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, M. Mayil Vaganan⁵**10.18805/IJARe.A-6128**

ABSTRACT

Background: Canna lily (*Canna indica* L.) is an edible herbaceous perennial plant in which flowers and rhizomes were commonly used as a food additive and its potentiality was not fully utilized in India. To stun these hindrances, morphological characterizations are needed to determine the genetic variability to improve flower quality and rhizome yield in canna lily.

Methods: In the present research, a field experiment was conducted during 2022-2023 in Botanical Garden, Tamil Nadu Agricultural University, Coimbatore, Tamil Nadu. Twelve accessions were investigated by using a randomized block design with 3 replications. All the observations for 23 quantitative traits were carried out at 0.05 and 0.01 probability.

Result: A wide range of genetic variability was observed, a high genetic coefficient of variation ranged from 8.49 to 75.62% and a phenotypic coefficient of variation ranged from 8.83 to 76.50% was observed in 20 traits except in days to fist bloom, rhizome diameter, number of nodes per rhizome. High heritability coupled with high genetic advance as a percent of mean was observed for 21 traits except in days to fist bloom and number of nodes per rhizome. Character association analysis revealed that stem diameter and inflorescence length showed highly significant and positively correlated with flower yield and rhizome yield per plant. Path analysis specified that the number of leaves per clump had a very high and positive direct effect on fresh flower yield per plant.

Key words: *Canna indica,* GCV, Genetic advance, Genetic variability, Heritability, PCV, Traits.

INTRODUCTION

The ornamental *Canna*, a single genus of family Cannaceae (Tanaka *et al*., 2009), comes under the order Zingiberales which consisting of eight families based on an update of the APG IV (Angiosperm Phylogeny Group) classification of the orders and families of angiosperm (APG *et al*., 2016; Byng *et al*., 2018). Recently, the genus *Canna* have been recognized and 20 species studied based on morphological and molecular analyses (Tanaka, 2001, 2008) *Canna* is characterized by its asymmetrical showy hermaphrodite flowers with 3-4 petaloid staminodes and one relatively modified as a staminodial labellum which is special structure for a place to pollination insects. A specialized one staminode modified as a stamen which bears pollen from a half anther. A narrower petal is the pistil, which is connected down to a three chambered ovary (Khoshoo and Mukherjee, 1970). The nutritional compositions of a *Canna* plant vary with climatic conditions. *Canna* leaf, seed and rhizome possess more carbohydrates, proteins, lipids, fibres, moisture and ash content. *Canna* seeds are enriched with more carbohydrates, lipids, proteins and fibre content when compared to the leaves and rhizomes, whereas leaves contains more moisture and ash content (Okonwu and Ariaga, 2016). Economic uses of *Canna* revealed each and every part of the plant having medicinal activity and the quantitative analysis revealed the presence of biomolecules

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How to cite this article: Baranidharan, R., Lourdusamy, D.K., Aruna, P., Rajamani, K., Chandrakumar, K., Karthikeyan, S. and Vaganan, M.M. (2023). Estimation of Genetic Variability and Character Association Analysis of Underutilized Ornamental Canna Lily (*Canna indica* L.). Indian Journal of Agricultural Research. 57(6): 717-724. doi: 10.18805/IJARe.A-6128.

Submitted: 21-06-2023 **Accepted:** 30-08-2023 **Online:** 21-09-2023

such as flavonoids, phenolic compounds, saponins, steroids, tannins and terpenoids (Darsini *et al*., 2015).

The natural variability in canna is more and for genetic improvement, germplasm collections represent mainly the source of variations in *Canna* morphological and anatomical characterization through molecular DNA markers (Akhi *et al*., 2021). In recent times, canna is the greatest source for the new base starch to employ complementarily with cassava starch which was evaluated on the basis of genetic characteristics, morphological traits and starch properties (Piyachomkwan *et al*., 2002). The morphological characterization was determined in C*anna indica* for genetic and phenotypic variability and grouping of varieties to improve edible canna varieties (Sari *et al*., 2016). The economic component's yield has a very complicated nature and is the outcome of the interaction of several factors that are present in both the plant and the environment in which it is cultivated. Selection must therefore take use of the heterogeneity within each component trait in order to maximize rhizome and flower yield. Together, correlation and path coefficient studies provide a comprehensive picture of the interactions and relative contributions of independent and dependent features on the dependent variable, enabling a plant breeder to use the best selection techniques to improve crops. A complete understanding of the strength and type of association between qualitative, quantitative traits are a necessity for the successful breeding programme. Therefore, the goal of the current experiment was to identify the main canna features that contribute to yield.

MATERIALS AND METHODS

The present study was conducted during 2022-2023 at Department of Floriculture and Landscape Architecture, Botanical Garden, Tamil Nadu Agricultural University, Coimbatore, Tamil Nadu. The experimental site is located at 11.01E latitude and 76.9W longitude at a mean altitude of 458.44±19 m above the mean sea level. Twelve *Canna indica* accessions were collected from different places of south India *viz*., Tamil Nadu, Kerala andhra Pradesh and Pondicherry (Table 1). The field trial was laid out in

randomized block design (RBD). The crop was grown in recommended spacing of 60×60 cm along with the recommended agronomic practices and plant protection measures. 20 plants were accommodated in each plot. The observations were taken after flowering for all the parameters and *Canna indica* accession (Ac. 1) first bloom at 55.67 (days) planting from main field. Among the 20 plants, five plants were selected randomly and tagged properly for each accessions and recorded the data *viz*., plant height (cm), stem diameter (cm), number of leaves per plant, number of tillers per plant, number of leaves per clump, leaf length (cm), leaf width (cm), leaf area (cm²), days to first bloom (days), number of inflorescence per plant, inflorescence length (cm), number of flowers per plant, single flower weight (g), flower length (cm), staminode length (cm), staminode width (cm), flower yield per plant (g), rhizome diameter (cm), rhizome fresh weight (cm), rhizome internode length (cm), number of nodes per rhizome, number of eyes per rhizome, rhizome yield per plant (g). ANOVA (Analysis of variance) to test the significant difference among the accessions for each character was computed and used for statistical analysis by using Agres software. The genetic variability parameters *viz*., phenotypic coefficient of variation (PCV), genetic coefficient of variation (GCV), heritability (*h 2*) was worked out by using the formula suggested by (Burtan and Devane, 1953), the genotypic and phenotypic correlation and genetic advance mean (GAM) were calculated by using the formula given by (Johnson *et al*., 1955) path coefficient analysis were evolved by the method given by (Dewey and Lu, 1959) and the scale value was suggested that the path coefficient analysis were given by Lenka and Mishra (1973) for the following traits of yield and its attributing characters were analyzed to make the effective selection.

RESULTS AND DISCUSSION

The present research was mainly focused on estimation of genetic variability and character association of *Canna* accessions to evaluate the extent of variability.

Table 1: Source and collection of canna lily accessions used in this study.

Estimation of genetic variability

The mean performance is the direct criteria to select the accessions from the diverse population. The mere selection based on the yield related contributing traits may also improve the yield of the population. The trait wise grand mean performance, standard deviation, mean range and coefficient of variation were furnished in the Table 2. To assess the extent of variability, phenotypic and genotypic coefficients of variation are the reliable parameters which will give us the idea of heritable and non-heritable portions of the variability. In the present research study, the higher values of PCV and GCV were less influenced by environment for all the traits. Phenotypic (PCV) coefficient of variation was slightly higher than genotypic (GCV) coefficient of variation for all the traits. High PCV and GCV were found in most of the traits. Phenotypic coefficient of variation ranged from 8.83 to 95.77% and genetic coefficient of variation ranged from 8.49 to 94.95% except in days to first bloom, rhizome diameter and number of nodes per rhizome. Significantly high value for genetic coefficient of variation was recorded in flower yield per plant (94.95%), number of

inflorescence per plant (75.62%), single flower weight (60.42%), inflorescence length (57.92%), number of flowers per plant (53.63%), staminode width (49.43%), rhizome fresh weight (45.89%), leaf area (42.35%), plant height (35.11%), number of leaves per clump (33.74%), stem diameter (31.36%), rhizome yield per plant (31.34%), flower length (30.7%), rhizome internode length (27.26%), leaf width (26.97%), number of leaves per plant (25.04%), staminode length (24.42%), leaf length (22.05%), rhizome diameter (21.09%), number of tillers per plant (20.40%), number of nodes per rhizome (15.22%), days to first bloom (8.49%). It indicated that though the characters are least influenced by environmental effect, a phenotypic variability in these characters was contributed by only additive gene inheritance and hence the improvement can be made by simple selection. The similar findings are in accordance with the results in turmeric (Suresh *et al*., 2020).

Heritability (*h 2* **) and genetic advance as percent of mean (GAM)**

All the traits were observed to have high heritability and genetic advance expressed as percentage of mean except

Note: PH: Plant height (cm); SD: Stem diameter (cm); NLP: Number of leaves per plant; NTP: Number of tillers per plant; NLC: Number of leaves per clump; LL: Leaf length (cm); LW: Leaf width (cm); LA: Leaf area (cm²); DFB: Days to first bloom (days); NIP: Number of inflorescence per plant; IL: Inflorescence Length (cm); NFP: Number of flowers per plant; SFW: Single flower weight (g); FL: Flower length (cm); SL: Staminode length (cm); SW: Staminode width (cm); FYP: Flower yield per plant (g); RD: Rhizome diameter (cm); RFW: Rhizome fresh weight (g); RIL: Rhizome internode length (cm); NNR: Number of nodes per rhizome; NER: Number of eyes per rhizome; RYP: Rhizome yield per plant (g).

 Volume 57 Issue 6 (December 2023) 721

in time taken for flowering (16.82%) which were shown medium genetic advances as per cent of mean (GAM) (Table 2). High value to estimate the broad sense heritability were recorded for the characters *viz*., Plant height (99.70%) followed by number of flowers per plant (99.40%), number of eyes per rhizome (98.80%), flower yield per plant (98.30%), number of inflorescence per plant (97.70%), staminode width (97.50%), stem diameter (97.30%), single flower weight (97.10%), rhizome fresh weight (96.30%), flower length (94.40%), rhizome yield per plant (93.50%), rhizome internode length (93.00%), days to first bloom (92.40%), leaf width (92.00%), staminode length (91.70%), inflorescence length (90.40%), leaf length (89.50%), rhizome diameter (87.40%), number of leaves per plant (87.30%), leaf area (86.80%), number of nodes per rhizome (82.00%) and number of leaves per clump (69.60%) and medium heritability were recorded in number of tillers per plant (59.30%). High heritability and high GAM indicates the presence of additive gene action with less environmental influence on these traits and an important factor for predicting the resultant effect for selecting the best accessions. Hence, it indicated the predominance of additive gene action ample scope for improving these traits would be effective for the direct selection. The findings are in accordance with the results of turmeric (Mishra *et al*., 2015) and (Luiram *et al*., 2018).

Character association analysis

In crop improvement programme, selection is very effective only when genetic variability is present. However, selections for some traits need to be correlated to explain easily the interrelationship among the traits and make easy to identify the elite accessions. Association analysis of different quantitative traits with flower and rhizome yield per plant on *Canna* accessions and their interrelationships were investigated though the study of correlation analysis which is suggested that the level of genotypic correlation were

higher as compared to their corresponding phenotypic correlations these indicates the inherent relationship and were studied in *Canna* (Table 3a and 3b). Among the 23 traits, inflorescence length (0.94**) was highly significant and positively correlated with rhizome yield per plant followed by plant height (0.92**), stem diameter (0.92**), leaf width (0.91**) leaf area (0.85**), number of flowers per plant (0.83**), flower yield per plant (0.83**), rhizome fresh weight (0.79**), rhizome diameter (0.78**), number of tillers per plant (0.76**), leaf length (0.72**), single flower weight (0.66**), flower length (0.62**), number of leaves per clump (0.53*), number of inflorescence per plant (0.52*), staminode length (0.52*), rhizome internode length (0.50*), staminode width (0.41*) while, number of nodes per rhizome (-0.71**), number of eyes per rhizome (-0.70**) were shown negatively correlated with rhizome yield. In the present study, research findings were related and reported in turmeric (Aarthi *et al*., 2022) and (Islam *et al*., 2008) in ginger.

Stem diameter (0.93**) was highly significant and positively correlated with flower yield per plant followed by single flower weight (0.89**), inflorescence length (0.74**), number of tillers per plant (0.71**), number of leaves per clump (0.70**), number of flowers per plant (0.64**), flower length (0.64**), staminode length (0.63**), leaf width (0.62**), staminode width (0.60**), plant height (0.57**), leaf area (0.48*). Inflorescence length (0.87**) was highly significant and positively correlated with fresh weight of rhizome per plant followed by leaf width (0.81**), stem diameter (0.80**), flower yield per plant (0.80**), number of flowers per plant (0.76**), leaf area (0.72**), rhizome diameter (0.65**), number of tillers per plant (0.64**), plant height (0.60**), single flower weight (0.58**), number of leaves per clump (0.54**), leaf length (0.51*), number of inflorescence per plant (0.46*), staminode length (0.40*), flower length (0.39*), staminode width (0.31*). The result revealed that the related findings were reported in turmeric (Sivakumar *et al*., 2020).

Table 4: Path coefficient analysis for quantitative traits in *Canna indica* L. accessions.

Traits	PH	SD	NTP	NLC	LA	RD	RFW	RIL	NNR	NER	Genotypic correlation with yield
PH.	3.84	-4.25	-1.35	1.79	-2.46	-1.40	2.90	1.11	-1.77	2.15	0.57
SD	2.75	-5.93	-2.03	4.16	-1.78	-1.03	3.86	0.45	-1.75	2.23	0.93
NTP	2.02	-4.68	-2.58	4.69	-1.73	-0.77	3.07	0.37	-1.69	2.02	0.71
NLC	1.11	-3.97	-1.94	6.22	-0.74	-0.20	2.59	-0.27	-2.52	0.42	0.70
LA	3.37	-3.77	-1.60	1.65	-2.80	-1.16	3.47	1.23	-2.12	2.21	0.48
RD	3.30	-3.75	-1.21	0.78	-1.99	-1.63	3.11	0.81	-0.99	2.16	0.58
RFW	2.32	-4.76	-1.64	3.35	-2.02	-1.05	4.81	0.43	-1.84	1.21	0.80
RIL	2.37	-1.47	-0.53	-0.94	-1.91	-0.73	1.14	1.80	-0.99	1.38	0.13
NNR	-2.06	3.14	1.31	-4.74	1.80	0.48	-2.68	-0.54	3.31	-0.58	-0.54
NER	-2.34	3.75	1.47	-0.74	1.75	0.99	-1.65	-0.71	0.54	-3.53	-0.45

Residual effect square: 0.224.

Note: PH: Plant height; SD: Stem diameter; NTP: Number of tillers per plant; NLC: Number of leaves per clump; LA: Leaf area; RD: Rhizome diameter; RFW: Rhizome fresh weight; RIL: Rhizome internode length; NNR: Number of nodes per rhizome; NER: Number of eyes per rhizome.

Path coefficient analysis

In path analysis were shown direct and indirect effects of ten variable traits on fresh flower yield per plant is given in Table 4. The estimates indicated that the number of leaves per clump (6.22) were exhibited very high and positive direct effect on fresh flower yield per plant followed by fresh rhizome weight (4.81), plant height (3.84), number of nodes per rhizome (3.31) and rhizome intermodal length (1.80). The results in accordance with similar findings reported in turmeric (Prajapati *et al*., 2014). The characters stem diameter (-5.93) followed by number of eyes per rhizome (-3.53), leaf area (-2.80), number of tillers per plant (-2.58) and rhizome diameter (-1.63) were shown very high and negative direct effect on fresh flower yield per plant. The research related findings were reported in turmeric (Suresh *et al*., 2019).

Considering the indirect effect, all the traits were shown high positive indirect effect on fresh flower yield per plant. Fresh weight of rhizome, number of eyes per rhizome, number of leaves per clump and rhizome internode length were shown very high and positive indirect effect on fresh flower yield per plant while, stem diameter, leaf area, number of tillers per plant, number of nodes per rhizome and rhizome diameter had very high but negative indirect effect on flower yield per plant. The results revealed that both direct and indirect effect play major role in choice of economic trait for selection criteria based on path analysis. The similar results were reported in turmeric (Verma *et al*., 2014).

CONCLUSION

The present study was to estimate genetic variability and association analysis among the quantitative traits to select the promising *Canna* accessions. The results revealed that among the *Canna* accessions Ac. 8 showed high flower yield per plant and rhizome yield per plant (329.90 g and 891.8 g) followed by Ac.10 (300.20 g and 836.2 g), Ac.3 (128.21 g and 746.3 g) and Ac.6 (106.03 g and 737.9 g). The characters plant height, stem diameter, leaf area, fresh weight of rhizome, number of tillers per plant, number of leaves per clump, number of eyes per rhizome and rhizome intermodal length are play important role in the genetic improvement of both flower and rhizome yield per plant in canna lily.

ACKNOWLEDGEMENT

The authors would like to thank Indian Council of Social Science Research (Doctoral fellowship), Ministry of Education for providing fund and Head of the Department Floriculture and Landscape Architecture, HC and RI, TNAU, Coimbatore. Our special thanks to technical assistants who were helped in completing the research.

Conflict of interest

The authors declare that they have no conflicts of interest.

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