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Original Research Paper

Assessment of genetic diversity in China aster [*Callistephus chinensis* (L.) Nees]

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ABSTRACT

China aster [*Callistephus chinensis* (L.) Nees] is a flowering annual mainly cultivated for loose flower and cut flower, bedding and pot culture. To assess the genetic diversity, 42 genotypes were evaluated for fourteen quantitative traits. The genotypes were found to be highly variable for the traits such as plant height, plant spread, flower stalk length, 100 flower weight, number of flowers per plant, weight of flowers per plant and flower yield per hectare. However, low variability was recorded for vase life and shelf life. The genotypes were broadly grouped into two clusters, which were further divided into cluster 1a, 1b and cluster 2a, 2b, respectively. All the genotypes in cluster 1a were vigorous and medium flowering, whereas, genotypes in cluster 1b were tall, erect, vigorous and late flowering. The cluster 2a comprises of the genotypes with short stature, small flower and early flowering, however, cluster 2b contains only two genotypes. In principal component analysis (PCA) PC1 was highly correlated to flower yield, weight of flowers/plant, flower stalk length and plant height and PC2 was highly positively correlated to shelf life and vase life and negatively correlated to 100 flower weight. The results suggested that the existing variation in China aster genotypes could be used for the development of trait-specific novel genotypes.

Keywords : China aster, cluster analysis, diversity, principal component analysis

INTRODUCTION

China aster [*Callistephus chinensis* (L.) Nees] is a diploid (2n=2x=18) flowering annual belonging to the family Asteraceae and is a native of China (Navalinskien *et al*., 2005). The genus *Callistephus* derives its name from two Greek words '*Kalistos*' and '*Stephos*' meaning 'most beautiful' and 'crown', respectively. In India, China aster ranks third among the flowering annuals after chrysanthemum and marigold (Chakraborty *et al*., 2019). China aster is winter season annual crop. It is commercially grown for loose andcut flower, which are used in flower decoration, preparation of bouquets and garlands. It is also used in landscape gardening as a bedding plant to provide colour break and mass effect. It is gaining popularity in India, because of ease in cultivation, array of colours and varied uses (Bhargav *et al*., 2016).

For any breeding programme, characterization and evaluation are crucial steps in developing a variety and further research. Cluster analysis and principal component analysis are two important parameters to determine the diversity of the crop. Considering the importance of the crop, the present investigation was carried out to assess the diversity among 42 genotypes of China aster based on the fourteen quantitative traits.

MATERIALS AND METHODS

The present study was conducted at the Division of Flower and Medicinal Crops, ICAR- Indian Institute of Horticultural Research, Bengaluru during 2015-16 and 2016-17. The experimental site was geographically located at 13° 58¹ N Latitude, 78°E Longitude and at an elevation of 890 m above mean sea level. The soil of experimental plot was red loamy with pH 7.35 and E.C. of 0.26 dsm^{-1}. A total of 42 genotypes including 21 varieties and 21 stabilized lines were evaluated for vegetative growth, flowering, yield and postharvest life in randomized complete block design with two replications. Twenty plants per replication were planted at a spacing of 30 x 30 cm

under open field conditions. The recommended agronomical practices were adopted to raise the crop. Five random plants were selected for recording the various quantitative traits *viz*., plant height (cm), number of leaves per plant, plant spread (cm), number of branches per plant, days to first flowering, flower stalk length (cm), flower head diameter (cm), 100 flowers weight (g), number of flowers per plant, weight of flowers per plant (g), duration of flowering (days), vase life (days) and shelf life (days).

Descriptive statistics (*e.g.*, range, standard deviation, mean, standard error of mean), clustering based on average linkage, and euclidian distance and principal component analysis (PCA) were calculated using XLSTAT (Addinsoft, 2017).

RESULTS AND DISCUSSION

The diversity among the China aster accessions for quantitative traits was high (Table 1). Wide range of variation was observed for most of the characters such as plant height (8.20-61.80 cm), plant spread (8.75-42.65 cm), flower stalk length (4.65-49.10 cm), 100 flower weight (105.00-548.25 g), number of flowers per plant (7.35-65.05), weight of flowers per plant (7.72-235.21 g), flower yield per hectare (6.48-197.57 q/ha). Highest variability was recorded for weight of flowers per plant, which directly represent the flower yield per hectare with a mean of 124.49 g and 104.57 q/ha, respectively having a C.V. of 48.65%. Minimum variability was observed for vase life (5.40-9.50 days) followed by shelf life (2.35-4.42 days) with a mean of 7.06 (C.V. 14.26%) and 3.42 days (C.V. 14.37%), respectively. Presence of such high genetic variability among the genotypes for these parameters will form the basis for effective selection of superior genotypes in China aster. Such wide variability for many quantitative traits was also reported by Gupta and Dutta (2005) and Banerji *et al*. (2012) in chrysanthemum, and Kumar *et al*. (2014) in bougainvillea.

Cluster analysis was carried out to distinguish possible groups among the populations using Ward method (Fig. 1). The Agglomerative hierarchical clustering (AHC) allows sub-division of 42 genotypes into two major clusters based on the correlation that exists between the morphological traits among the genotypes. In the present study, cluster 1 comprised of 33 populations, which was further divided into two sub-groups cluster Ia contains 18 genotypes and Ib contains 15 genotypes. Nine genotypes were classified into cluster 2, which was again divided into two sub-clusters group IIa and group IIb containing 7 and 2 genotypes, respectively.

In cluster Ia, all the genotypes were vigorous, medium flowering with big flowers, whereas, genotypes in cluster Ib were tall and erect, vigorous, late flowering with big flowers. Except genotype IIHRJ22, all the genotypes in cluster IIa belong to the Japanese

Table 1 : Descriptive statistics of quantitative traits in China aster genotypes

Trait	Range		Mean ± SE(m)	CV (%)
	Minimum	Maximum		
Plant height (cm)	8.20	61.80	45.50 ± 0.66	24.97
Number of leaves/plant	9.20	32.35	19.50 ± 0.86	22.13
Plant spread (cm)	8.75	42.65	24.54 ± 0.72	32.59
Number of branches/plant	6.65	17.60	12.08 ± 0.30	19.83
Days to first flowering	46.85	100.15	66.71 ± 0.71	16.92
Flower stalk length (cm)	4.65	49.10	35.62 ± 0.72	29.34
Flower head diameter (cm)	3.54	6.74	5.39 ± 0.07	15.96
100 flowers weight (g)	105.00	548.25	292.02 ± 2.66	31.98
Number of flowers/plant	7.35	65.05	40.92 ± 0.46	34.82
Weight of flowers/plant (g)	7.72	235.21	124.49 ± 2.06	48.65
Duration of flowering (days)	16.58	34.40	24.92 ± 0.30	19.53
Flower yield/ hectare (q/ha)	6.48	197.57	104.57 ± 1.73	48.65
Vase life (days)	5.40	9.50	7.06 ± 0.12	14.26
Shelf life (days)	2.35	4.42	3.42 ± 0.08	14.37

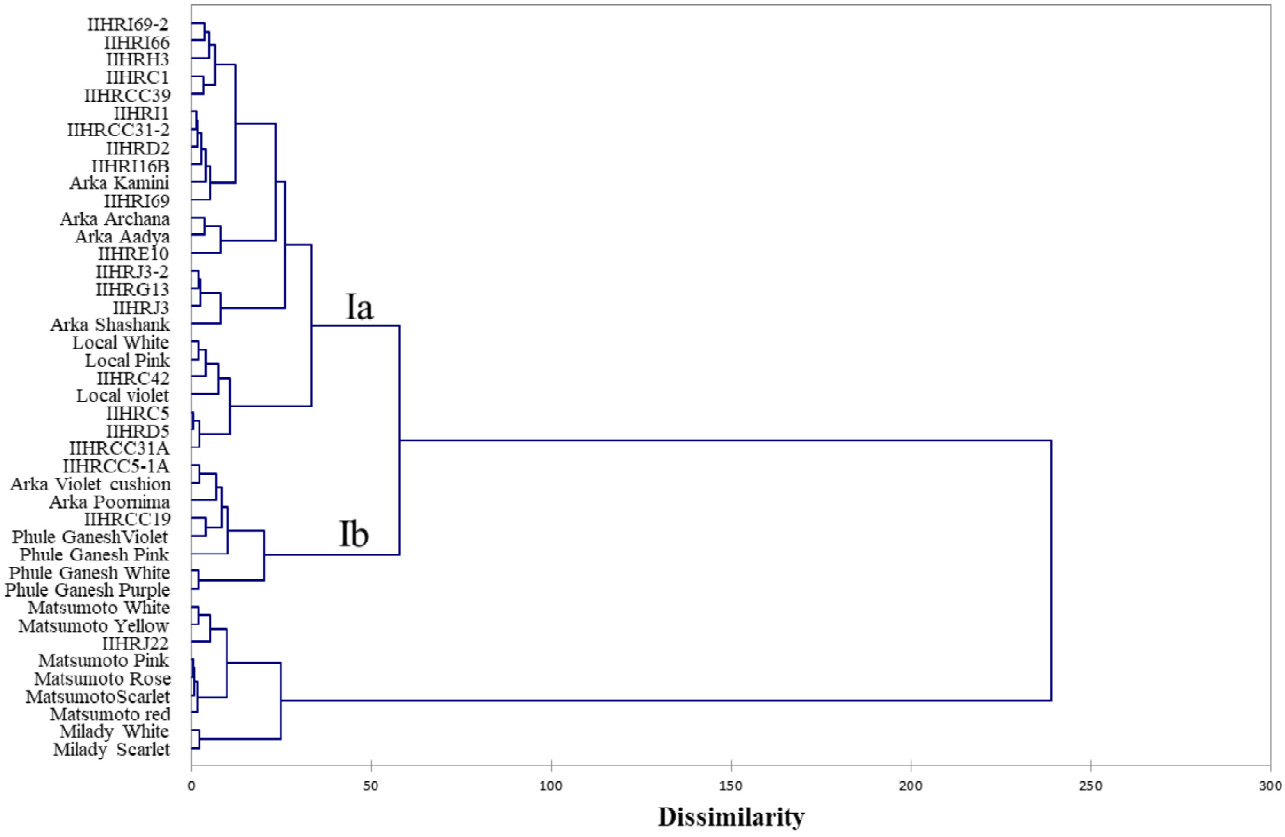

Fig. 1 : Dendrogram showing genetic relationship among 42 China aster genotypes based on morphological data

originated short stature, early flowering and small flowered genotypes, however, IIb contains only two European originated genotypes namely Milady Scarlet and Milady White. Similar results were also obtained by Kumar *et al*. (2011) in snapdragon, and Bharathi and Jawaharlal (2014) in marigold. It was observed that genotypes representing particular geographic regions were grouped together. The heterogeneous origin of genotypes, place of release, different ploidy levels often grouped together in the same cluster, suggesting the ancestral relationship between the various genotypes (Bellundagi *et al*., 2013). For further improvement in the morphological and yield parameters, genotypes may be selected on the basis of genetic divergence. Crossing between highly genetic divergent genotypes could yield better results (Singh *et al.,* 2016). Therefore, genotypes may be chosen for crossing on the basis of genetic divergence as depicted in the dendrogram. Based on the cluster distance, genotypes belonging to Matsumoto series, Milady Scarlet and Milady White, and genotypes belonging to Phule Ganesh, Arka, IIHRJ3-2 and IIHRG13 were most divergent. Therefore, crossing among the most divergent genotypes can achieve improvement in the morphological and yield attributes by getting desirable transgressive segregants.

To determine the most significant characteristics of the data set and also to determine the distances between the genotypes based on the data obtained on morphological traits, set of 42 genotypes used for cluster analysis were subjected to Principal Component Analysis (PCA) (Table 2). The analysis also helped to understand the contribution of morphological characters across the genotypes. The first two components of the seven considered accounted for most of the variation. The first principal component (PC1) explained 55.66% of the total variation and was positively correlated to all the traits; highly correlated to flower yield, weight of flowers/ plant, flower stalk length and plant height. The PC2 explained 10.55% of total variation and was highly positively correlated to shelf life and vase life, and negatively to 100 flower weight (Table 2). Because PC1 and PC2 accounting 66.21% of cumulative variance the compounds, a scatterplot was made for both (Fig. 2).

Table 2 : Principal component analysis in China aster genotypes

Variable	PC1	PC2	PC3	PC4	PC5	PC6	PC7
Eigen value	7.79	1.48	1.19	0.95	0.71	0.54	0.46
Cumulative variance (%)	55.66	66.21	74.68	81.49	86.57	90.41	93.70
Plant height (cm)	0.82	0.29	0.22	-0.25	-0.09	-0.02	-0.22
Number of leaves/plant	0.72	-0.25	-0.41	-0.19	0.05	0.39	0.02
Plant spread (cm)	0.82	-0.05	-0.27	0.38	-0.03	-0.04	-0.12
Number of branches/plant	0.75	-0.02	-0.17	0.43	-0.15	0.20	-0.17
Days to first flowering	0.71	0.04	-0.47	-0.36	0.24	0.12	0.04
Flower stalk length (cm)	0.86	0.13	0.30	-0.12	-0.05	0.08	-0.26
Flower head diameter (cm)	0.80	-0.08	-0.11	-0.05	-0.34	-0.31	-0.17
100 flowers weight (g)	0.81	-0.33	-0.17	-0.03	-0.22	-0.23	0.25
Number of flowers/plant	0.75	-0.02	0.56	0.04	0.24	0.17	-0.01
Weight of flowers/plant (g)	0.88	-0.30	0.28	-0.01	0.05	-0.03	0.22
Duration of flowering (days)	0.61	0.27	-0.18	0.25	0.59	-0.32	-0.04
Flower yield/hectare (q)	0.88	-0.30	0.28	-0.01	0.05	-0.03	0.22
Vase life (days)	0.46	0.67	-0.10	-0.41	-0.09	-0.09	0.13
Shelf life (days)	0.38	0.70	0.02	0.39	-0.20	0.17	0.30

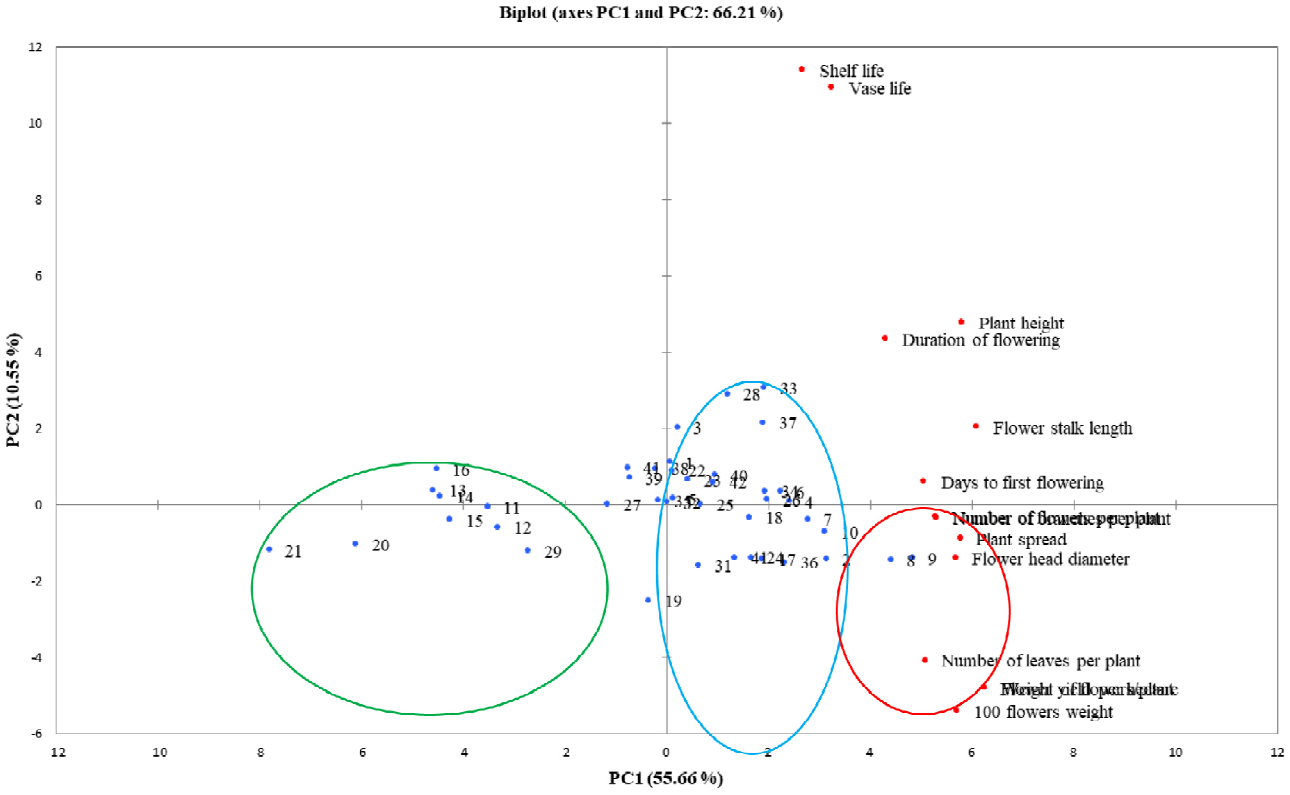

Fig. 2 : Principal Component Analysis (PCA) of China aster genotypes based on morphological characters

1. Arka Kamini 2, Arka Poornima, 3. Arka Shashank, 4. Arka Violet Cushion, 5. Arka Aadya, 6. Arka Archana, 7. Phule Ganesh Pink, 8. Phule Ganesh Purple, 9. Phule Ganesh White, 10. Phule Ganesh Violet, 11. Matsumoto Yellow, 12. Matsumoto White, 13. Matsumoto Rose, 14. Matsumoto Scarlet, 15. Matsumoto Red, 16. Matsumoto Pink, 17. Local Pink, 18. Local White, 19. Local Violet, 20. Milady Scarlet, 21. Milady White, 22. IIHRD5, 23. IIHRC5, 24. IIHRC42, 25. IIHRCC39, 26. IIHRCC5-1A, 27. IIHRCC31-2, 28. IIHRJ3, 29. IIHRJ22, 30. IIHRI1, 31. IIHRI66, 32. IIHRCC31A, 33. IIHRG13, 34. IIHRI69-2, 35. IIHRD2, 36. IIHRCC19, 37. IIHRJ3-2, 38. IIHRI69, 39. IIHRI16B, 40. IIHRH3, 41. IIHRE10, 42. IIHRC1.

Large variation was recorded in traits such as shelf life, vase life, plant height, 100 flower weight as mentioned by the relative length of the vectors in the biplot diagram. The biplot also signifies the positive correlation between the parameters *viz*., shelf life, vase life, plant height, duration of flowering, days to first flowering and 100 flower weight, flower yield per hectare, weight of flowers per plant and number of leaves per plant as indicated by the acute angle.

The genotypes like Matsumoto, Milady Scarlet and Milady White which were short and early flowering formed a group in one quadrant and all are comparatively late flowering genotypes which are, tall with big flowers formed another group and intermediate medium flowering forms the group in between. Most of the morphological traits contributed equally in grouping of genotypes except vase life and shelf life, which were distributed away from the genotypes. The result of PCA is consistent with that of the cluster analysis. A similar pattern was also observed for hips traits in *Rosa* sp. (Verma *et al*., 2013) and in pea (Esposito *et al*., 2007).

CONCLUSION

This study indicated that the quantitative traits are useful for preliminary evaluation of genetic diversity in China aster. PCA revealed that number of flowers per plant, flower yield per hectare, flower stalk length, plant height and plant spread are key traits contributing to the maximum variation among the genotypes. The cluster analysis showed significant genetic variability among the evaluated China aster genotypes, which may provide an excellent opportunity for crop improvement through hybridization between the genotypes of different clusters, to assemble desirable traits with higher heterotic potential.

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