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Genetic variability, heritability and genetic advance in F_2 segregating population of cross Arka Kamini × AAC-1 in China aster (*Callistephus chinensis* (L.) Nees)

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Abstract

The aim of the present study was to evaluate genetic variability in F_2 population of cross Arka Kamini x AAC-1 in China aster. The investigation was conducted in Kittur Rani Channama College of Horticulture, Arabhavi during 2021-22. The genotypic coefficient of variation was lower than phenotypic coefficient of variation for all traits studied. The estimates of PCV and GCV were high for number of flowers per plant, individual flower weight, flower yield per plant. High heritability was noticed in most of characters studied except days for 50 percent flowering and flower yield per plant. High heritability associated with high genetic gain was exhibited by plant height, plant spread in both directions, number of branches, days to flower bud initiation, duration of flowering, number of flowers per plant, individual flower weight, stalk length, flower diameter and shelf life. The progenies which expressed characters with high heritability coupled with high genetic advance would be effective for advancement to next generation for developing high yielding China aster cultivars.

Keywords: China aster, coefficient of variation, genetic variability, heritability, genetic gain

1. Introduction

China aster [*Callistephus chinensis* (L.) Nees.] is a semi-hardy annual flower crop belongs to family Asteraceae with chromosome number of (2n = 18). China aster is a geitonogamous crop and the natural crossing is approximately 10 percent (Fleming, 1937) [3]. The crop is cultivated as a cut and loose flower, and is also for garden landscaping and used as a potted plant (Hay *et al.*, 1976) [5]. In India, it is grown by small and marginal farmers in Tamil Nadu, Karnataka, Andhra Pradesh, Maharashtra and West Bengal. The increasing popularity of China aster in major cities of India has led to its cultivation on a commercial scale.

The success of a crop improvement program relies on genetic variability existing in available genotypes, which may be contributed either due to genetic constitution of cultivars or difference in growing environment. The criterion for genetic improvement of any crop involves creation and utilization of variability. Generally, the amount of variability generated in the early segregating generations is more than compared to later generations. Thus, segregating F_2 population provides an opportunity for selection of desirable segregants. The consumer preferences changes from time to time; stressed the importance of research in developing high yielding with attractive flower colour and form. The breeding of China aster to improve both its qualitative and quantitative traits is necessary. Thus, the present study was undertaken to examine the magnitude of variability, heritability, genetic advance, and genetic advance as percent mean for different growth, flowering, quality and yield parameters among segregating F_2 populations.

2. Materials and Methods

The present study was carried out in Department of Floriculture and Landscape Architecture, KRC College of Horticulture, Arabhavi, University of Horticultural Sciences, Bagalkot during 2021-22. The experiment composed of 200 F_2 progenies of cross Arka Kamini and AAC-1, and parental genotypes. The F_2 population is developed by selfing F_1 hybrids of Arka Kamini × AAC-1. The experiment was laid out in randomized block design with no replication. The healthy, well established, uniformly grown forty-five days old seedlings were transplanted into main field at a spacing of 30 cm x 30 cm in ridge and furrow system. Irrigation was given immediately after transplanting followed by subsequent irrigation at regular intervals depending on weather condition. Normal crop management practices were followed. The data on growth, flowering, quality and yield parameters were recorded from five plants selected randomly in each parental line and each individual plant of F_2 population. The genetic parameters such as mean, range, phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) was computed as per the method suggested by Burton and DeVane (1953) [2]. Heritability (broad sense), genetic advance and genetic gain was calculated following the formula proposed by Johnson *et al.* (1955) [6].

3. Results

The estimates of coefficient of variation for fifteen traits in F_2 population of Arka Kamini x AAC-1 was presented in table 1. It was observed that PCV was higher than GCV for all morphological and yield attributing traits studied. The estimates of PCV and GCV were high (> 20%) for number of flowers per plant (29.92, 28.11), individual flower weight (31.28, 29.91), flower yield per plant (42.99, 27.84) and stalk length (23.62, 22.90), respectively. High PCV and moderate GCV were noted in shelf life (20.28, 19.73), plant spread (E-W) (21.17, 18.66) and number of branches (21.83, 18.15). Low PCV and GCV was estimated in days for 50 percent flowering (2.53, 1.62). High heritability was noticed in most of characters studied except days for 50 percent flowering (41.07%) and flower yield per plant (41.93%). The estimates of genetic advance and genetic advance expressed as percent of mean (genetic gain) for fifteen traits in F_2 population of Arka Kamini x AAC-1 was given in Table 1. The estimates of genetic gain were high in all characters excluding stem girth (15.42), days to first flower bud opening (14.80) and days to 50 percent flowering (2.14). High heritability associated with high genetic gain was exhibited by plant height (14.66, 32.90), plant spread (N-S) (70.02, 28.82), plant spread (E-W) (77.65, 33.87), number of branches (69.15, 31.09), days to flower bud initiation (93.11, 25.70), duration of flowering (95.33, 29.44), number of flowers per plant (88.25, 54.39), individual flower weight (91.42, 58.90), stalk length (93.99, 45.74), flower diameter (78.13, 20.76) and shelf life (94.58, 39.52).

Table 1: Genetic parameters of different morphological and yield attributing traits

Sl. No.	Source of variation/ characters	Range		Mean	Coefficient of variation		Heritability (%)	Genetic advance (%)	Genetic gain (%)
		Min.	Max.		PCV (%)	GCV (%)			
1	Plant height (cm)	18.90	58.20	44.55	16.98	16.46	94.06	14.66	32.90
2	Plant spread (N-S) (cm)	13.20	49.10	23.36	19.98	16.72	70.02	6.73	28.82
3	Plant spread (E-W) (cm)	13.40	42.30	24.26	21.17	18.66	77.65	8.22	33.87
4	Number of branches per plant	8.00	21.00	14.71	21.83	18.15	69.15	4.57	31.09
5	Stem girth (cm)	1.02	1.85	1.40	11.81	9.40	63.42	0.22	15.42
6	Days to flower bud initiation	49.00	67.00	54.65	13.40	12.93	93.11	14.04	25.70
7	Days to first flower opening	54.00	78.00	64.54	10.58	8.72	67.93	9.55	14.80
8	Days for 50 percent flowering	64.00	89.00	76.83	2.53	1.62	41.07	1.65	2.14
9	Duration of flowering	22.00	33.00	29.11	14.99	14.64	95.33	8.57	29.44
10	Number of flowers per plant	12.00	43.00	22.85	29.92	28.11	88.25	12.43	54.39
11	Individual flower weight (g)	0.95	4.64	2.44	31.28	29.91	91.42	1.44	58.90
12	Flower yield per plant (g)	16.20	136.40	55.73	42.99	27.84	41.93	20.7	37.14
13	Stalk length (cm)	12.30	31.70	22.76	23.62	22.90	93.99	10.41	45.74
14	Flower diameter (cm)	3.40	7.10	5.60	12.90	11.40	78.13	1.16	20.76
15	Shelf life (days)	2.00	6.00	4.03	20.28	19.73	94.58	1.59	39.52

PCV- Phenotypic co-efficient of variation; GCV- Genotypic co-efficient of variation

4. Discussion

The estimates of genetic parameters like coefficient of variation, broad sense heritability, genetic advance and genetic advance as percent of mean (genetic gain) for fifteen characters were worked out to understand the extent to which variations observed due to genetic factors. In F_2 population, there was a wide range of variability for all traits studied among all progenies; these can be exploited through selection. The high PCV and GCV were revealed for characters namely number of flowers per plant, individual flower weight, flower yield per plant and stalk length. High PCV and moderate GCV was noticed in in shelf life, plant spread (E-W) and number of branches. These findings suggested that, the presence of maximum variability among F_2 progenies studied and these traits can prove to be effective in improving the crop through selection and breeding. Low coefficient of variation, *i.e.*, PCV and GCV were revealed by days for 50 percent flowering. The result shows that chance of improving of these traits by direct visual selection is low. Similar results were obtained by Khangjarakpam *et al.* (2014) [7], Ramya *et al.* (2019) [11] in China aster and Prakash *et al.* (2017) [10] in chrysanthemum.

The PCV and GCV alone does not provide reliable information about assessment of variation that is heritable and therefore, estimation of heritability becomes imperative. The high heritability estimate values were noted for plant height, plant spread in both directions, number of branches, stem girth, days to flower bud initiation, days to first flower bud opening, duration of flowering, number of flowers per plant, individual flower weight, stalk length, flower diameter and shelf life. The result indicates that expression of heritability in these characters were less influence by environment and give a reliable indication of expected amount of improvement through selection. These results are in close conformity with the findings of Prakash *et al.* (2017) [10] and Telem *et al.* (2017) [13] in crysanthemum; Anuja and Jahnavi (2012) [1] in French marigold; Tirakannanavar *et al.* (2015) [14], Nishchitha (2016) [9], Kumari *et al.* (2017) [8] and Harishkumar *et al.* (2018) [4] in China aster.

High heritability estimate coupled with high genetic advance as percent of mean was observed for plant height, plant spread in both directions, number of branches, days to flower bud initiation, duration of flowering, number of flowers per plant, individual flower weight, stalk length, flower diameter and shelf life suggesting that, the gene action is mostly of additive type and therefore, direct selection of such trait will be rewarding. These results were in line with work of Sahu and Sharma (2014) [12] in chrysanthemum; Tirakannanavar *et al.* (2015) [14], Nishchitha (2016) [9], and Harishkumar *et al.* (2018) [4] in China aster.

5. Conclusion

The study revealed existence of a wide range of variability progenies of cross Arka Kamini × AAC-1 for different growth, flowering, quality and yield parameters. The progenies which expressed characters with high heritability associated with high genetic advance would be effective for advancement to next generation for developing novel high yielding China aster cultivars.

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