2 - Heritability in broad sense, GA-Genetic Advance, GAM- Genetic advance as per cent of mean

Conclusion

The present investigation revealed the presence of considerable genetic variability among the F_5 populations of China aster for various growth, flowering and yield-related traits. Characters such as number of branches, stem girth, shelf life, length of ray florets, disc diameter, flower yield per plant and total yield per hectare, which exhibited high heritability coupled with high genetic advance, can be effectively exploited through direct selection and utilized for the development of high yielding China aster genotypes in future breeding programmes.

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