



## Interaction studies through character association, divergence and coefficient of variation in chrysanthemum (*Chrysanthemum morifolium*)

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### ABSTRACT

*Chrysanthemum morifolium* (Ramat.) holds one of the most pertinent constituents of global floriculture market. The study was carried out during 2021–22 and 2022–23 at Punjab Agricultural University, Ludhiana, Punjab to categorise diverse chrysanthemum genotypes based on their response groups, morphological variability and their selection for breeding new genotypes. The present investigations comprehensively assessed the morphological parameters of 20 chrysanthemum genotypes collected from leading Indian research institutes across cut, loose and pot genotypes. Coefficient of variance, heritability, genetic advance and path coefficient analysis were done. Analysis of variance revealed significant responses in different morphological, floral and reproductive traits. A high coefficient of variation (>20%), heritability and genetic advance were revealed in flower number/plant (FN), number of ray florets, thickness of ray florets, plant height, days to 50% flowering accounting a significant genetic control. Plant height showed maximum positive correlations with most of traits. High heritability with regard to flower number, ray florets, days to flower opening, plant height and spread except for primary branches. The high value of genetic advance was recorded for traits; number of ray florets and flower number demonstrating that after choosing the top 5% high yielding genotypes as parents, the traits in a new generation can increase significantly. Path coefficient attributed nine traits as positive and seven traits as negative with direct effects on number of flowers/plant. The findings highlighted the importance of integrated trait selection strategies to develop high-performing chrysanthemum cultivars with enhanced ornamental value and adaptability to diverse growing conditions.

**Keywords:** Chrysanthemum, Coefficient of variation, Genetic diversity, Response groups

*Chrysanthemum morifolium* (Ramat.), a herbaceous plant belonging to the family Asteraceae, is native to the northern hemisphere primarily Asia and Europe (Zhao *et al.* 2010). It possesses diverse ploidy levels ( $2n = 2x = 18$  to  $90$ ), cultivated species being hexaploids ( $2n = 6x = 54$ ,  $n=9$ ), and a complex history of about 200 species (Liu *et al.* 2012, Wang *et al.* 2014a, Wang *et al.* 2014b, Mekapogu *et al.* 2022). This flower is recognised as ‘Queen of the East’ or ‘Autumn Queen’, ranking second as spray and seventh as standard type and contributing a share of 0.0041% (Eisa *et al.* 2022, Mekapogu *et al.* 2023). India has a total export of 18.29 MT of chrysanthemum flowers accounting for 60.91 lakhs/ 6 million globally (Anonymous 2022–23). Chrysanthemum is a popular crop due to its diverse growth habits, flower colours, sizes, shapes, post-harvest quality, and uses (Mohit and Bala 2024). Effective breeding requires knowledge of trait variability and types to achieve targeted objectives through genetic diversity analysis (Kaur *et al.* 2016). Genetic variability is influenced by factors such as

genetic background, breeding history, and geographic origin (Liu *et al.* 2020). Broad-sense heritability (H) estimates heritable genetic variance, while genotypic (GCV) and phenotypic (PCV) coefficients of variation help to assess the extent of variability (Kadium *et al.* 2023, Rasheed *et al.* 2023). Character association analysis ascertains the direct and indirect impacts of morphological, physiological and agronomic trait on the flower production and quality. This involves the correlation, path coefficient and regression analysis to evaluate trait associations. Considerably, key traits like flower diameter, stem length, number of branches and days to flowering are the traits of multiple interacting with one another, including the governance of multiple genes making improvements. Thus, understanding effect of key traits, helps breeders to prioritize traits for selection to develop market acceptable cultivars (Zhang *et al.* 2021). Considering these aspects, the present study aimed to assess the extent of variability among 20 chrysanthemum genotypes that was achieved through correlation, path coefficient, and genetic diversity analysis.

### MATERIALS AND METHODS

The study was carried out during 2021–22 and 2022–23

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at Punjab Agricultural University, Ludhiana (30°54' N, 75°48' E; at an elevation of 248 m amsl), Punjab. The research trial area maintains a large number of accessions of chrysanthemum and is located in the North-Western Plain Zone of India. The maximum temperature went up to 25°C during July–November and the minimum temperature recorded was 15°C during nights with rainfall of 600–700 mm per annum during the two growing years. The soil type of this experimental area was sandy soil. A completely randomized design (CRD) was followed to place the earthen pots in three replications (n=3), each having five pots with three rooted cuttings per pot. Twenty diverse chrysanthemum genotypes having commercial significance were selected for morphological characterisation (Fig. 1). The selection was based on their demand for various purposes and hence, the grouping of all 20 genotypes was made into cut, loose and pot culture. The selected varieties were evaluated for various growth and flowering parameters and the genetic analysis comprising of coefficients of variability, genotypic and phenotypic correlation and path analysis was performed on the traits to observe their suitability, heritability and genetic advancement.

The recorded data on various parameters was arranged and analysed for ANOVA by employing the statistical design CRD in R-software (Version 4.2.2) (Gopinath *et al.* 2020) and grouping was done according to Tukey's test ( $p \leq 0.05$ ) using Minitab software (Version 16). Variance in quantitative traits (phenotypic, genotypic and environmental variances) and their respective coefficient of variance were calculated using the formula (Burton and De Vane 1953) to estimate heritability. The percent genotypic coefficient of variance (GCV), phenotypic coefficient of variance (PCV) and environmental co-efficient of variance (ECV) were calculated as per Burton (1952) and heritability was

calculated as per the formula given by Weber and Moorty (1952). Genetic advance expected from selecting 5% of superior progeny was calculated as per Johnson *et al.* (1955). The variability was partitioned into replications, genotypes and error (Al-Jibouri *et al.* 1958). The significance of genotypic and phenotypic coefficients of correlation were matched to table "t" values at (n-2) degrees of freedom, as suggested by Fisher and Yates (1963) where 'n' specifies the number of genotypes.

## RESULTS AND DISCUSSION

**Genetic variability, phenotypic and genotypic coefficient of variation for different traits:** Twenty commercial genotypes with variable attributes were tested against variability (Table 1, Fig. 2). The phenotypic variance (PV) ranged from 0.01 (thickness of ray florets, TRF) to 14107.52 (number of ray florets, NR) and the genotypic variance (GV) varied from 0.01 (TRF) to 13948.07 (NR). A high degree of PCV and GCV were estimated for Number of ray florets (NR) (83.26 and 82.79) followed by the Flower number (FN) (80.02 and 79.64), TRF (45.52 and 42.28), Plant height (PH) (37.21 and 35.37), Stem girth (SG) (33.93 and 31.77), Flowering diameter (DF) (cm) (32.34 and 30.41), Primary branches (PB) (29.61 and 20.11), Internodal length (INTR) (27.00 and 22.06) and Bud diameter (BD) (22.72 and 21.72). Further, ECV% varied from 2.20 (days to fifty percent flowering, D50)–21.73 (PB). PCV, GCV and ECV were estimated and categorised as low (<10%), moderate (10–20%) and high (>20%) (Subramaniam and Menon 1973).

From Table 1, moderate degrees of FD (17.09 and 14.66), PS (14.57 and 12.90) and D50 (11.53 and 11.32) were observed. The ECV was reported as high for PB (21.73) and medium for TRF (16.74), INTR (15.57), SG (6.76), PH (11.57), DF (11.00), while low for NR (8.85), FD (8.79),

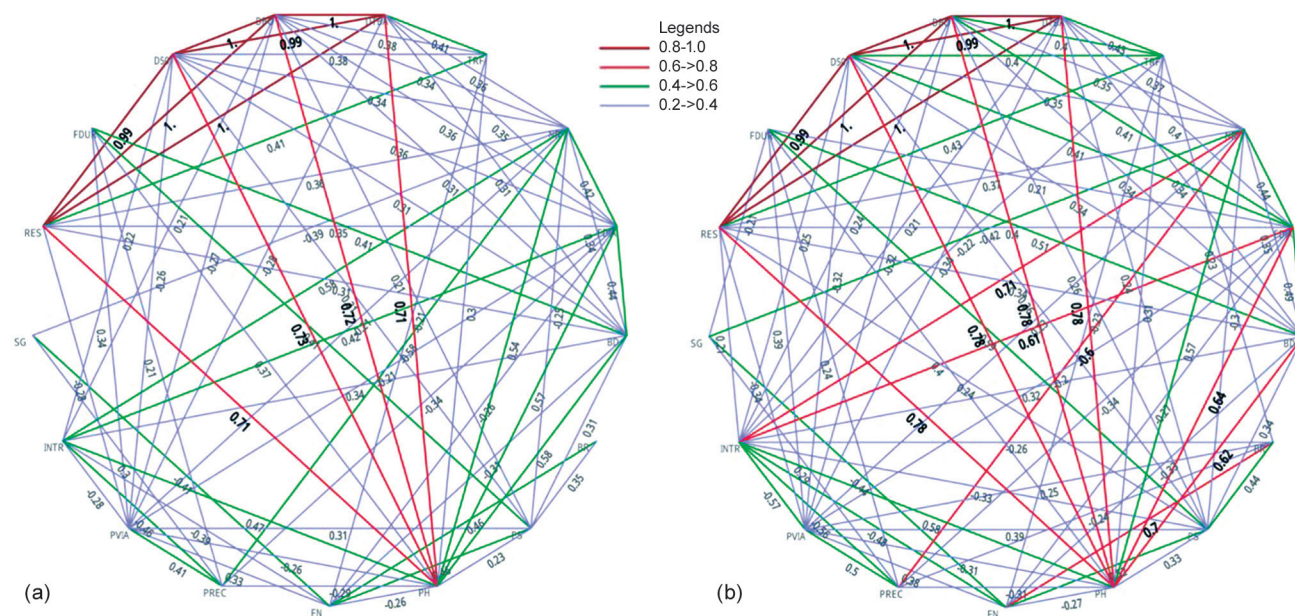


Fig. 1 (a) Phenotypic and (b) Genotypic correlations between flower number/plant (FN) and other morphological and flowering traits. The dark red line denotes for  $R^2=0.8-1.0$ ; red line denotes for  $0.6-0.8$ ; green line denotes for  $0.4-0.6$  and blue line denotes for  $0.2-0.4$ .

Table 1 Estimates of genetic variability and descriptive statistics of various vegetative and flowering traits of chrysanthemum

Trait	Mean	Range	Mean sum of squares		Variance			Coefficient of variation			(h <sub>b</sub> <sup>2</sup> ) %	GA	GAM %
			Genotypes (degrees of freedom=19)	Error (degrees of freedom=38)	GV	PV	EV	GCV (%)	PCV (%)	ECV (%)			
PH	37.47	10.00-65.00	546.12 ***	18.81	175.76	194.57	18.80	35.37	37.21	11.57	90.00	25.95	69.25
PB	6.20	2.45-10.00	6.49	1.82	1.55	3.37	1.82	20.11	29.61	21.73	46.12	1.74	28.13
SG	3.98	1.90-8.47	5.04	0.22	1.60	1.83	0.22	31.77	33.93	11.90	87.70	2.44	61.30
PS	28.49	20.00-44.01	44.28***	3.71	13.52	17.23	3.71	12.90	14.57	6.76	78.46	6.70	23.54
INTR	2.40	1.20-3.60	0.98***	0.14	0.28	0.42	0.14	22.06	27.00	15.57	66.76	0.89	37.13
DTBA	88.80	65.00-117.00	386.26	6.51	126.58	133.09	6.51	12.66	12.99	2.87	95.11	22.60	25.45
DBO	107.75	82.00-139.00	475.71 ***	6.51	156.40	162.91	6.51	11.60	11.84	2.36	96.00	25.24	23.42
D50	115.50	89.00-148.00	519.49 ***	6.51	170.99	177.50	6.51	11.32	11.53	2.20	96.33	26.43	22.89
BD	8.58	5.28-12.81	10.77***	0.32	3.48	3.80	0.32	21.72	22.72	6.67	91.38	3.67	42.78
DF	5.09	2.00-9.32	7.51***	0.31	2.39	2.71	0.31	30.41	32.34	11.00	88.42	3.00	58.92
NR	142.65	10.00-438.00	42004***	159	13948.07	14107.52	159.44	82.79	83.26	8.85	98.87	241.91	169.58
TRF	0.30	0.80-0.10	0.05***	0.00	0.01	0.01	0.00	42.28	45.52	16.74	86.29	0.24	80.91
FD	28.65	19.87-40.00	59.28***	6.34	17.64	23.99	6.34	14.66	17.09	8.79	73.55	7.42	25.90
FN	78.85	20.00-304.99	11869.10 ***	37.50	3943.86	3981.36	37.50	79.64	80.02	7.76	99.06	128.75	163.29

\*\*\* Significance at 0.001% level of significance; \* Significance at 5% level; \*\*Significance at 1% level. Diagonal values signify direct effects; Rest values signify indirect effects; Residual effect at genotypic level= SQRT (1- 1.0818) and at phenotypic level= 0.4771. GV, Genotypic variance; PV, Phenotypic variance; EV, Environmental variance; GCV, Genotypic co-efficient of variance; PCV, Phenotypic co-efficient of variance; ECV, Environmental co-efficient of variance; (h<sub>b</sub><sup>2</sup>) %, Heritability; GA, Genetic advance; GAM%, Genetic advance as mean (%); PH, Plant height (cm); PB, Primary branches; SG, Stem girth (mm); PS, Plant spread (cm<sup>2</sup>); INTR, Internodal length (cm); DTBA, Days for bud appearance; DBO, Days taken for bud opening; D50, Days to 50% flowering; BD, Bud diameter (mm); DF, Diameter of flower (cm); NR, Number of ray florets; TRF, Thickness of ray floret (mm); FD, Flowering duration (days); FN, Flower number.

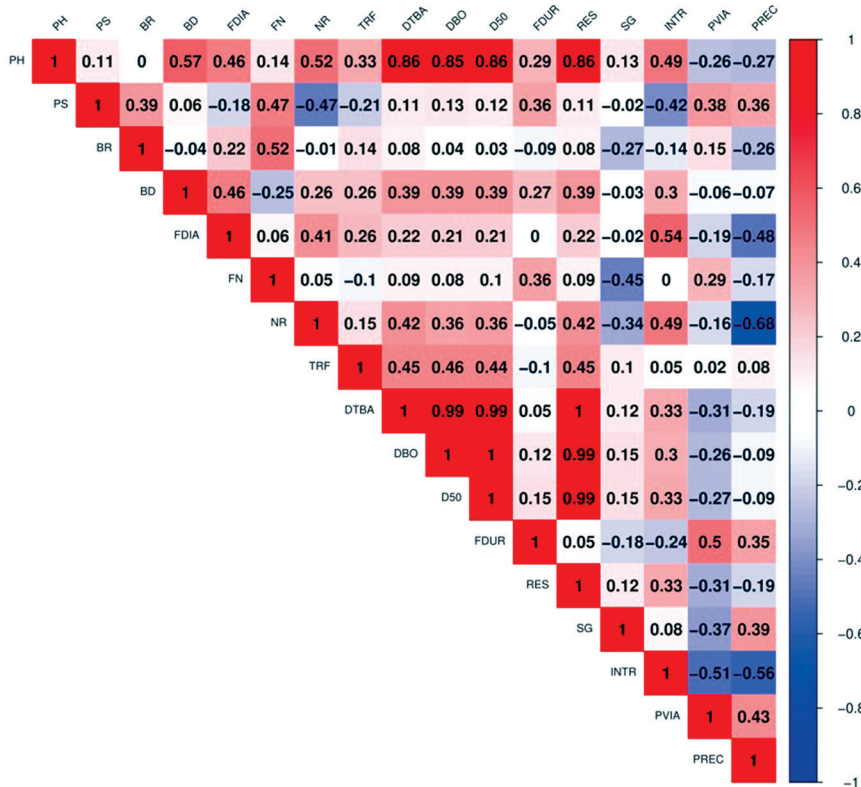


Fig. 2 A cumulative genotypic and phenotypic correlogram for 17 horticultural attributes recorded in the study.

The colour bar represents the gradation from red to blue with red denoting highest R<sup>2</sup> values while blue denoting lowest R<sup>2</sup> values; PH, Plant height (cm); PS, Plant spread (cm<sup>2</sup>); BR, Number of primary branches; BD, Bud diameter (mm); FDIA, Flower diameter(mm); FN, Number of flowers/plant; NR, Number of ray florets/flower; TRF, Thickness of ray florets (mm); DTBA, Days to bud appearance; DBO, Days to bud opening; D50, Days to fifty percent flowering; FDUR, Flower duration (days); RES, Response behaviour (weeks); SG, Stem girth (mm); INTR, Internodal length (cm); PVIA, Pollen viability; PREC, Pollen receptivity

FN (7.76), PS (6.76), BD (6.67), and D50 (2.20), thereby, indicating that the genetic variability is due to genotype and negligible influence of environment on these traits. The percent heritability was estimated and characterized as low (<30%), moderate (30–60%) and high (>60%), as suggested by Robinson *et al.* (1949). The results revealed that all traits possessed a high heritability i.e. FN (99.06), NR (98.87), DTBA (95.11), D50 (96.33), DBO (96.00), BD (91.38), PH (90.00), DF (88.42), SG (87.70), PS (78.46), TRF (86.29), FD (73.55), except for primary branches (46.12). The genetic advance (GA) and genetic advance as a percent of the mean (GAM %) were estimated and characterized as low (<10%), moderate (10–20%) and high (>20%). The high value of GA was recorded for traits; NR (241.91) and FN (128.75) demonstrating that the average NR and FN in a new generation can increase significantly. Most of the traits showed a high GAM%, viz. FN (163.29%), NR (169.58%), TRF (80.91%), PH (69.25%), SG (61.30%), DF (58.92%), BD (42.78%), INTR (37.13%), PB (28.13%), FD (25.90%), DTBA (25.45%), PS (23.54%), DBO (23.42%) and D50 (22.89%).

The dataset suggested a broad range of GCV and PCV

values across different traits among chrysanthemums like FN, NR, TRF and PH accounting for a substantial genetic control. Hence, these traits are highly amenable to genetic improvement (Shim *et al.* 2016a, 2016b, Kim *et al.* 2024). In contrast, traits such as DBO and D50 showed lower GCV and PCV values, implying that such traits are less influenced by genetic factors and more by environmental conditions as reported by Shim *et al.* (2016a). The GCV and PCV values are in congruence with the similar findings of Kameswari *et al.* (2015), Telem *et al.* (2017), Henny *et al.* (2021), Bennurmath *et al.* (2022), Kumar *et al.* (2022) and Gurung *et al.* (2023) for PH, INTR, BD, FD, NR and NF. Considering SG, similar readings were obtained from the discoveries of Baskaran *et al.* (2009); while for PS and BR, Kumar *et al.* (2015) and Henny *et al.* (2021) gave complementary findings. Traits such as FN, NR, DBO, D50 and PH constantly exhibited high H. The high H in FN and NR indicated a phenotypic variation being contributed by genetic makeup and PH implied its historical importance in cut chrysanthemum breeding programmes (Zhang *et al.* 2023). In contrast to our findings, Kim *et al.* (2024) showed lowest heritability for number of flowers (NOF) (0.37). Genetic progress predicts that, after

one cycle of selection intensity, the genotypic value of the new population will improve relative to the base population (Singh 2001). NR, FN and PH with high GAM% of more than 20% have indicated additive gene effect. These findings were well established by Shrivani *et al.* (2024) and Gurung *et al.* (2023).

*Path co-efficient analysis at genotypic and phenotypic level:* Path coefficient analysis (Table 2) was conducted using FN as the dependent trait. The low residual effects at genotypic (1–1.0818) and phenotypic (0.4771) levels indicated that the traits selected were appropriate. At the genotypic level, DTBA (127.856) showed the highest positive direct effect, followed by DBO (16.833), PH (1.00), BR (0.904). Negative direct effects were observed for BD (-0.271) and INTR (-0.169), RES (-131.748), D50 (-13.297), FDIA (-0.539), TRF (-0.515), NR (-0.285), FD (-0.056), and PS (-0.02). At the phenotypic level, DTBA (33.348) again had the highest positive direct effect, followed by DBO (6.589), PH (0.502), SG (-0.497), BR (0.455), PS (0.317), BD (-0.313) and NR (0.028). Negative direct effects were found for SG (-0.497), BD (-0.313), RES (-36.043), D50 (-4.118), FDIA (-0.289), TRF (-0.277),

Table 2 Path coefficient analysis showing direct (diagonal) and indirect (of the diagonal) effects of different quantitative traits on flower yield (flower number/plant) of chrysanthemum

Trait	PH	PS	BR	BD	FDIA	NR	TRF	DTBA	DBO	D50	FD	RES	SG	INTR	Cr. w/s FN
PH	G 1.000	0.327	0.073	0.622	0.645	0.572	0.313	0.776	0.782	0.785	0.397	0.776	0.066	0.579	-0.274
P	0.502	0.116	-0.028	0.290	0.287	0.273	0.149	0.358	0.363	0.365	0.186	0.358	0.035	0.235	-0.261**
G	-0.007	-0.020	-0.009	-0.007	-0.003	0.006	0.000	-0.005	-0.005	-0.005	-0.012	-0.005	0.001	0.007	0.519
P	0.073	0.317	0.110	0.097	0.042	-0.080	-0.014	0.059	0.065	0.067	0.129	0.059	-0.011	-0.062	0.458
G	0.066	0.395	0.904	-0.016	0.177	0.005	0.206	0.091	0.100	0.111	-0.034	0.091	-0.152	-0.232	0.696**
P	-0.025	0.158	0.455	-0.004	0.068	0.003	0.071	0.050	0.052	0.055	0.017	0.050	-0.042	-0.058	0.464**
G	-0.169	-0.092	0.005	-0.271	-0.132	-0.095	-0.034	-0.091	-0.091	-0.091	-0.137	-0.091	0.002	-0.088	-0.327*
P	-0.181	-0.096	0.003	-0.313	-0.139	-0.107	-0.037	-0.096	-0.097	-0.097	-0.127	-0.096	0.002	-0.107	-0.311**
G	-0.348	-0.090	-0.106	-0.263	-0.539	-0.236	-0.044	-0.215	-0.219	-0.220	-0.112	-0.215	0.042	-0.326	-0.270*
P	-0.165	-0.038	-0.043	-0.128	-0.289	-0.121	-0.013	-0.101	-0.104	-0.105	-0.051	-0.102	0.010	-0.122	-0.261*
G	-0.163	0.085	-0.002	-0.100	-0.125	-0.285	-0.009	-0.106	-0.101	-0.100	-0.006	-0.106	0.120	-0.203	-0.163
P	0.015	-0.007	0.000	0.010	0.012	0.028	0.001	0.010	0.010	0.010	0.001	0.010	-0.011	0.016	-0.163*
G	-0.161	0.001	-0.117	-0.064	-0.042	-0.016	-0.515	-0.220	-0.208	-0.206	0.083	-0.220	-0.051	0.114	-0.229**
P	-0.082	0.012	-0.043	-0.033	-0.012	-0.009	-0.277	-0.113	-0.107	-0.106	0.042	-0.113	-0.023	0.035	-0.207
G	99.214	30.287	12.852	43.087	51.072	47.590	54.679	127.856	127.305	126.921	19.110	127.856	-7.700	27.269	-0.104*
P	23.825	6.189	3.690	10.265	11.715	12.009	13.559	33.348	33.203	33.099	3.977	33.348	-2.507	6.451	-0.104*
G	13.171	4.318	1.860	5.658	6.841	5.960	6.791	16.761	16.833	16.823	2.870	16.760	-0.427	4.045	-0.098*
P	4.772	1.354	0.747	2.037	2.378	2.268	2.534	6.560	6.589	6.585	0.910	6.560	-0.273	1.408	-0.099*
G	-10.436	-3.496	-1.627	-4.466	-5.421	-4.655	-5.321	-13.200	-13.289	-13.297	-2.354	-13.199	0.241	-3.290	-0.095*
P	-2.998	-0.873	-0.493	-1.275	-1.496	-1.404	-1.571	-4.087	-4.115	-4.118	-0.593	-4.087	0.141	-0.901	-0.096*
G	-0.022	-0.033	0.002	-0.029	-0.012	-0.001	0.009	-0.008	-0.010	-0.010	-0.056	-0.008	0.012	0.002	0.199
P	-0.048	-0.053	-0.005	-0.053	-0.023	-0.003	0.020	-0.015	-0.018	-0.019	-0.129	-0.016	0.016	0.013	0.169*
G	-102.252	-31.223	-13.207	-44.387	-52.628	-49.042	-56.320	-131.748	-131.178	-130.782	-19.688	-131.748	7.932	-28.125	-0.104
P	-25.752	-6.691	-3.986	-11.094	-12.665	-12.981	-14.644	-36.043	-35.885	-35.773	-4.307	-36.043	2.710	-6.971	-0.104
G	-0.040	0.042	0.102	0.005	0.047	0.254	-0.060	0.036	0.015	0.011	0.129	0.036	-0.603	-0.013	-0.445**
P	-0.035	0.017	0.046	0.003	0.017	0.192	-0.041	0.037	0.021	0.017	0.061	0.037	-0.497	-0.004	-0.411**
G	-0.098	0.056	0.044	-0.055	-0.103	-0.121	0.038	-0.036	-0.041	-0.042	0.006	-0.036	-0.004	-0.169	-0.483*
P	-0.124	0.052	0.034	-0.090	-0.112	-0.153	0.033	-0.051	-0.056	-0.058	0.026	-0.051	-0.002	-0.264	-0.394**

\* Significance at 5% level; \*\*Significance at 1% level; \*\*Significance at 0.1% level. Diagonal values signify direct effects; Rest values signify indirect effects; Residual effect at genotypic level =  $\sqrt{1 - 1.0818}$  and at phenotypic level = 0.4771; PH, Plant height (cm); PS, Plant spread (cm<sup>2</sup>); BR, Number of primary branches; BD, Bud diameter (mm); FDIA, Flower diameter (cm); NR, Number of ray florets; TRF, Thickness of ray floret (mm); DTBA, Days to bud appearance; DBO, Days to bud opening; D50, Days to 50% flowering; FD, Flowering duration; RES, Response; SG, Stem girth (mm); INTR, Internodal length; FN, Flower number.

Table 3 Estimation of genotypic (G) and phenotypic (P) correlation among various morphological attributes of chrysanthemum

TRAIT	PH	PS	BR	BD	FDJA	NR	TRF	DTBA	DBO	D50	FDUR	RES	SG	INTR	FN
PH	G	1.00**													
	P	1.00													
PS	G	0.33	1.00**												
	P	0.23	1.00												
BR	G	0.07	0.44	1.00**											
	P	-0.06	0.35**	1.00											
BD	G	0.62	0.34	-0.02	1.00**										
	P	0.58***	0.31*	-0.01	1.00										
FDJA	G	0.64*	0.17	0.20	0.49	1.00**									
	P	0.58***	0.13	0.15	0.44***	1.00									
NR	G	0.57**	-0.30	0.01	0.35	0.44	1.00**								
	P	0.55**	-0.25	0.01	0.34**	0.42***	1.00								
TRF	G	0.31*	0.00	0.23	0.12	0.08	0.03	1.00**							
	P	0.30*	-0.04	0.16	0.12	0.04	0.03	1.00							
DTBA	G	0.78**	0.24	0.10	0.34*	0.40*	0.37	0.43	1.00**						
	P	0.72***	0.19	0.11	0.31*	0.35**	0.36**	0.41**	1.00						
DBO	G	0.78**	0.26	0.11	0.34	0.41	0.35	0.40	1.00**	1.00**					
	P	0.73***	0.21	0.11	0.31*	0.37**	0.34**	0.39**	1.00***	1.00					
D50	G	0.78**	0.26	0.12	0.34	0.41	0.35	0.40	0.99**	1.00	1.00**				
	P	0.73***	0.21	0.12	0.31*	0.37**	0.34**	0.39**	1.00***	1.00***	1.00				
FD	G	0.40	0.59*	-0.04	0.51	0.21	0.02	-0.16	0.15	0.17	0.18	1.00**			
	P	0.38**	0.41**	0.04	0.47**	0.18	0.03	-0.15	0.12	0.14	0.14	1.00			
RES	G	0.78	0.24	0.10	0.34	0.40	0.37	0.43	1.00	1.00	0.99	1.00**			
	P	0.72***	0.19	0.11	0.31*	0.35**	0.36**	0.41**	1.00***	1.00***	1.00***	1.00			
SG	G	0.07**	-0.07	-0.17	-0.01	-0.08	-0.42**	0.10**	-0.06	-0.03	-0.21	-0.06	1.00**		
	P	0.07	-0.03	-0.09	-0.01	-0.03	-0.40**	0.08**	-0.08	-0.04	-0.12	-0.08	1.00		
INTR	G	0.58**	-0.33	-0.26	0.32	0.61	0.71	-0.22	0.21	0.24	0.25	0.21	0.02**	1.00**	
	P	0.50***	-0.20	-0.13	0.35**	0.42***	0.58***	-0.13	0.19	0.21	0.22	0.19	0.01**	1.00	
FN	G	-0.27	0.52	0.70**	-0.33	-0.27	-0.16*	-0.23	-0.10*	-0.10*	0.20*	-0.10	-0.44*	-0.48*	1.00**
	P	-0.26**	0.46	0.46**	-0.31	-0.26	-0.16**	-0.21	-0.10*	-0.10**	0.17*	-0.10	-0.41	-0.39	1.00

\* Significance at 5% level; \*\*Significance at 1% level; \*\*\*Significance at 0.1% level. Diagonal values signify direct effects; Rest values signify indirect effects; Residual effect at genotypic level= SQRT(1- 1.0818) and at phenotypic level= 0.4771; PH, Plant height (cm); PS, Plant spread (cm<sup>2</sup>); BR, Number of primary branches; BD, Bud diameter (mm); FDJA, Flower diameter (cm); NR, Number of ray florets; TRF, Thickness of ray floret (mm); DTBA, Days to bud appearance; DBO, Days to bud opening; D50, Days to 50% flowering; FD, Flowering duration; RES, Response; SG, Stem girth (mm); INTR, Intermodal length; FN, Flower number.

INTR (-0.264) and FD (-0.129).

Correlation analysis can only determine the relationship between variables without establishing a cause-and-effect link, which may confuse breeders when selecting the optimal combination. Conversely, path coefficient analysis, by breaking down the genotypic association into direct and indirect effects, evaluates the significance of flower number/plant. This study revealed that most traits positively influenced flower production, aligning with earlier findings for plant height (Suvija *et al.* 2016), plant spread (Kameshwari *et al.* 2015, Bennurmah *et al.* 2022), and flower diameter (Gurung *et al.* 2023). The direct and indirect effects correspond with previous reports by Kumar *et al.* (2015), Telem *et al.* (2017) and Bindhushree *et al.* (2019).

*Phenotypic and genotypic correlation for morphological traits:* The phenotypic correlation was influenced by external factors, reducing the overall correlation expression (Table 3). Plant height showed strong, positive, and significant correlations with flowering traits, DBO (0.73), D50 (0.73), DTBA (0.72), and RES (0.72), followed by BD and NR (0.58 each) and INTR (0.50) at the 0.01% level. PH was also positively correlated with FD (0.38) at 1% and TRF (0.30) at 5%, but negatively correlated with FN (-0.26) at 5%. Plant spread (PS) correlated positively with FD (0.41) and BR (0.35) at 1%, while BD and PVIA (0.31) at 5%. FN (0.46) at 1% level. There was significant value ( $R^2$ ) obtained for number of branches (BR), having a higher positive correlation with FN (0.46) at  $p=0.01$ . Considering the association between bud-diameter (BD) and other traits, it was concluded that BD had significant positive correlations with FDIA (0.44) at 0.1%, NR (0.34), FDUR

(0.47), INTR (0.35) at 1% and DTBA, DBO, RES (0.31) at  $p=0.05$ , respectively. Number of ray florets (NR) showed to be positively and significantly correlated with INTR (0.58) at  $p=0.001$ , RES (0.36), D50 (0.34), DTBA (0.36) at  $p=0.1$  while negatively correlated with SG (-0.40) and FN (-0.16) at  $p=0.1$ . There was positive correlation of thickness of ray florets (TRF) at  $p=0.1$  among DTBA (0.41), DBO (0.39), D50 (0.34), and RES (0.41). Corresponding to days to bud appearance (DTBA), it was instigated that traits such as DBO, D5, and RES of  $R^2$  value =1.00 each, were positively associated at  $p=0.01$  with DTBA while FN (-0.10) displayed negative correlation at  $p=0.05$ . The  $R^2$  values attained for flowering traits like DBO and D50 were shown to be associated with response behaviour positively (1.00) at 0.1% significance, while negative in case of FN (-0.10) at  $p=0.05$ . The same correlation was also attained between each other at  $p=0.001$ . Both SG (-0.44) and INTR (-0.48) were also linked to FN negatively at  $p=0.05$ . The correlation phenotypic correlation matrix is displayed in Table 3 showing maximum phenotypic correlation values,  $R^2$  of DBO with D50 and DTBA each (1.00) while it was 0.99 between D50 and DTBA. The trait RES showed a  $R^2$  of 1.00 with DBO and DTBA while it was 0.99 with D50.

Genotypic correlation coefficients were higher than phenotypic ones, indicating strong genetic control and genotype-environment interactions (Table 3). Significant genotypic correlations were observed among several traits. Plant height showed strong positive associations with FDIA (0.64), NR (0.57), TRF (0.631), DTBA (0.31), DBO and D50 (0.78 each), SG (0.07), and INTR (0.58) at 1–5% significance, while RES (0.78) was positive but



Fig. 3 Pictorial depiction of flowers of 20 chrysanthemum genotypes used for evaluation (scale bar = 2 cm).

non-significant. Plant spread was non-significant positively correlated with FD (0.59) and negatively with INTR (-0.33). Branch number correlated positively with FN (0.70,  $p=0.01$ ) but negatively with INTR (-0.6) while bud diameter was positively linked to DTBA (0.34) significantly at  $p=0.05$  and FD (0.51) non-significantly while negatively association was observed with FN (-0.33).

Flower duration (FDUR) was observed to show INTR to be the positive trait for association (0.61) at non-significant level. Number of ray florets (NR) depicted significant negative correlation with SG (-0.42) and FN (-0.16) at 1% and 5% respectively whereas maximum correlations with INTR (0.71) non-significantly. Thickness of ray florets (TRF) was positively associated with SG (0.10) significantly at 1% and maximum non-significant  $R^2$  values for RES and DTBA (0.43) while negative association with FN. Days to bud appearance (DTBA), days to bud opening (DTBO) and days to fifty percent flowering (D50) depicted a negative correlation with FN (-0.10) at  $p=0.05$  along with SG in the case of D50. SG showed positive correlation with INTR (0.02) and negative with FN (-0.44) at  $p=0.1$ . INTR showed only negative correlation with FN at  $R^2$  as -0.48 at 5% level of significance. RES demonstrated non-significant correlations. Table 3 displayed maximum genotypic correlation values of DBO with D50 and DTBA (1.00) each while it was 0.99 between D50 and DTBA. The trait RES showed a high positive path coefficient value with DBO and DTBA while it was 0.99 with D50.

These findings are in parallel with works of Suvija *et al.* (2016) who obtained negative and significant correlation of DTBA with FY/plant (-0.029), NF/plant (-0.128) and PH (-0.093). Khangjarakpam *et al.* (2015), Bennurmth *et al.* (2022) and Gurung *et al.* (2023) signified the positive correlations of PH with FY. The results obtained for number of branches were same as suggested by Misra *et al.* (2013). The current outcomes of plant spread were similar to the studies conducted by Priya *et al.* (2022) in chrysanthemum. Thus, at both phenotypic and genotypic level, these characteristics can be enhanced by choosing genotypes with larger flower yield to boost ornamental value and stay relevant in the market, although, it is the genotypic correlation coefficient that provides a measure of the genetic association between different characteristics, aiding in breeding strategies (Tiwari and Upadhyay 2011).

This study revealed the genetic closeness and diversity among chrysanthemum genotypes, providing valuable insights for selecting suitable parents in breeding programmes. The observed variability can aid in developing improved lines with desirable commercial traits. Morphological characterization also supports the use of genotypes for various ornamental purposes and helps align flowering responses with market demands.

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