



RESEARCH ARTICLE

Genetic variability and trait association studies in *Celosia* accessions for growth and yield characters

Priyadharsini R¹, Rajadurai K R^{1*}, Beulah A², Madhan Mohan M³, Venkatesan K¹ & Rajesh S⁴

¹Department of Floriculture and Landscaping, Tamil Nadu Agricultural University, Horticultural College and Research Institute, Periyakulam 625 604, India

²Department of Post Harvest Technology, Tamil Nadu Agricultural University, Horticultural College and Research Institute, Periyakulam 625 604, India

³Department of Plant Breeding and Genetics, Tamil Nadu Agricultural University, Agricultural Research Station, Vaigai Dam, Periyakulam 625 604, India

⁴Centre for Plant Molecular Biology and Biotechnology, Tamil Nadu Agricultural University, Coimbatore 641 003, India

*Email: rajadurai.kr@tnau.ac.in



ARTICLE HISTORY

Received: 18 January 2025

Accepted: 03 March 2025

Available online

Version 1.0 : 09 March 2025



Additional information

Peer review: Publisher thanks Sectional Editor and the other anonymous reviewers for their contribution to the peer review of this work.

Reprints & permissions information is available at https://horizonepublishing.com/journals/index.php/PST/open_access_policy

Publisher's Note: Horizon e-Publishing Group remains neutral with regard to jurisdictional claims in published maps and institutional affiliations.

Indexing: Plant Science Today, published by Horizon e-Publishing Group, is covered by Scopus, Web of Science, BIOSIS Previews, Clarivate Analytics, NAAS, UGC Care, etc See https://horizonepublishing.com/journals/index.php/PST/indexing_abstracting

Copyright: © The Author(s). This is an open-access article distributed under the terms of the Creative Commons Attribution License, which permits unrestricted use, distribution and reproduction in any medium, provided the original author and source are credited (<https://creativecommons.org/licenses/by/4.0/>)

CITE THIS ARTICLE

Priyadharsini R, Rajadurai KR, Beulah A Madhan Mohan M, Venkatesan K, Rajesh S. Genetic variability and trait association studies in *Celosia* accessions for growth and yield characters. Plant Science Today (Early Access). <https://doi.org/10.14719/pst.7281>

Abstract

Improving the yield and other characteristics of a crop requires an understanding of the type and extent of variability present in the plant material as well as the relationships between the traits. This study focuses on thirty-five accessions of *Celosia* species, evaluated for genetic variability in 19 quantitative and qualitative traits, to understand the associations between these characters and their contribution to flower yield. The objective of the work was to investigate the genetic variability and association between traits to rationally improve the yield of *Celosia* species. The data used in this study were assessed at 70 days after transplanting (DAT) to complete flowering in all *Celosia* accessions for its growth and yield. From the results of the analysis, the trait, single flower weight had the larger estimates of GCV (41.9 %) and PCV (46.29 %) of all parameters that were recorded. For most traits examined, higher estimates of heritability were recorded, particularly for plant spread (E-W) (99 %), while significant genetic advance per mean was in single flower weight (78.14 %). Leaf length (0.34) and seed weight (0.81) showed a significant positive correlation with the number of flowers per plant, indicating strong potential for increasing yield. The parameters like plant height (0.8132) and leaf length (0.7602) had the most direct impact on flower yield, according to the path analysis results. Based on this conclusion, it appears that *Celosia* species can be improved by analyzing the features acquired from selection criteria based on genetic parameters and employing them for improved crop yield in future breeding works.

Keywords

breeding; correlation; estimates; heritability; improvement; selection

Introduction

Celosia spp. is an annual, dicotyledon herbaceous plant that grows to a height of 2 to 5 feet and is used for both ornamental and therapeutic purpose. It belongs to the genus *Celosia*, family Amaranthaceae and class Magnoliopsid. Some of the common names of *Celosia* are cockscomb, crested celosia, yellow toreador, red cockscomb, foxtail amaranth, fire-flame bush, shinaji tea and woodfordia. The Greek word celosia means "burned" because the flower head resembles a flame. Other names for the flower include brain comb, velvet flower, flame head and flamingo (1).

In addition to tropical and subtropical areas like Africa, India, Southern America, it is primarily found in southern China (2). Celosia leaves are simple, saggitate (arrow-shaped), with pinnate venation, measuring 2-4 inches in length and exhibiting a variety of colours, including purple, scarlet and bright green, with an alternate leaf arrangement (3). Celosia has a colourful, flattened seed that is small, kidney-shaped and has a diameter of 1 to 1.5 mm. It is primarily black and lustrous, with a thin, crumbly seed coat (4). The stem is upright, thick and branched with green or red-tinged, ridged and an almost flat at the top. The simple, petiolate leaves are alternate, with a blade that is long-elliptical to ovally lanceolate, measuring 5-13 cm long, 2-6 cm wide. The leaf apex is either acuminate or attenuate, while the base gradually narrows and becomes decurrent, with entire margins. They have juicy, flat spikes that resemble crests. *C. argentea* Linn., *C. cristata* Linn., *C. isertii* Linn. and *C. spicata* Linn. are the most significant among approximately 60 species of Celosia because of their leafy vegetable diet and ornamental value (5).

There are two major types of *Celosia* inflorescences: the plume or plumosa type and the cristata type. The fluffy, feathery crown of the plumosa group is essentially made up of tiny flowers. Its colours are essentially red and yellow. In contrast, the cristata group features tight blossoms with a velvety texture that some people compare to brain tissue. The flower head is coloured in a variety of hues, including deep red, dark pink and golden yellow. There are several flowers at the down middle (6). There are five perianthial segments, which are elliptically ovate, pointed at the tip and pale crimson to purplish red, yellowish white, or yellow. Five stamens are present in each flower and their filaments are united to form a cup at the base.

An important strategy for crop development programme is the selection process, which depends on the genetic variation present in a population. Genetic variability analysis is found very helpful in choosing the right plant species (7). The correlation coefficient shows the type of link between the features where path analysis separates the correlation coefficients into measures of direct and indirect impacts, giving insight into how each character contributes directly and indirectly to yield. Since yield is a complicated trait that is influenced by numerous component traits, it may not always be feasible to select for superior yielding genotypes in any selection method (8). In light of the foregoing context, the current study was carried out with the aim of estimating the overall genetic variability and figuring out the heritability of particular agronomic parameters as well as correlation and path analysis among significant traits for selection criteria aimed at increasing yield in *Celosia* spp accessions.

Materials and Methods

Sources of Celosia accessions and Study Location

The *Celosia* species evaluated in this study were totally 35 accessions and they were collected from different geographical locations of Tamil Nadu. Among these, 5 accessions were collected from National Bureau of Plant Genetic Resources

(NBPGR), New Delhi. Among the total collected species of celosia, 34 accessions belong to the species *C. cristata* and 1 accession belongs to *C. argentea*.

The experiment was conducted in the year 2024 during the month of March to June at the research farm of the Department of Floriculture and Landscape Architecture, Horticultural College and Research Institute, Periyakulam with latitudinal position of 10.12645 N and longitudinal position of 77.59682 E and altitude of 356 m above mean sea level, Tamil Nadu Agricultural University.

Experimental Design and Method of Planting

The *Celosia* accessions were raised for 25 days in the nursery in portrays before transplanting to the field. The crop was grown using established processes from the Crop Production Guide, which included suitable agronomic practices. The seedlings raised in the nursery were transplanted in the field arranged in Randomized Block Design (RBD) with three replications. The plant population were maintained in the area of 463m² with the spacing of 30 × 30 cm and number of plants per replication were maintained with 9 plants.

Collection and Data Analysis

Data collection on growth parameters began 30 Days after transplanting (DAT), while flowering parameters were assessed at 60 DAT and continued till 70 DAT to complete flowering in all *Celosia* accessions. Data collected on growth and flowering parameters are represented in Table 1. Weighing balances and the metre rule were used to create the quantitative data, while developed scales were utilized for recording other data. TNAUSTAT statistical software were used to analyze the resulting data. All data were subjected to analysis of variance (ANOVA) and means were separated using Least Significant Differences (LSD). The relationships among the quantitative and qualitative traits were established using Pearson correlation coefficient. The genetic variability analysis was done using the statistical package R version 4.4.

Table 1. Morphological characters recorded in *Celosia* accessions

S.No	Vegetative characters	Flowering characters
1.	Plant height (cm)	Days for first flowering
2.	Leaf length (cm)	Days for 50% flowering
3.	Leaf breadth (cm)	No. of flowering branch
4.	Plant spread (E-W) (cm)	Single flower weight (g)
5.	Plant spread (N-S) (cm)	Inflorescence length (cm)
6.	Stem girth (cm)	Flower length (cm)
7.	Number of leaves	Flower width (cm)
8.	Number of branches	No. of flowers/ plant
9.	-	Weight of flowers/ plant (g)
10.	-	Days for 50% senescence
11.	-	Seed weight (g)

Genotypic (GCV) and phenotypic coefficient of variation (PCV) were calculated using previously mentioned formula (9), heritability in the broad sense (h^2) (10) and genetic advance as per the method described earlier (11). The correlation coefficients were determined the degree of a character's relationship with yield as well as among the variables that contribute to yield. The correlation between genotype and phenotype was calculated using formula given elsewhere (11). The path coefficient analysis to figure out the direct and indirect impacts of the various characters on yield was also calculated (12).

Results and Discussion

Phenotypic and genotypic coefficient of variability

Estimates of genetic components of *Celosia* accessions are shown in Table 2 and Fig. 1. Results of the analysis revealed that PCV % was higher than GCV % for all the traits studied. This showed that traits under study were more influenced by the environmental factors like soil quality, rainfall, temperature as they contribute fluctuations in plant growth. Most of the studied parameters of *Celosia* accessions exhibited high GCV and PCV estimates. The presence of substantial variability in these qualities is indicated by the highest values of GCV and PCV. The parameter single flower weight was documented with highest GCV (41.9 %) and high PCV (46.29 %) of all others. The moderate estimates of GCV and PCV were recorded for days for 50 % senescence (15.41 % and 18.23 %), days for first flowering (11.70 % and 13.52 %) and days for 50 % flowering (11.44 % and 16.48 %).

The environment had a significant influence in the phenotypic expression and inheritance of the measured traits, as evidenced by the disparity between estimates of genotypic (GCVs) and phenotypic coefficients of variation (PCVs) for nearly all of the observed traits. High GCV and PCV were observed for the characters like single flower weight, number of leaves and plant spread (E-W) indicating that additive gene action contributed to these genotypes which implies that direct selection will readily improve the observed parameter. Moderate and high GCV and PCV estimates in *Celosia* accessions suggest that traits such as single flower weight are suitable for selection. Every parameter in the study had a higher PCV than the GCV, suggesting that the environment was influencing the traits. Similar study was conducted in Chrysanthemum where they reported that high amount of phenotypic and genotypic variation was observed for the characters like, number of flowers per plant, peduncle length of terminal flower, length of outer ray florets, flower diameter and peduncle thickness of terminal flower suggesting the presence of large amount of variability which supports the current study (13). Another work in Carnation were also reported about the genetic variability and its importance for selection of superior qualities of the crop (14).

Heritability

The degree of correlation between a trait's phenotype and breeding value, or genotype, has been defined as heritability. Consequently, the proportion of phenotypic variance attributable to genetic variance is known as heritability (15). A reliable indicator of the way traits are passed down from parents to their offspring is heritability. There are three levels of heritability: low (less than 30 %), medium (30 % - 60 %) and high (more than 60 %). The estimated values of heritability are presented in Table 2 and Fig. 1. Plant breeders can choose genotypes from a wide genetic population with the use of heritability estimations. Consequently, high heritability aids in the efficient selection of a specific trait (16). In this study, the broad sense heritability was high (>60 %) for most of the plant characters. Higher estimates of heritability in broad sense were documented for the most of the characters studied such as plant spread (E-W) (99 %), plant spread (N-S) (91 %), flower length (89 %), number of flowers / plant (88 %), inflorescence length (87 %), plant height (84 %), number of leaves (82 %), single flower weight (81 %), seed weight/plant (80 %), flower width (77 %), stem girth (77 %), days for first flowering (74 %), leaf length (73 %), number of branches (71 %), number of flowering branches (68 %) and leaf breadth (63 %) where the moderate level of heritability was found in days for 50 % flowering (48 %). The environmental influence is moderate for days for 50% flowering.

High heritability of the observed traits in *Celosia* indicated that genetic factors play a significant role in controlling these traits. The high heritability helps in the effective selection of the particular character representing that these characters were predominant in additive gene action. Similar studies were done in *Celosia argentea* where they reported the results according to the heritability estimates as plant height and dry matter content showed moderate environmental influence, whereas harvest index showed no environmental influence in expression and the environmental influence was negligible for number of leaves per plant, stem weight and stem diameter (7). Similar study in chrysanthemum discussed that heritability in the broadest sense for the traits was strong, ranging from 0.92 (leaf length-width ratio) to 0.99 (flower diameter and number of blooms per plant) (13).

Table 2. Genetic parameters of *Celosia* accessions at 70 DAT

S.No.	Characters	GCV (%)	PCV (%)	Heritability (Broad sense)	Genetic advance	Genetic advance as percentage of mean
1.	Plant height	23.32	25.40	0.84	25.14	44.09
2.	Leaf length	24.99	29.09	0.73	2.88	44.25
3.	Leaf breadth	22.39	28.09	0.63	1.28	36.79
4.	Plant Spread (N-S)	32.31	33.85	0.91	20.42	63.54
5.	Plant Spread (E-W)	33.56	33.65	0.99	20.83	68.95
6.	Stem girth	30.84	35.02	0.77	2.04	55.94
7.	Number of leaves	37.57	41.37	0.82	148.90	70.30
8.	Number of branches	27.63	32.61	0.71	10.30	48.23
9.	Days for first flowering	11.70	13.52	0.74	8.01	20.87
10.	Days for 50% flowering	11.44	16.48	0.48	8.32	16.37
11.	Number of flowering branches	27.46	33.18	0.68	9.33	46.83
12.	Single flower weight	41.90	46.29	0.81	4.08	78.14
13.	Inflorescence length	28.71	30.61	0.87	9.56	55.48
14.	Flower length	30.14	31.78	0.89	31.78	10.06
15.	Flower width	30.61	34.83	0.77	4.52	55.41
16.	Number of flowers / plant	29.98	31.81	0.88	11.00	58.22
17.	Days for 50% senescence	15.41	18.23	0.71	4.96	26.84
18.	Seed weight/plant	36.11	40.15	0.80	2.64	66.90
19.	Weight of flowers / plant	37.86	43.30	0.76	0.36	68.19

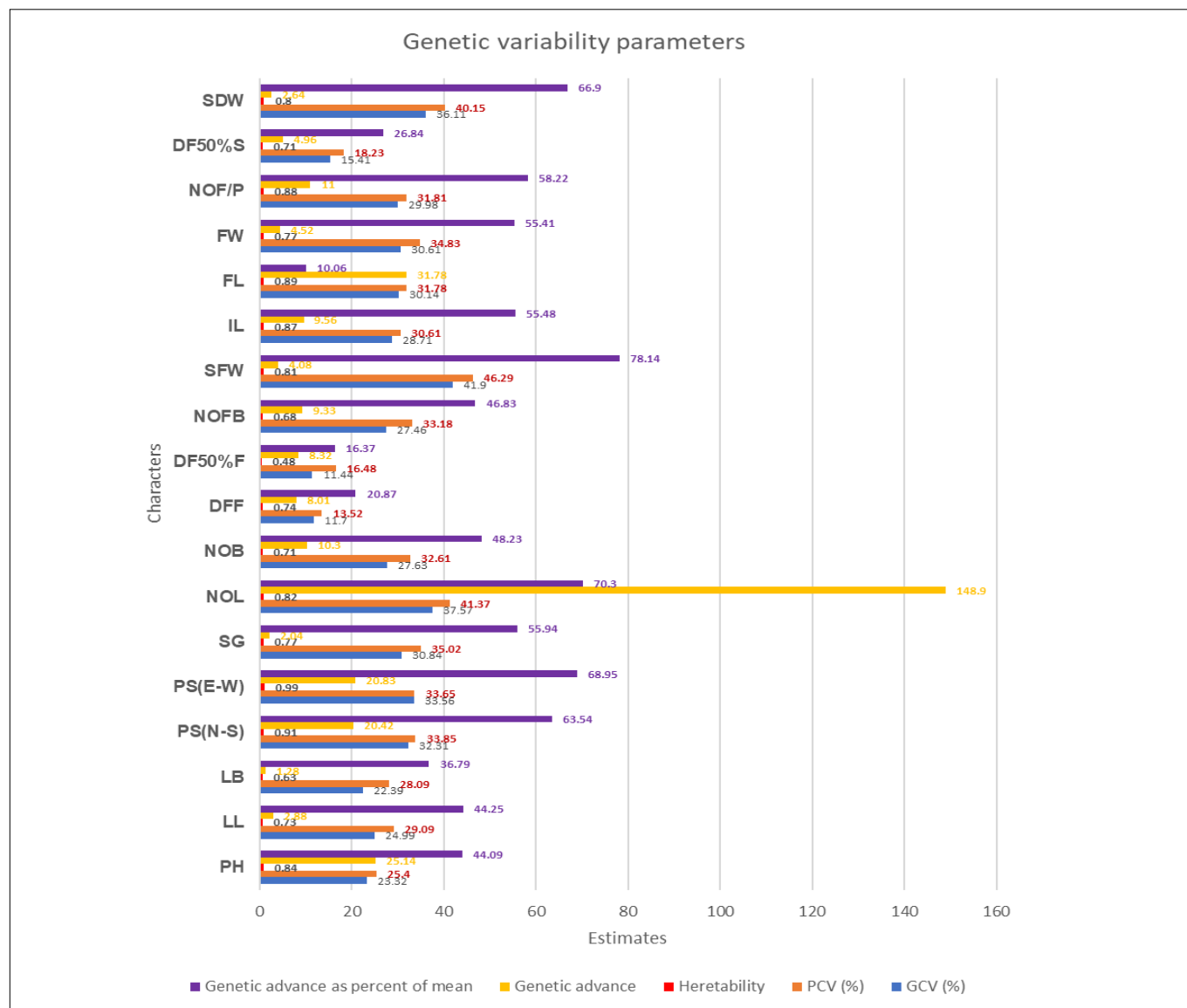


Fig. 1. Graphical representation of genetic variability parameters.

(*Traits: PH= Plant height, LL=Leaf length, LB= Leaf breadth, PS(N-S)= Plant spread at N-S, PS(E-W)=Plant spread at E-W, SG=Stem girth, NOL=Number of leaves, NOB= Total number of branches, DFF=Days for first flowering, DF50%F=Days for 50% flowering, NOFB= Number of flowering branches, SFW= Single flower weight, IL=Inflorescence length, FL=Flower length, FW= Flower width, NOF/P= Number of flowers per plant, DF50%S=Days for 50% flower senescence, SDW= Seed weight, WOF/P= Weight of flowers per plant)

Genetic advance (GA) as percent of mean

When selection is applied on the base population, the genetic advance serves as a helpful indicator of the effective and efficient selection progress that may be anticipated. In this present study, majority of the characters revealed the high genetic advance as percent of mean (>20 %), whereas some parameters like days for 50 % flowering and flower length exhibited the moderate genetic advance as percent of mean (10-20 %) which is indicated in Table 1 and Fig. 1. The parameters that has high genetic advance per mean are Single flower weight (78.14 %), number of leaves (70.3 %), plant spread (E-W) (68.95 %), weight of flowers/plant (68.19 %), seed weight/plant (66.9 %), plant spread (N-S) (63.54 %), number of flowers/plant (58.22 %), stem girth (55.94 %), inflorescence length (55.48 %), flower width (55.41 %), number of branches (48.23 %), number of flowering branches (46.83 %), leaf length (44.25 %), plant height (44.09 %), leaf breadth (36.79 %), days for 50 % flower senescence (26.84 %) and days for first flowering (20.87 %). Some of the traits like single flower weight, number of leaves with high estimates of

genetic advance further strengthens its usefulness for selection unlike days for 50 % senescence and days for first flowering with low estimates of genetic advance.

The high GAM observed in some of the evaluated traits of *Celosia* showed that additive gene action could regulate characters to the greatest extent possible and that there was a high likelihood of exploiting this feature for selection-based genetic improvement. This reveals that selection is important for improving these traits. Similar studies were done in *Celosia argentea* where he described that in contrast to stem diameter and weight, which have low estimates of both heritability and genetic advance, an unusually high estimate of genetic advance for dry matter content further enhances its utility for selection (16). In marigold, high advance per mean coupled with high heritability was achieved for some of the vegetative and flowering traits which can be considered for the future breeding works (17, 18). Another study in Indian rose showed high genetic advance for weight of flower, number of petals per flower and number of flowers per plant which supports the current study (19).

Correlation studies

The correlation coefficients between various characters were calculated at the genotypic and phenotypic level (Tables 3, 4) and (Fig. 2, 3) and represented as correlogram in Fig. 4. The correlogram approach was used to visually represent the correlation between multiple variables, making it easier to identify patterns, strengths and directions of relationships within the dataset. It helps in quick determination of important links using correlograms, which offer a more structured and intuitive method of interpreting complex interrelationships than numerical correlation matrices. The plant breeder benefits when desirable traits have a positive association with one another since it promotes the simultaneous improvement of both traits (20). According to genotypic correlation, weight of flowers per plant which is the economic yield of the plant showed the positive and significant correlation with only two characters which are leaf length (0.34) and seed weight (0.81), where all the other characters were found with both positive and negative with non-significant correlation with number of flowers per plant.

Plant height exhibited highly significant and positive correlation with leaf breadth (0.51) and significant positive correlation with some other characters such as plant spread (N-S) (0.38), plant spread (E-W) (0.38), number of flowering branches (0.37), number of flowers per plant (0.38), days for 50 % flower senescence (0.36), seed weight (0.38). A non-significant negative correlation was found with leaf length (-0.22) and all other characters were non-significant positively correlated. Leaf length showed a highly significant positive correlation with flower length (0.64) and a positive correlation with leaf breadth (0.40), inflorescence length (0.41) and weight of flowers per plant (0.34), where all other characters showed both positive and negative non-significant correlation with leaf length. Leaf breadth showed a highly positive significant correlation with plant spread (N-S) and plant spread (E-W) which are on par with each other (0.75) and has positive significant correlation with some characters

such as stem girth (0.53), number of flowering branches (0.34), flower length (0.36), number of flowers per plant (0.35). Plant spread (N-S) was highly positive and significantly correlated with some characters like plant spread (E-W) (1.01), stem girth (0.49), number of leaves (0.45), total number of branches (0.55), number of flowering branches (0.59), number of flowers per plant (0.58) and showed positive significant correlation with days for 50 % flower senescence (0.36). Plant spread (E-W) and stem girth showed highly significant positive correlation with number of flowering branches (0.60), number of flowers per plant (0.58), total number of branches (0.55), stem girth (0.48), number of leaves (0.47), days for 50 % flower senescence (0.38) and days

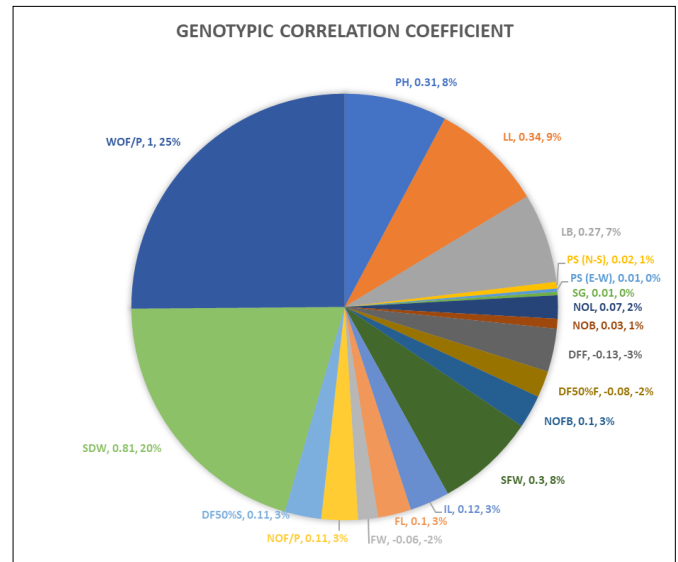


Fig. 2. Genotypic coefficient of correlation among different traits in *Celosia* accessions (*Traits: PH= Plant height, LL=Leaf length, LB= Leaf breadth, PS(N-S)= Plant spread at N-S, PS(E-W)=Plant spread at E-W, SG=Stem girth, NOL=Number of leaves, NOB= Total number of branches, DFF=Days for first flowering, DF50%F=Days for 50% flowering, NOFB= Number of flowering branches, SFW= Single flower weight, IL=Inflorescence length, FL=Flower length, FW= Flower width, NOF/P= Number of flowers per plant, DF50% S=Days for 50%flower senescence, SDW= Seed weight, WOF/P= Weight of flowers per plant).

Table 3. Genotypic correlation among 19 characters in *Celosia* accessions

Traits	PH	LL	LB	PS(N-S)	PS(E-W)	SG	NOL	NOB	DFF	DF50%F	NOFB	SFW	IL	FL	FW	NOF/P	DF50%S	SDW	WOF/P
PH	1**	-0.22	0.51**	0.38*	0.38*	0.14	0.29	0.32	0.30	0.31	0.37*	0.05	0.06	0.12	0.27	0.38*	0.36*	0.38*	0.31
LL		1**	0.40*	0.00	0.00	0.18	-0.23	-0.20	-0.30	-0.22	-0.17	0.10	0.41*	0.64**	-0.09	-0.14	-0.10	-0.00	0.34*
LB			1**	0.75**	0.76**	0.53**	0.21	0.21	0.25	0.12	0.34*	0.07	0.23	0.36*	-0.10	0.35*	0.24	0.17	0.27
PS(N-S)				1**	1.01**	0.49**	0.45**	0.55**	0.25	0.33	0.59**	0.05	0.08	0.09	0.02	0.58**	0.36*	0.12	0.02
PS(E-W)					1**	0.48**	0.47**	0.55**	0.26	0.33*	0.60**	0.05	0.06	0.08	0.00	0.58**	0.38*	0.14	0.01
SG						1**	0.47**	0.55**	0.26	0.33*	0.60**	0.05	0.06	0.08	0.00	0.58**	0.38*	0.14	0.01
NOL							1**	0.79**	0.07	0.05	0.79**	0.49**	0.25	0.05	0.34*	0.75**	0.27	0.39*	0.07
NOB								1**	0.18	0.09	1.11**	0.24	0.02	-0.07	0.26	1.02**	0.39*	0.41*	0.03
DFF									1**	0.98**	0.14	-0.03	-0.26	-0.16	-0.39*	0.15	0.07	0.07	-0.13
DF50%F										1**	0.17	0.03	-0.36*	-0.24	-0.22	0.09	0.05	0.14	-0.08
NOFB											1**	0.24	0.04	-0.04	0.30	1.09**	0.46**	0.44**	0.10
SFW												1**	0.34*	0.21	0.14	0.27	-0.03	0.28	0.30
IL													1**	0.89**	0.32	0.12	-0.17	-0.07	0.12
FL														1**	0.16	0.00	-0.13	-0.13	0.10
FW															1**	0.30	0.07	0.00	-0.06
NOF/P																1**	0.41*	0.43**	0.11
DF50%S																	1**	0.30	0.11
SDW																		1**	0.81**
WOF/P																			1**

*significant at $p=0.05$, **significant at $p=0.01$, Traits : PH= Plant height, LL=Leaf length, LB= Leaf breadth, PS(N-S)= Plant spread at N-S, PS(E-W)=Plant spread at E-W, SG=Stem girth, NOL=Number of leaves, NOB= Total number of branches, DFF=Days for first flowering, DF50%F=Days for 50% flowering, NOFB= Number of flowering branches, SFW= Single flower weight, IL=Inflorescence length, FL=Flower length, FW= Flower width, NOF/P= Number of flowers per plant, DF50% S=Days for 50%flower senescence, SDW= Seed weight, WOF/P= Weight of flowers per plant

Table 4. Phenotypic correlation among 19 characters in *Celosia* accessions

Traits	PH	LL	LB	PS(N-S)	PS(E-W)	SG	NOL	NOB	DFF	DF50 %F	NOFB	SFW	IL	FL	FW	NOF/P	DF50 %S	SDW	WOF/P
PH	1**	-0.15	0.35**	0.32**	0.35**	0.05	0.19*	0.22*	0.29**	0.12	0.32**	0.08	0.06	0.12	0.24*	0.34**	0.25**	0.33**	0.24*
LL		1**	0.27**	0.022	-0.00	0.18	-0.17	-0.15	-0.18	-0.16	-0.12	0.10	0.37**	0.51**	-0.10	-0.10	-0.09	0.00	0.34**
LB			1**	0.58**	0.61**	0.37**	0.22*	0.25**	0.16	0.12	0.21*	0.07	0.23*	0.29**	-0.05	0.28**	0.18	0.16	0.19*
PS (N-S)				1**	0.96**	0.40**	0.41**	0.44**	0.17	0.20*	0.47**	0.01	0.08	0.09	0.03	0.53**	0.30**	0.11	0.02
PS (E-W)					1**	0.42**	0.43**	0.47**	0.23*	0.23*	0.49**	0.04	0.06	0.07	0.00	0.55**	0.32**	0.13	0.01
SG						1**	0.43**	0.49**	0.00	0.00	0.48**	0.06	0.25**	0.16	0.05	0.58**	0.23*	0.25**	0.18
NOL							1**	0.68**	-0.01	0.09	0.62**	0.44**	0.25**	0.04	0.28**	0.65**	0.18	0.35**	0.08
NOB								1**	0.08	0.07	0.81**	0.20*	0.04	-0.06	0.21*	0.88**	0.34**	0.31**	0.02
DFF									1**	0.59**	0.14	0.01	-0.16	-0.10	-0.26**	0.10	-0.39	0.02	-0.04
DF										1**	-0.00	-0.00	-0.24*	-0.19*	-0.06	0.06	-4.00	0.07	-0.04
50%F											1**	0.25**	0.10	-0.03	0.23*	0.84**	0.28**	0.35**	0.08
NOFB												1**	0.34**	0.19	0.13	0.19*	-0.09	0.24*	0.23*
SFW													1**	0.80**	0.27**	0.09	-0.16	-0.03	0.13
IL														1**	0.15	0.00	-0.11	-0.11	0.10
FL															1**	0.25**	0.02	-0.01	-0.10
FW																1**	0.36**	0.34**	0.09
NOF/P																	1**	0.24*	0.08
DF																		1**	0.65**
50%S																			1**
SDW																			
WOF/P																			

*significant at $p=0.05$, **significant at $p=0.01$; Traits : PH= Plant height, LL=Leaf length, LB= Leaf breadth, PS(N-S)= Plant spread at N-S, PS(E-W)=Plant spread at E-W, SG=Stem girth, NOL=Number of leaves, NOB= Total number of branches, DFF=Days for first flowering, DF50%F=Days for 50% flowering, NOFB= Number of flowering branches, SFW= Single flower weight, IL=Inflorescence length, FL=Flower length, FW= Flower width, NOF/P= Number of flowers per plant, DF50% S=Days for 50%flower senescence, SDW= Seed weight, WOF/P= Weight of flowers per plant

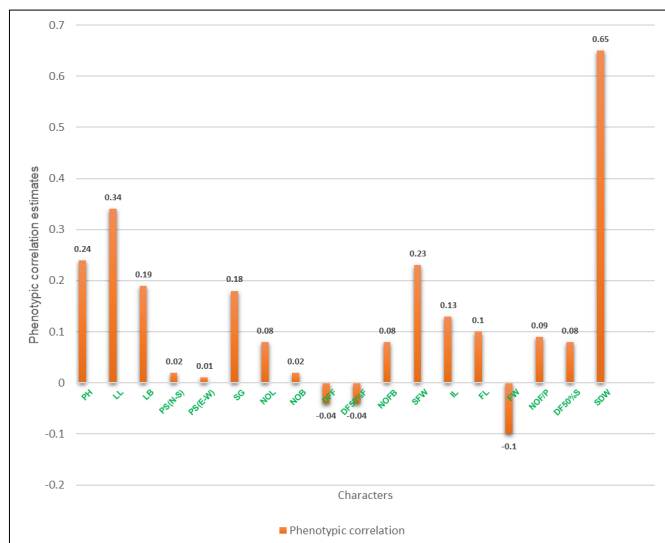


Fig. 3. Phenotypic coefficient of correlation among different traits in *Celosia* accessions (*Traits: PH= Plant height, LL=Leaf length, LB= Leaf breadth, PS(N-S)= Plant spread at N-S, PS(E-W)=Plant spread at E-W, SG=Stem girth, NOL=Number of leaves, NOB= Total number of branches, DFF=Days for first flowering, DF50%F=Days for 50% flowering, NOFB= Number of flowering branches, SFW= Single flower weight, IL=Inflorescence length, FL=Flower length, FW= Flower width, NOF/P= Number of flowers per plant, DF50% S=Days for 50%flower senescence, SDW= Seed weight, WOF/P= Weight of flowers per plant).

for 50 % flowering (0.33). Highly significant and positive correlation for number of leaves were found with total number of branches and number of flowering branches (0.79), number of flowers per plant (0.75), single flower weight (0.49), seed weight (0.39) and flower weight (0.34). The total number of branches were found to be highly significantly correlated with number of flowering branches (1.11), number of flowers per plant (1.02), seed weight (0.41), days for 50% flower senescence (0.39). The character days for first flowering has highly significant positive correlation with days

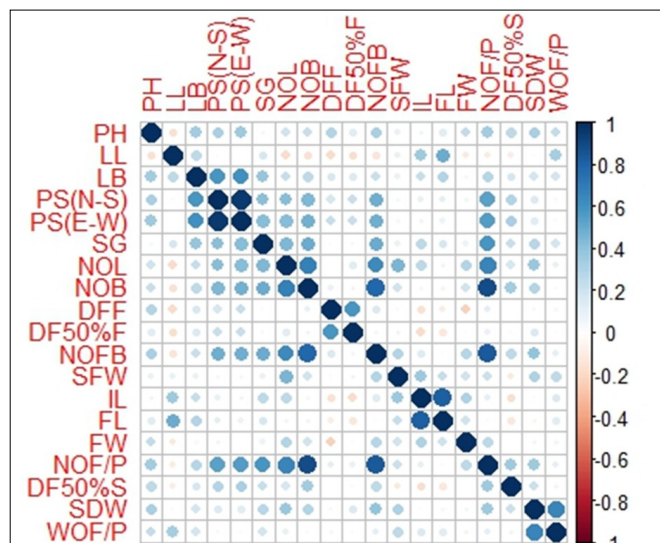


Fig. 4. Correlogram for the 19 attributes recorded in the study (*Traits: PH= Plant height, LL=Leaf length, LB= Leaf breadth, PS(N-S)= Plant spread at N-S, PS(E-W)=Plant spread at E-W, SG=Stem girth, NOL=Number of leaves, NOB= Total number of branches, DFF=Days for first flowering, DF50%F=Days for 50% flowering, NOFB= Number of flowering branches, SFW= Single flower weight, IL=Inflorescence length, FL=Flower length, FW= Flower width, NOF/P= Number of flowers per plant, DF50% S=Days for 50%flower senescence, SDW= Seed weight, WOF/P= Weight of flowers per plant).

for 50% flowering (0.98) and has significant negative correlation with flower width (-0.39). The character days for 50 % flowering has significant negative correlation with inflorescence length (-0.36) and all other characters has non-significant correlation. Number of flowering branches were found with highly positive significant correlation with the characters number of flowers per plant (1.09), seed weight (0.44) and days for 50 % flower senescence (0.46). Single flower weight has positive significant correlation with inflorescence length (0.34). Number of flowers per plant has positive significant correlation with seed weight (0.43), days

for 50 % flower senescence (0.41). Similar studies have been conducted in flower crops such as carnation for flower yield between ten vegetative, eight qualitative and four flowering traits for eight genotypes which has influence for the better selection of the trait with relation to yield of the crop (21). In the current study, selection based on leaf length and seed weight will contribute for increased weight of flowers which was supported by the previous work done in the crop *Celosia*, where the selection is based on the fruit length at maturity was recommended to favour the increase in leaf biomass (22). Similar work done in China aster for flower yield per plant with other characters of the crop such as number of leaves, number of secondary branches per plant and plant spread which influences the flower yield per plant. Hence the selection based on these characters will promote the yield which also validates the outcome of current study (23).

The flower yield in *Celosia* showed good positive relationship with vegetative character such as leaf length and one of the flowering parameters, seed weight. This may have resulted in the major contribution for the required yield of the plant (Weight of flowers per plant) and other flower parameters such as inflorescence length, flower diameter, flower length etc. Hence, the selection of above stable characters will help for improving the yield. These qualities ought to be prioritized when choosing *Celosia* for crop improvement. The ultimate objective of a breeding program is to select desired genotypes from a genetically heterogeneous pool of germplasm. A complex quantitative characteristic that depends on the interactions of growth conditions is plant production. Breeders may find it difficult to select the best combination because correlation analysis can only estimate the link between factors. Because correlation analysis is incapable of demonstrating cause and effect, it merely assesses the direction and intensity

of connections between components, which may make it difficult for breeders to choose the optimal combination. Breeders' capacity to make precise selections for the best possible trait improvement is also limited by correlation analysis's ability to identify intricate interactions like gene-environment interactions and epistasis. However, path coefficient analysis evaluates the significance of yield-attributing variables by breaking down the genotypic connection into direct and indirect effects. In order to determine the precise contribution of each characteristic to plant production, a path coefficient analysis was carried out (24).

Path Coefficient analysis

To determine the relative contribution of each parameter under study with the weight of flowers per plant based on calculated indirect and direct impacts, path coefficient analysis was performed (Table 5. Fig. 5). Yield is a complex and polygenic trait, direct selection for yield may not be a dependable strategy because to its strong environmental influence. Finding the component characters is therefore crucial to determine the yield enhancement. Path analysis is hence a crucial technique for separating the correlation coefficients into the direct and indirect impacts of the independent and dependent variables. As a result, correlations and path analysis together would provide a deeper understanding of the connections that exist between various character combination (25).

Direct effect on yield

The characters that had shown direct positive effect on yield of the plant were plant height (0.8132), leaf length (0.7602), plant spread (E-W) (0.4820), stem girth (0.1969), days for 50 % flowering (0.4752), single flower weight (0.0556), inflorescence length (1.1612), number of flowers per plant

Table 5. Path coefficient analysis showing direct (diagonal) and indirect effects of different quantitative traits on weight of flowers/plant

Traits	PH	LL	LB	PS (N-S)	PS(E-W)	SG	NOL	NOB	DFF	DF50%F	NOFB	SFW	IL	FL	FW	NOF/P	DF50%S	SDW	WOF/P
PH	1**	-0.22	0.51**	0.38*	0.38*	0.14	0.29	0.32	0.30	0.31	0.37*	0.05	0.06	0.12	0.27	0.38*	0.36*	0.38*	0.31
LL		1**	0.40*	0.00	0.00	0.18	-0.23	-0.20	-0.30	-0.22	-0.17	0.10	0.41*	0.64**	-0.09	-0.14	-0.10	-0.00	0.34*
LB			1**	0.75**	0.76**	0.53**	0.21	0.21	0.25	0.12	0.34*	0.07	0.23	0.36*	-0.10	0.35*	0.24	0.17	0.27
PS(N-S)				1**	1.01**	0.49**	0.45**	0.55**	0.25	0.33	0.59**	0.05	0.08	0.09	0.02	0.58**	0.36*	0.12	0.02
PS(E-W)					1**	0.48**	0.47**	0.55**	0.26	0.33*	0.60**	0.05	0.06	0.08	0.00	0.58**	0.38*	0.14	0.01
SG						1**	0.47**	0.55**	0.26	0.33*	0.60**	0.05	0.06	0.08	0.00	0.58**	0.38*	0.14	0.01
NOL							1**	0.79**	0.07	0.05	0.79**	0.49**	0.25	0.05	0.34*	0.75**	0.27	0.39*	0.07
NOB								1**	0.18	0.09	1.11**	0.24	0.02	-0.07	0.26	1.02**	0.39*	0.41*	0.03
DFF									1**	0.98**	0.14	-0.03	-0.26	-0.16	-0.39*	0.15	0.07	0.07	-0.13
DF50%F										1**	0.17	0.03	-0.36*	-0.24	-0.22	0.09	0.05	0.14	-0.08
NOFB											1**	0.24	0.04	-0.04	0.30	1.09**	0.46**	0.44**	0.10
SFW												1**	0.34*	0.21	0.14	0.27	-0.03	0.28	0.30
IL													1**	0.89**	0.32	0.12	-0.17	-0.07	0.12
FL														1**	0.16	0.00	-0.13	-0.13	0.10
FW															1**	0.30	0.07	0.00	-0.06
NOF/P																1**	0.41*	0.43**	0.11
DF50%S																	1**	0.30	0.11
SDW																		1**	0.81**
WOF/P																			1**

*significant at $p=0.05$, **significant at $p=0.01$ (*Traits: PH= Plant height, LL=Leaf length, LB= Leaf breadth, PS(N-S)= Plant spread at N-S, PS(E-W)=Plant spread at E-W, SG=Stem girth, NOL=Number of leaves, NOB= Total number of branches, DFF=Days for first flowering, DF50%F=Days for 50% flowering, NOFB= Number of flowering branches, SFW= Single flower weight, IL=Inflorescence length, FL=Flower length, FW= Flower width, NOF/P= Number of flowers per plant, DF50% S=Days for 50%flower senescence, SDW= Seed weight, WOF/P= Weight of flowers per plant)

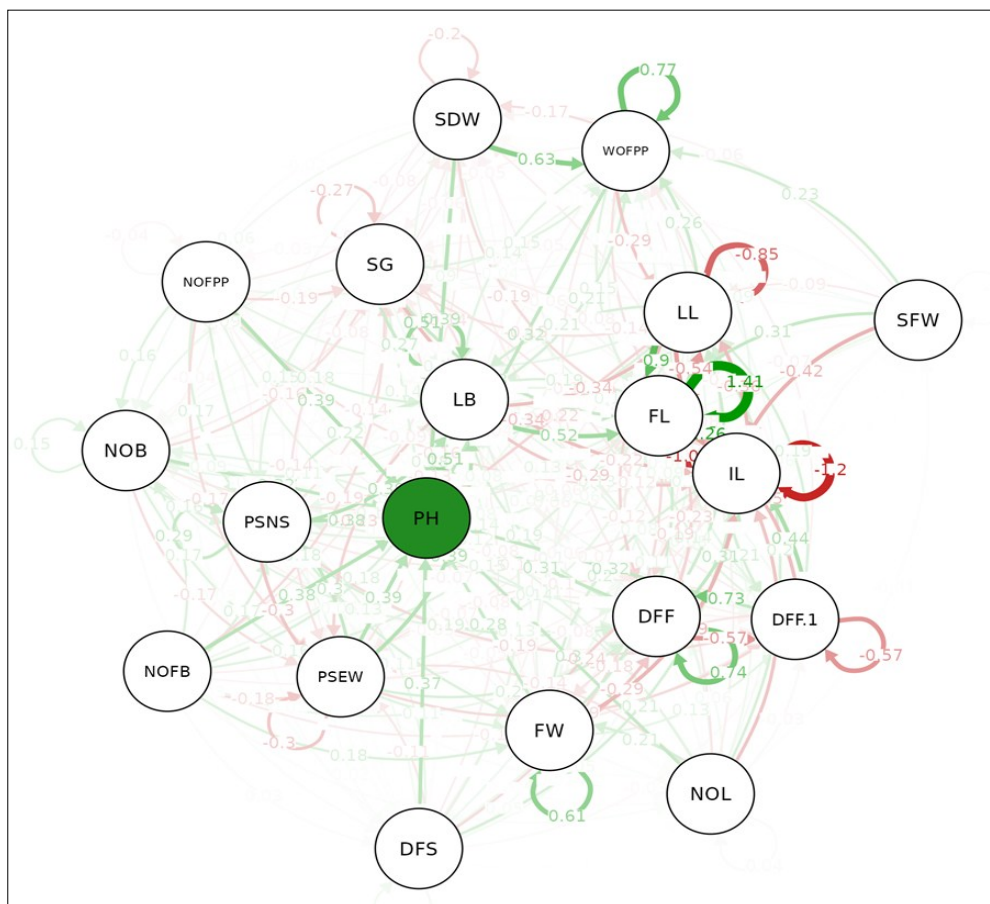


Fig. 5. Genotypic path diagram for 19 traits of *Celosia* accessions.

(*Traits: PH= Plant height, LL=Leaf length, LB= Leaf breadth, PS(N-S)= Plant spread at N-S, PS(E-W)=Plant spread at E-W, SG=Stem girth, NOL=Number of leaves, NOB= Total number of branches, DFF=Days for first flowering, DF50%F=Days for 50% flowering, NOFB= Number of flowering branches, SFW= Single flower weight, IL=Inflorescence length, FL=Flower length, FW= Flower width, NOF/P= Number of flowers per plant, DF50%S=Days for 50%flower senescence, SDW= Seed weight, WOF/P= Weight of flowers per plant).

(0.0848) and seed weight (0.5080). The findings were related for certain characters like plant height, number of flowers per plant for China aster (24) which showed the direct positive effect towards yield of the crop. In this study, the direct negative effect on flower yield was contributed by leaf breadth (-0.3263), plant spread (N-S) (-0.4927), number of leaves (-0.1445), total number of branches (-0.1645), days for first flowering (-0.6532), number of flowering branches (-0.0435), flower length (-1.3054), flower width (-0.5023), days for 50% flower senescence (-0.0612).

The selection based on the characters which had direct negative effect will have an adverse effect on the flower yield of *Celosia* and direct positive effect will have positive effect for the yield improvement of *Celosia*. Path analysis improves the accuracy of selecting features for better *Celosia* cultivars by revealing insight into the mechanisms by which traits affect yield. Similar work in Hibiscus reported that the days taken for first flowering, petal length, petal width and days taken for bud initiation showed direct negative effect on flower yield of Hibiscus having adverse effect on yield which also supports the current study (26). Another work done in gerbera concluded that the flowering traits like days required to first-flower opening, flower stalk length, number of ray florets and stalk diameter showed positive direct effect and positive significant correlation with flower yield per plant while flower diameter, days to 50 % flowering and dry weight of flower exhibited negative impact and significant correlation with number of flowers per plant.

Indirect effect on yield

Plant height exhibited high order of positive indirect effect on flower weight per plant (yield) via seed weight (0.1980), days for 50 % flowering (0.1513) and plant spread (E-W) (0.1861). In contrast, maximum and minimum negative indirect effect were extended by the characters like flower width (-0.1405) and days for first flowering (-0.2020). Leaf length had the higher positive indirect effect on yield through inflorescence length (0.4863) and the maximum and minimum negative indirect effect on the characters days for 50 % flowering (-0.1056) and flower length (-0.8378). Leaf breadth contributed for higher positive indirect effect on yield via plant height (0.4172) whereas maximum and minimum negative indirect effect by days for first flowering (0.1648) and flower length (-0.4778). Plant spread (N-S) showed the higher positive indirect effect on yield through plant height (0.3107) and the maximum and minimum negative indirect effect by flower length (-0.1266) and leaf breadth (-0.2471). Plant spread (E-W) contributed the high order of positive indirect effect on flower yield via plant height (0.3141) and the maximum and minimum negative indirect effect through days for first flowering (-0.1732) and plant spread (N-S) (-0.4983). Stem girth contributed for higher positive indirect effect on yield through inflorescence length (0.3306) and the maximum and minimum negative indirect effect by leaf breadth (-0.1738) and flower length (-0.2734). Number of leaves had the higher positive indirect effect on flower yield via inflorescence length (0.2964) and the maximum and

minimum negative indirect effect by flower width (-0.1728) and plant spread (N-S) (-0.2260). The total number of branches exhibited the high order of positive indirect effect on yield through plant spread (E-W) (0.2699) and the maximum and minimum negative indirect effect via number of leaves (-0.1144) and plant spread (N-S) (-0.2743). The parameter days for first flowering contributed for higher positive indirect effect on yield of the plant through days for 50% flowering (0.4697) and the maximum and minimum negative indirect effect through plant spread (N-S) (-0.1263) and inflorescence length (-0.3025). The parameter days for 50 % flowering exhibited the high order positive indirect effect on yield via flower length (0.3228) and the maximum and minimum negative indirect effect via plant spread (N-S) (-0.1641) and inflorescence length (-0.4263).

The number of flowering branches had the higher positive indirect effect on yield through plant height (0.3089) and the maximum and minimum negative indirect effect via leaf breadth (-0.1141) and plant spread (N-S) (-0.2921). The single flower weight bestowed the high order positive indirect effect on yield through inflorescence length (0.4026) and the lower negative indirect effect via flower length (-0.2854) where others are negligible for comparison. The inflorescence length rendered the high order positive indirect effect on yield via leaf length (0.3183) and maximum negative indirect effect on flower width (-0.1509). The flower length had the high order positive indirect effect on yield through leaf length (0.4879) and the maximum negative indirect effect via days for 50 % flowering (-0.1175). The flower width exhibited the higher positive indirect effect on yield through inflorescence length (0.3760) and the maximum and minimum negative indirect effect via days for 50 % flowering (-0.1067) and flower length (-0.2159). The number of flowers per plant rendered the higher positive indirect effect on yield via plant height (0.3141) and the maximum and minimum negative indirect effect through days for first flowering (-0.1040) and plant spread (N-S) (-0.2881). The parameter days for 50 % flower senescence showed the higher positive indirect effect on yield through plant height (0.2973) and the maximum and minimum negative indirect effect via plant spread (N-S) (-0.1783) and inflorescence length (-0.2023). Seed weight had the high positive indirect effect on yield through plant height (0.3169) and the negative indirect effect estimates were negligible for the study.

According to the path analysis results, plant height has a major impact on flower weight per plant (yield), mostly through positive indirect effects on plant spread (E-W), seed weight and days to 50 % flowering. Since these characteristics act as critical bridges, increasing plant height may result in higher yield by augmenting these crucial factors. Flower width and days to initial blooming, on the other hand, have detrimental indirect impacts, suggesting that reducing their impact could further maximize yield results. For breeding endeavours, to increase overall flower production, this research emphasizes the significance of selecting for plant height and its related positive contributors while reducing the impact of traits with detrimental indirect impacts. Similar to the current study, some of other researchers have studied the path analysis on various crops like China aster (23) where

they discussed that maximum indirect negative effect of test weight estimate was via number of flowers per plant to the yield of the crop, so the selection of the trait with test weight should be made crucial. Another work in *Rosa* spp. (27) also reported about the character association, direct and indirect effect estimates of the traits which determine the effectiveness on yield where floral diameter is crucial trait since it influences flower and petal fresh weight favourably, supporting the intuitive comprehension of larger blooms carrying more weight.

The estimated residual effect for the path analysis with 19 characters was 0.0369. The lower residual effect indicated that the characters chosen for path analysis were adequate and appropriate. Within the scope of path analysis conducted in the current study, it is therefore, suggested that the characters such as inflorescence length, plant height, leaf length are the leading main components of flower yield which shall be given high priority in the selection programme.

Conclusion

Genetic diversity and the inheritance of desirable traits are fundamental to the success of crop breeding programs. In this experiment, high heritability and high genetic advance as per cent over mean was recorded for the traits viz, plant height, plant spread (N-S), plant spread (E-W), number of leaves and flower length. High genetic advancement as a percentage over mean and high heritability suggest that additive gene components predominate. Therefore, there is a lot of possibilities to enhance these characters through direct selection. From the correlation studies it is concluded that selection should be made on the basis of higher average leaf length and seed weight to bring desired improvement in the yield of *Celosia* accessions. The path coefficient analysis concluded that direct selection for yield improvement in *Celosia* accessions can be performed using the characters such as plant height, leaf length, plant spread (E-W), stem girth, days for 50 % flowering, single flower weight, inflorescence length, number of flowers per plant and seed weight. To improve breeding efficiency, future studies should combine contemporary genomic and computational techniques with genetic factors, correlation and path analysis. The identification of genes influencing complex traits can be facilitated by genome-wide association studies (GWAS) and genomic selection (GS), which enable more accurate selection than is possible with traditional correlation estimations. In order to comprehend genotype-environment interactions and guarantee trait stability under various climatic situations, it is imperative to expand multi-environment trials. Integrating molecular markers with traditional selection methods will enhance breeding strategies for climate resilience and productivity.

Acknowledgements

This article forms the part of Ph.D thesis of the first author of Department of Floriculture & Landscape architecture submitted to Tamil Nadu Agricultural University, Coimbatore and the work was supported by all the co-authors.

Authors' contributions

RP carried out writing original draft, formal analysis, editing. KRR had done investigation, visualisation, supervision. AB helped in review and editing. MM contributed for formal analysis and data curation. KV had participated in performing validation, reviewing. SR helped for formal analysis and reviewing.

Compliance with ethical standards

Conflict of interest: The authors disclose that none of their personal ties or known conflicting financial interests might have appeared to have influenced the work described in this study.

Ethical issues: None

References

- Woo K, Ko J, Song S, Lee J, Kang J, Seo M. Antioxidant compounds and antioxidant activities of the methanolic extracts from Cockscomb (*Celosia cristata* L.) flowers. *Planta Med.* 2011;77(12):PM78. <https://doi.org/10.1055/s-0031-1282836>
- Surse S, Shrivastava B, Sharma P, Sharma J, Gide P. Pharmacognostic standardisation of whole plant of *Celosia argentea* var. *cristata* (L.). *Int J Pharm Res Scholars.* 2014;3(3):387-92.
- Rubini D, Sudhakar D, Anandaragopal K. Phytochemical investigation and anthelmintic activity of *Celosia cristata* leaf extract. *Int Res J Pharm.* 2012;3(5):3353-6.
- Wang Y, Lou Z, Wu QB, Guo ML. A novel hepatoprotective saponin from *Celosia cristata* L. *Fitoterapia.* 2010;81(8):1246-52. <https://doi.org/10.1016/j.fitote.2010.08.011>
- De Bao WDG, Jie X, Qin W. The nutritional components of *Celosia cristata* L cv Plumosa. *J Plant Resour. Environ.* 1994;3(3):32-5.
- Gholizadeh A, Kapoor H. Modifications in the purification protocol of *Celosia cristata* antiviral proteins lead to protein that can be N-terminally sequenced. *Protein Pept. Lett.* 2004;11(6):551-61. <https://doi.org/10.2174/0929866043406210>
- Oyetunde OA, Olayiwola MO, Osho BT. Genetic diversity and trait profiles of some amaranthus genotypes. *Adv Hort Sci.* 2021;35(3):277-84. <https://doi.org/10.36253/ahsc-10523>
- Saikia J, Shadeque A, Bora G. Genetic studies in cucumber. 2. Heritability and genetic advance of yield components. *Haryana J Hort Sci.* 1995;24:73-76. <https://www.cabidigitallibrary.org/doi/full/10.5555/19971601163>
- Burton GW. Quantitative inheritance in grasses. *Proceedings of 6th International Grassland Congress; 1952 17-23; August Pennsylvania State College.* 1: 277-283.
- Lush JL. Intra-sire correlations or regressions of offspring on dam as a method of estimating heritability of characteristics. *J Anim Sci.* 1940;1:293-301. <https://doi.org/10.2527/jas1940.19401293x>
- Johnson HW, Robinson HF, Comstock RE. Estimates of genetic and environmental variability in soybeans. *Agron J.* 1955;47:314-18. <http://doi.org/10.2134/agronj1955.00021962004700070009x>
- Dewey DR, Lu K. A correlation and path-coefficient analysis of components of crested wheatgrass seed production. *Agron J.* 1959;51(9):515-18. <https://doi.org/10.2134/agronj1959.00021962005100090002x>
- Kumar S, Kumar M, Singh MK, Kumar S, Kumar S. Variability study in chrysanthemum (*Dendranthema grandiflora* Tzvelev). *Progr. Agric.* 2015;47(2):271-74. <https://doi.org/10.5958/2249-5258.2015.00049.4>
- Rajib Roychowdhury RR, Jagatpati Tah JT. Evaluation of genetic parameters for agro-metrical characters in carnation genotypes. *Afr Crop Sci J.* 2011;19:183-88.
- Hallauer AR, Carena MJ, Miranda Filho JD. Quantitative genetics in maize breeding. Springer Science & Business Media[e-book]. Springer New York, NY. 2010. <https://doi.org/10.1007/978-1-4419-0766-0>
- Oyetunde OA, Otusanya GO, Lawal IT, Oduntan AO, Olalekan OJ. Genetic diversity, discriminant and trait association analyses of accessions. *Acta Hort. Regiotecturae.* 2022;25(2):189-96. <https://doi.org/10.2478/ahr-2022-0023>
- Singh KP, Raju D, Prasad K, Bharadwaj C. Studies on genetic variability, heritability and genetic advance in French marigold (*Tagetes patula*) genotypes. *J Ornament Hort.* 2009;12(1):30-4.
- Patel M, Chawla S, Chavan S, Shah H, Patil SD. Genetic variability, heritability and genetic advance studies in marigold (*Tagetes spp.*) under the South Gujarat region. *Electron J Plant Breed.* 2019;10(1):272-76.
- Panwar S, Singh KP, Namita N. Assessment of variability, heritable components and grouping of Indian rose. *Indian J Agric Sci.* 2012;82(10):875-80. <https://doi.org/10.56093/ijas.v82i10.24180>
- Rashmi R, Chandrashekar S. Evaluation of genetic variability, heritability and genetic advances in gladiolus (*Gladiolus hybridus* L.) genotypes. *The Bioscan.* 2016;11(3):1829-32.
- Naik BH. Correlation studies in carnation (*Dianthus caryophyllus* L.). *Journal of Horticultural Sciences.* 2014;9(1):38-42. <https://doi.org/10.24154/jhs.v9i1.216>
- Olawuyi O, Bamigbegbin B, Bello O. Genetic variation of morphological and yield characters of *Celosia argentea* L. germplasm. *J Basic Appl Sci Int.* 2016;13:160-69.
- Naikwad D, Kandpal K, Patil M, Hugar A, Kulkarni V. Correlation and path analysis in China aster [*Callistephus chinensis* (L.) Nees]. *Int J Curr Microbiol Appl Sci.* 2018;7(2):3353-62. <https://doi.org/10.20546/ijcmas.2018.702.401>
- Zafar SA, Aslam M, Khan H, Sarwar S, Rehman RS, Hassan M et al. Estimation of genetic divergence and character association studies in local and exotic diversity panels of soybean (*Glycine max* L.) genotypes. *Phyton.* 2023;92(6). <https://doi.org/10.32604/phyton.2023.027679>
- Kumar S, Kumar R, Gupta R, Sephia R. Studies on correlation and path-coefficient analysis for yield and its contributing traits in cucumber. *Crop improv.* 2011;38(1):18-23.
- Krishna H, Taj A. Genetic variability, Correlation and Path analysis studies in thirty *Hibiscus rosa-sinensis* L. Genotypes for yield and its attributes. *Agron J.* 2022; 47:314-18.
- Visalakshi M, Muthulakshmi R, Ganga M, Thamaraiselvi SP, Ganesh S, Vasanth S. Studies on correlation analysis, path analysis and genetic diversity in Rosa (*Rosa spp.*). *Plant Sci Today.* 2024;11(3). <https://doi.org/10.14719/pst.4017>