



Evaluating genetic variability and trait interrelationships through correlation and path coefficient analysis in garden stock (*Matthiola incana*) genotypes

DEVARAI LAVA KUMAR¹, M K SINGH^{1*}, NAMITA¹, SAPNA PANWAR¹, NAVEEN SINGH¹, ADITI KUNDU¹, AMOLKUMAR U SOLANKE² and SARIKA³

ICAR-Indian Agricultural Research Institute, New Delhi 110 012, India

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ABSTRACT

The present study was carried out during 2022–23 and 2023–24 at ICAR-Indian Agricultural Research Institute, New Delhi to analyse their genetic variability, correlations and trait associations influencing inflorescence production in garden stock (*Matthiola incana* L.). Thirty-six genotypes of garden stock were assessed, for 13 vegetative and floral traits. Analysis of variance indicated the significant differences amid genotypes for all the considered characters. The wide variation recorded for plant spread (542.99–2070.30 cm²) followed by the leaf area/plant (404.75–1625.90 cm²), inflorescence length (18.04–38.85 cm) and inflorescence count/plant (1.00–18.58). Higher genotypic and phenotypic coefficient of variation were documented for inflorescence count/plant, leaf area/plant, distance between two florets, inflorescence length, plant height, leaf count/plant, plant-spread, days for first floral bud initiation and first flowering indicating substantial genetic variability for breeding. All the traits exhibited higher heritability (62.02–90.80%), with inflorescence count/plant (90.80%). Most of the observed characters had shown higher heritability united with a high genetic advance as a percent mean, showing strong additive gene action with favourable response to selection. Inflorescence count/plant unveiled positive and highly significant correlation with leaf count/plant, plant spread and leaf area plant. Cause and effect analysis using correlation coefficients revealed the inflorescence count/plant had a positive and very high effect with leaf count/plant (0.738), leaf area/plant (0.448), plant spread (0.362), stem girth (0.281) and days to first bud flowering (0.274). These traits, can be preferred as key indicators for selection criteria along with other agronomically important traits in stock breeding programme for greater inflorescences per plant and other ornamental potential.

Keywords: Broad-sense heritability, Genotypic coefficient, Path analysis, Stock, Ornamental

Stock [*Matthiola incana* (L.)] belonging to family Brassicaceae, is a commercially important winter annual grown extensively for bedding displays, potted plants and cut flowers, across the temperate and the subtropical regions (Tatsuzawa *et al.* 2012). Valued for its fragrant spikes, diverse colour palette and long vase life. Stock ranks among the top ten cut flowers in European and Asian markets (Sun *et al.* 2024). Beyond ornamental use, single-flowered types serve as industrial sources of linolenic acid-rich seed oil (55–65 %) and different anthocyanin-based natural dyes can be extracted from stock flowers (Taviano *et al.* 2020, Nuraini *et al.* 2020). Despite its economic significance, stock cultivation in India remains constrained by limited adapted germplasm, narrow genetic base in commercial cultivars and inadequate knowledge of trait interrelationships affecting yield and quality.

Efficient breeding programmes require comprehensive understanding of genetic variability, heritability and trait associations within available germplasm. Phenotypic (PCV) and genotypic (GCV) coefficients of variation quantify the extent of variability, while heritability estimates partition genetic form and environmental effects (Burton and De-Vane 1953). Correlation analysis identifies the traits relationships, but often fails to distinguish their effects from direct and indirect components, enabling breeders to identify key selection criteria for yield improvement (Dewey and Lu 1959). In stock, number of inflorescences per plant determine both cut flower production and bedding use. The systematic genetic elucidating its relationship with vegetative and floral traits remain scarce, particularly under Indian subtropical conditions.

Previous studies on stock have largely emphasized morphological characterization (Eid *et al.* 2009) and pigment analysis (Tatsuzawa *et al.* 2012), while genetic diversity studies remain poorly explored. Therefore, the present study aimed to systematically evaluate indigenous stock collections to assess genetic variability and identify

¹ICAR-Indian Agricultural Research Institute, New Delhi;

²ICAR-National Institute of Plant Biotechnology, New Delhi;

³ICAR-Indian Agricultural Statistics Research Institute, New Delhi.

*Corresponding author email: singh_markandey@yahoo.com

potential resources for breeding improvement. Given the expanding floriculture industry in India and increasing demand for winter flowers, identification of high-yielding genotypes adapted to subtropical environments is essential.

The present investigation aimed to analyse genetic variability and interrelationships among growth and floral traits in garden stock to identify key traits contributing to inflorescence yield.

MATERIALS AND METHODS

The present study was carried out during 2022–23 and 2023–24 at ICAR-Indian Agricultural Research Institute, New Delhi. Thirty-six diverse garden stock genotypes, maintained in the Research Farm of Floriculture and Landscaping-Indian Agriculture Research Institute germplasm collection, were evaluated, representing variation in flower colour (white, pink, purple, lavender, yellow), flower form (single and double) and growth habit. Genotypes were coded as G₁–G₃₆ for analysis (Table 1).

The experiment was laid out in a completely randomized design (CRD) comprising three replications per genotype, with 15 plants/replication. Plants grown in 10-inch diameter earthen pots filled with a potting mixture comprising of soil, Farmyard manure and sand (2:1:1, v/v/v). Seeds were sown in nursery beds during the first week of October and healthy seedlings were transplanted to pots after 30 days (November first week) at the 4–5 true leaf stage. Plants were maintained under open field conditions with overhead irrigation using hosepipe fitted with rose, at two-day intervals. Fertilization consisted of 200:150:150 mg NPK/pot applied in two doses at 15-day intervals starting two weeks after transplanting. Standard pest and disease management practices were followed (For aphid control, imidacloprid @1 ml/L, two sprays in weekly interval and for fusarium wilt, potting media was drenched with 1% copper oxychloride after pot filling).

Observations were taken on randomly chosen five healthy and well-grown plants in each replication for 13 biometric traits as followed. Vegetative traits measured included, plant height (cm; from soil-surface to shoot apex); leaf count/plant (fully expanded leaves); leaf area/plant (cm²; measured by LI - 3100C leaf area meter, LI-COR Biosciences., USA); plant spread (cm²; E-W × N-S) and stem girth (mm; measured 5 cm above soil surface using digital vernier calipers).

Floral traits recorded included, days to first flower bud initiation (from transplanting), days to first flowering (from transplanting to opening of first floret), florets/inflorescence (counted on primary spike), distance between florets (cm; average of five consecutive florets on primary spike), floret-diameter (cm; average of five fully opened florets); inflorescence length (cm; from base to tip of primary spike during harvesting stage) and inflorescence/plant (total number of flower spikes are counted per plant throughout the season without harvesting). Duration of flowering (out of 15 plants per replication, five plants measured till last flowering on plants in pots).

Analysis of variance (ANOVA) was calculated following standard procedures using R software (version 4.3.1). Data from both years were pooled after testing homogeneity of error variance using Bartlett's test. Phenotypic (PCV) and genotypic (GCV) coefficients of variation were assessed in accordance to Burton and De-Vane (1953). Broad-sense heritability (h^2_b) was measured as the ratio of genotypic-variance to phenotypic-variance and genetic advance as percent of mean (GAM%) at 5% selection intensity was computed following Johnson *et al.* (1955).

Genotypic and phenotypic correlation coefficients were done using variance-covariance components. Path coefficient analysis was assessed following Dewey and Lu (1959) with inflorescence/plant as the dependent variable and remaining 12 traits as the independent variables. The direct and indirect effects were computed using correlation coefficients and residual effects were determined. All statistical analysis was performed using 'agricolae' and 'ggplot2' packages in R. Significance was tested at $p \leq 0.05$, 0.01 and 0.001 probability levels.

RESULTS AND DISCUSSION

The analysis of variance, uncovered significant variations among all the stock genotypes for all 13 traits indicated that there is a substantial genetic variability exists amid the genotypes, suggesting considerable potential for enhancing the horticultural characteristics through selection-based breeding in stock (Table 2).

Assessment of genetic parameters for the vegetative and floral traits: The degree of variability, including the range and estimations of genetic parameters like PCV, GCV, heritability (h^2_b), and genetic advance as per cent of the mean for the several vegetative and floral traits were analyzed (Table 3).

The highest variation range was reported by plant spread (542.99–2070.30 cm²) followed by the leaf area/plant (404.75–1625.90 cm²), leaf count/plant (27.48–129.60), inflorescence length (18.04–38.85 cm) and inflorescence count/plant (1.00–18.58) for the selected genotypes. The displayed phenotypic variance was great and was highly significant for all the 13 characters, signifying ample variability amongst the genotypes selected for this study. However, the variance between GCV and the PCV was minimal, suggesting that the phenotypical expressions of genotypes may be primarily controlled genetically, with only a minor incentive from the environment, inferring that phenotypical variance serve as a consistent indicator of genotypical variance. Comparable results were confirmed by Parmar *et al.* (2024) in Tulips and Gurung *et al.* (2023) in chrysanthemums. Higher phenotypic and genotypic coefficients of variation were documented for inflorescence count/plant (55.55% and 53.46%), leaf area/plant (52.38% and 50.28%), distance between two florets (51.81% and 51.74%), inflorescence length (46.05% and 45.32%), plant height (41.86% and 41.60%), leaf count/plant (38.68% and 35.53%), plant spread (37.35% and 37.24%), days for first flower bud initiation (30.06% and 28.91%) and days for

Table 1 Salient features of garden stock genotypes

Genotype	code	Floret colour (RHS colour chart)	Growth habit		Flower form
			Plant height	Branching	
G ₁	MiSRPr-1-22	Strong reddish purple (A)	Dwarf	Branched	Double
G ₂	MiSPr-1-22	Strong purple (A)	Dwarf	Branched	Double
G ₃	MiDPrP-1-22	Deep purplish pink (A)	Dwarf	Branched	Double
G ₄	MiDP-1-22	Deep purple (A)	Dwarf	Branched	Double
G ₅	MiW-1-22	White (C)	Dwarf	Branched	Double
G ₆	MiVPPr-1-22	Very Pale purple (C)	Dwarf	Branched	Double
G ₇	MiW-2-22	White (C)	Dwarf	Branched	Single
G ₈	MiVPPr-2-22	Very Pale purple (C)	Dwarf	Branched	Single
G ₉	MiDPrP-2-22	Deep purplish pink (A)	Dwarf	Branched	Single
G ₁₀	MiDP-2-22	Deep purple (A)	Dwarf	Branched	Single
G ₁₁	MiSPr-2-22	Strong purple (A)	Dwarf	Branched	Single
G ₁₂	MiSRPr-2-22	Strong reddish purple (A)	Dwarf	Branched	Single
G ₁₃	MiSRPr-3-22	Strong reddish purple (B)	Dwarf	Branched	Double
G ₁₄	MiSRPr-4-22	Strong reddish purple (B)	Dwarf	Branched	Double
G ₁₅	MiSRPr-5-22	Strong reddish purple (A)	Dwarf	Branched	Double
G ₁₆	MiSRPr-6-22	Strong reddish purple (A)	Dwarf	Branched	Single
G ₁₇	MiW-5-22	White (C)	Dwarf	Branched	Double
G ₁₈	MiW-6-22	White (C)	Dwarf	Branched	Single
G ₁₉	MiSPr-3-22	Strong purple (A)	Medium	Branched	Single
G ₂₀	MiW-3-22	White (C)	Medium	Branched	Single
G ₂₁	MiW-4-22	White (C)	Medium	Branched	Double
G ₂₂	MiSPr-4-22	Strong purple (A)	Medium	Branched	Double
G ₂₃	MiVPPr-3-22	Very pale purple (D)	Medium	Branched	Single
G ₂₄	MiVPPr-4-22	Very pale purple (D)	Medium	Branched	Double
G ₂₅	MiLPr-1-22	Light purple (D)	Medium	Branched	Single
G ₂₆	MiPPr-1-22	Pale purple (B)	Medium	Branched	Single
G ₂₇	MiDPrP-3-22	Deep purplish pink (C)	Tall	Unbranched	Single
G ₂₈	MiDPrP-4-22	Deep purplish pink (C)	Tall	Unbranched	Double
G ₂₉	MiSPr-5-22	Strong purple (A)	Tall	Unbranched	Single
G ₃₀	MiSPr-6-22	Strong purple (A)	Tall	Unbranched	Double
G ₃₁	MiPYG-1-22	Pale Yellow green	Tall	Unbranched	Double
G ₃₂	MiPYG-2-22	Pale Yellow green	Tall	Unbranched	Single
G ₃₃	MiW-7-22	White (C)	Tall	Branched	Double
G ₃₄	MiW-8-22	White (C)	Tall	Branched	Single
G ₃₅	MiW-9-22	White (C)	Tall	Unbranched	Double
G ₃₆	MiW-10-22	White (C)	Tall	Unbranched	Single

Mi, *Matthiola incana*; SRPr and W, Colour codes taken from RHS colour chart for floret colour, like SRPr, Strong reddish purple and W, White; 22, Year of consideration (2022); Plant height, Dwarf:<30 cm, Medium:>30cm to 50 cm and Tall: >50 cm; Flower form, Single: 4 petals/floret, Double: 30–60 petals/floret.

Table 2 Analysis-of-variance for vegetative and floral traits in garden stock genotypes

Character	DF	PH	LCP	LAP	PS	SG	DFBI	DFF	NFI	DB2F	FD	IL	DOF	NIP
Treatment	35	885.74**	2672.91**	379059.8**	372366**	4.73**	102.92**	183.21**	39.25**	2.19**	0.50**	2.19**	79.92**	87.43**
Error	72	1.31	6.66	448.26	757.15	0.07	0.35	0.73	0.21	0.01	0.01	1.04	0.63	0.06
Total	107	290.61	878.80	124293.2	122311.5	1.59	33.90	60.42	12.98	0.72	0.17	262.27	26.57	0.14

PH, Plant height (cm); LCP, Leaf count/plant; LAP, Leaf area/plant (cm²); PS, Plant spread (cm²); SG, Stem girth (mm); DFBI, Days to flower bud initiation; DFF, Days for first flowering; NFI, Number of florets/inflorescence; DB2F, Distance between two florets (cm); FD, Floret diameter (cm); IL, Inflorescence length (cm); DOF, Duration of flowering (days); NIP, Number of inflorescence/plant.

Table 3 Genetic parameters for various traits in garden stock genotypes

Character	Mean ± SD	Range		GCV (%)	PCV (%)	Heritability (%)	GA as per cent of mean
		Minimum	Maximum				
Plant height	41.17 ± 17.15	25.83	73.55	41.60	41.86	89.68	45.73
Leaf count/plant	77.36 ± 29.64	27.48	129.60	35.53	38.68	71.25	39.08
Leaf area/plant	679.44 ± 353.01	404.75	1625.90	50.28	52.38	81.64	57.51
Plant spread	945.17 ± 350.20	542.99	2070.30	37.24	37.35	78.40	56.48
Stem girth	9.49 ± 1.40	7.31	12.72	11.63	13.41	62.02	26.53
Days to flower bud initiation	19.55 ± 6.27	10.27	29.23	28.91	30.06	88.40	31.30
Days for first flowering	30.39 ± 7.32	18.92	46.38	24.66	25.82	88.78	32.54
Floret count/inflorescence	18.47 ± 3.60	12.04	24.84	19.54	19.69	85.45	39.93
Distance between two florets	1.65 ± 0.85	0.67	3.34	51.74	51.81	89.73	46.44
Floret diameter	3.57 ± 0.41	3.00	4.53	11.37	11.62	85.76	22.92
Inflorescence length	28.06 ± 16.24	18.04	38.85	45.32	46.05	90.65	37.30
Duration of flowering	35.50 ± 5.14	23.85	67.52	16.76	18.54	85.62	54.49
Inflorescence count/plant	9.72 ± 5.36	1.00	18.58	53.46	55.55	90.80	59.20

GCV, Genotypic coefficient of variation; PCV, Phenotypic coefficient of variation.

first flowering (25.82% and 24.66%), respectively. Moderate projections of PCV and GCV were observed for floret count/inflorescence (19.69% and 19.54%), flowering duration (18.54% and 16.76%), stem girth (13.41% and 11.63%) and floret-diameter (11.62% and 11.37%). Similar type of findings was stated by Kumar *et al.* (2023) in dahlia and Nataraj *et al.* (2021) in China Aster, documenting high PCV and GCV values for the traits plant height, plant spread, leaf count, while moderate values for flower diameter and stem girth.

Relying solely on GCV and PCV is inadequate, as it only quantifies the genetic diversity magnitude (Burton 1952). A more meaningful evaluation requires simultaneous analysis of GCV, heritability estimates and genetic advance values to provide a comprehensive basis for identifying elite genotypes and predicting response to selection, which enables breeders to distinguish between high variation due to high heritability versus variation driven by the environmental factors (Johnson *et al.* 1955). High level heritability (>60%) observed in most of the traits are ranging from 62.02% (stem girth) to 90.80% (inflorescence count/plant). All the characters exhibited genetic advance as per cent of mean estimations exceeding 20%, with values ranging from 22.92% (floret-diameter) and 59.20% (inflorescence count/plant). High heritability values, tied

up with substantial genetic gains, indicate the presence of additive-gene effects, providing considerable potential for efficient selection. Higher level of heritability combined with greater predictable genetic advance was documented for flower count in chrysanthemum (Telem *et al.* 2017) and plant height, plant spread in the China Aster (Rai *et al.* 2017).

Correlation coefficients (phenotypic and genotypic) for various traits in garden stock genotypes: Phenotypic and genotypic correlation study is a statistical approach employed to identify the type and degree of association amid the traits, especially those are highly heritable and economically significant (Khangjarakpam *et al.* 2015). Correlation coefficients for various traits on the primary trait of interest i.e. inflorescence count/plant have been calculated and are represented in Fig. 1 and Fig. 2. Inclusively, the genotypic correlation coefficients are recorded higher than the phenotypic correlation coefficient values, possibly by reason of the interaction amid the genotypes and environment.

The correlation coefficient (genotypic and phenotypic) results showed that the inflorescence count/plant unveiled a genotypic positive and highly considerable connection with the leaf count/plant (r = 0.97, 0.96), leaf area/plant (r = 0.84, 0.83) and plant spread (r = 0.60, 0.60). Therefore, there is potential for direct selection of these traits to

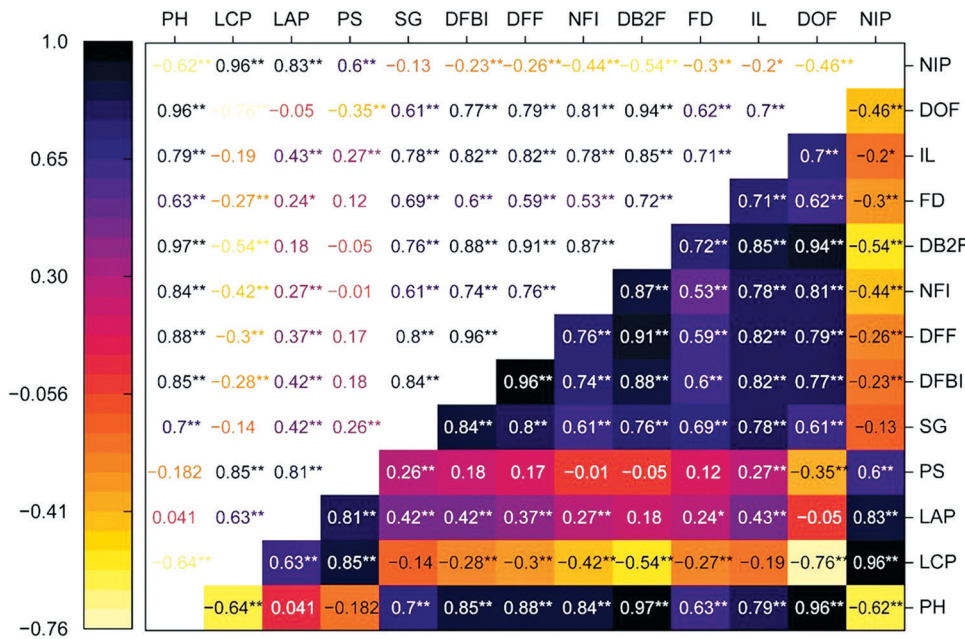


Fig. 1 Phenotypic correlations for vegetative and floral traits in garden stock genotypes. *Significant at $p=0.05$ and **Significant at $p=0.01$. PH, Plant height (cm); LCP: Leaf count/plant; LAP, Leaf area/plant (cm^2); PS, Plant spread (cm^2); SG, Stem girth (mm); DFBI, Days to flower bud initiation; DFF, Days for first flowering; NFI, Number of florets/inflorescence; DB2F, Distance between two florets (cm); FD, Floret diameter (cm); IL, Inflorescence length (cm); DOF, Duration of flowering (days); NIP, Number of inflorescence/plant.

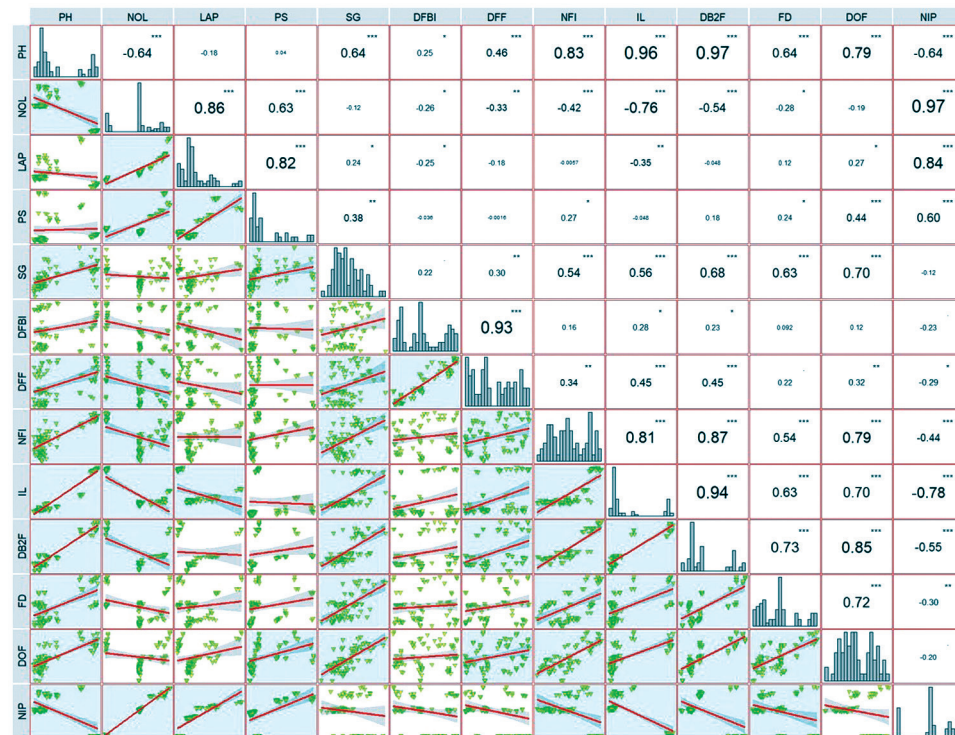


Fig. 2 Genotypic correlations for vegetative and floral traits in garden stock genotypes. *Significant at $p=0.05$; **Significant at $p=0.01$ and ***Significant at $p=0.001$. PH, Plant height (cm); LCP: Leaf count/plant; LAP, Leaf area/plant (cm^2); PS, Plant spread (cm^2); SG, Stem girth (mm); DFBI, Days to flower bud initiation; DFF, Days for first flowering; NFI, Number of florets/inflorescence; DB2F, Distance between two florets (cm); FD, Floret diameter (cm); IL, Inflorescence length (cm); DOF, Duration of flowering (days); NIP, Number of inflorescence/plant.

improve the inflorescence count/plant. The correlation examination recommends that the stock genotype with higher leaf count/plant, wider plant spread and more leaf area/plant tend to produce more inflorescence/plant. This recommends that direct selection for these traits would effectively enhance inflorescence production. Parallel findings reported in spray chrysanthemums for plant spread and leaf count (Gantait and Pal 2014, Shinghala *et al.* 2024).

In genotypic correlation analysis, leaf count/plant exhibited a significant and positive association with plant spread ($r = 0.86$) and leaf area/plant ($r = 0.63$), indicating that genotypes with higher leaf count tend to develop broader canopy architecture and increased photosynthetic surface. Similarly, leaf area/plant showed significant positive correlations with plant spread ($r = 0.82$), stem girth ($r = 0.43$) and flowering duration ($r = 0.44$). Plant spread was also positively and significantly correlated with stem girth ($r = 0.38$), floret count/inflorescence ($r = 0.27$), floret-diameter ($r = 0.24$) and flowering duration ($r = 0.43$). These findings are closely aligned by the reports of the Cordea *et al.* (2008) in stock and Gurung *et al.* (2023) in chrysanthemums.

The dependent variable (inflorescence count/plant) exhibited significant negative correlations with plant height ($r = -0.64, -0.62$), days to first flowering ($r = -0.29, -0.26$), floret-diameter ($r = -0.30, -0.30$), inter-floret spacing ($r = -0.55, -0.54$) and inflorescence length ($r = -0.78, -0.20$). These results showed that genotypes with dwarf stature, early flowering and compact

inflorescence traits tend to produce a higher inflorescence count/plant. Overall, the observed correlations highlight that vegetative traits such as leaf number, leaf area and plant spread positively contribute to floral productivity, whereas longer inflorescence length and other quality traits showed an inverse relationship with inflorescence count in stock under the present study, which are parallel with the reportings of Henny *et al.* (2021) in chrysanthemums and Kumar *et al.* (2024) in globe amaranth.

Path coefficient analysis in garden stock genotypes: Path coefficient study split the correlation between two characters into their direct and indirect contributions. Selecting the inflorescence count/plant as a dependent trait, the phenotypic and genotypic correlation coefficients were further analysed to divide their direct and indirect contributions (Table 4).

The cause-and-effect associations between the inflorescence count/plant, at phenotypic level represented high and direct effect with the leaf count/plant (0.532), days

to first flowering (0.183), leaf area/plant (0.105), plant spread (0.104), stem girth (0.067), inflorescence length (0.038) and floret count/inflorescence (0.005). Sahu *et al.* (2018) noted highest positive direct effect of plant spread and leaf count/plant on the flower count at phenotypic level. The negative and direct effect logged through flowering duration (-0.532), plant height (-0.247), distance between two florets (-0.197), days to flower bud initiation (-0.074) and floret-diameter (-0.014). Parallel negative effect results on flower yield/plant represented by first bud initiation (days) and 50% flowering (days) in marigold (Poulose *et al.* 2020). All had negative coefficients, signifying that a rise in these factors resulted in a reduction in the inflorescence count per plant.

At the genotypical level positive and the straight effect was observed for leaf count/plant (0.738), plant spread (0.362), leaf area/plant (0.448), stem girth (0.281) and days to first-flowering (0.274). These findings are similar with the results of Khangjarakpam *et al.* (2015) in China aster

Table 4 Phenotypic and genotypic path analysis of garden stock genotypes

Character		PH	LCP	LAP	PS	SG	DFBI	DFF	NFI	DB2F	FD	IL	DOF	r
PH	P	-0.247	-0.341	0.004	-0.019	0.047	-0.063	0.162	0.005	-0.192	-0.009	0.030	-0.511	-0.644***
	G	-0.776	-0.061	-0.018	0.431	-0.201	-0.073	0.244	-0.043	0.109	0.209	-0.074	0.757	-0.636***
LCP	P	-0.159	0.532	0.066	0.089	-0.009	0.020	-0.055	-0.002	0.106	0.004	-0.007	0.406	0.975***
	G	-0.695	0.738	-0.283	-0.032	0.038	0.023	-0.083	0.022	-0.060	-0.090	0.018	-0.601	0.971***
LAP	P	0.010	0.334	0.105	0.085	0.028	-0.031	0.067	0.001	-0.036	-0.003	0.016	0.025	0.845***
	G	0.044	0.988	0.448	-1.931	-0.121	-0.036	0.101	-0.014	0.020	0.078	-0.041	-0.037	0.836***
PS	P	-0.045	0.454	0.086	0.104	0.017	-0.013	0.032	0.001	0.010	-0.002	0.010	0.186	0.601***
	G	-0.196	0.375	-0.366	0.362	-0.074	-0.015	0.048	0.001	-0.005	0.040	-0.025	-0.276	0.612***
SG	P	0.172	-0.073	0.045	0.027	0.067	-0.062	0.147	0.003	-0.149	-0.010	0.030	-0.324	-0.127
	G	0.770	-0.650	-0.194	-0.626	0.281	-0.072	0.226	-0.032	0.086	0.231	-0.075	0.487	-0.122
DFBI	P	0.210	-0.147	0.044	0.019	0.056	-0.074	0.176	0.004	-0.174	-0.008	0.031	-0.409	-0.272**
	G	0.923	-0.310	-0.191	-0.423	-0.240	-0.085	0.267	-0.038	0.099	0.196	-0.077	0.607	-0.231
DFF	P	0.219	-0.161	0.039	0.018	0.054	-0.072	0.183	0.004	-0.180	-0.008	0.031	-0.420	-0.297**
	G	0.960	-0.444	-0.166	-0.414	-0.232	-0.082	0.274	-0.039	0.102	0.198	-0.078	0.624	-0.293*
NFI	P	0.207	-0.222	0.028	-0.001	0.041	-0.055	0.139	0.005	-0.171	-0.007	0.030	-0.431	-0.440**
	G	0.911	-0.005	-0.121	0.013	-0.175	-0.063	0.210	-0.051	0.098	0.176	-0.074	0.641	-0.437***
DB2F	P	0.240	-0.285	0.019	-0.005	0.051	-0.065	0.167	0.005	-0.197	-0.010	0.032	-0.498	-0.546**
	G	0.048	-0.549	-0.081	0.114	-0.216	-0.075	0.251	-0.045	-0.111	0.236	-0.079	0.735	-0.772***
FD	P	0.157	-0.146	0.025	0.013	0.046	-0.044	0.109	0.003	-0.142	-0.014	0.027	-0.331	-0.297**
	G	0.699	-0.322	-0.109	-0.294	-0.201	-0.052	0.168	-0.028	0.082	-0.322	-0.067	0.496	-0.545***
IL	P	0.194	-0.099	0.046	0.028	0.052	-0.061	0.151	0.004	-0.167	-0.010	0.038	-0.373	-0.197**
	G	0.860	-0.899	-0.197	-0.648	-0.227	-0.071	0.230	-0.041	0.096	0.234	-0.092	0.555	-0.300**
DOF	P	0.238	-0.406	-0.005	-0.036	0.041	-0.057	0.145	0.004	-0.185	-0.009	0.027	-0.532	-0.775**
	G	0.041	-0.637	0.021	0.834	-0.175	-0.066	0.219	-0.042	0.105	0.204	-0.066	-0.783	-0.205

R, Phenotypic and genotypic correlation coefficient of number of inflorescences/plant; P, Phenotypic level; G, Genotypic level
 Character sequence; PH, Plant height (cm); LCP, Leaf count/plant; LAP, Leaf area/plant (cm²); PS, Plant spread (cm²); SG, Stem girth (mm); DFBI, Days to flower bud initiation; DFF, Days for first flowering; NFI, Number of florets/inflorescence; DB2F, Distance between two florets (cm); FD, Floret diameter (cm); IL, Inflorescence length (cm); DOF, Duration of flowering (days); Residual value, genotypic, -0.046 and phenotypic, 0.078; *Significant at $p=0.05$, **Significant at $p=0.01$ and ***Significant at $p=0.001$

at genotypic level. The negative direct effect showed by the inflorescence length (-0.783), plant height (-0.776), floret-diameter (-0.322), distance between two florets (-0.111), flowering duration (-0.092), days to flower bud initiation (-0.085) and floret count/inflorescence (-0.051). Similar negative indirect effects were also reported in stock for the character, number of cut flowers/m² by flowering duration, floret-diameter and stalk length, highlighting increase in these traits leads to decrease in inflorescence count (Saketh 2023). A minimal residual impact from the genotypic and the phenotypic path analysis (-0.046 and 0.078, respectively) indicates that the traits selected for the path analysis were suitable to explain variation in inflorescence count, validating the model effectiveness. This implies the chosen traits are biologically and statistically relevant determinants of reproductive capacity in stock.

The comprehensive genetic variability and correlation analysis provided a strong foundation for development of improved garden stock cultivars with desirable horticultural traits by prioritizing few trait targets for selection. Thus, the overall analysis underscores that for the inflorescence count/plant, plant spread, leaf count/plant, leaf area/plant, stem girth and days to first flowering are the primary traits that can be targeted for selection for enhancing the ornamental and commercial potential of stock for garden uses. The traits like leaf area/plant, stem girth and days to early flowering provide substantial indirect contributions to inflorescence production and should be considered in multi-trait selection strategies. Plant height and inflorescence length showed strong negative direct effects on the inflorescence count. Breeders aiming to maximize inflorescence production should actively select for dwarf branching growth habits and avoid tall non-branching genotypes, as the inverse relationship between plant height and inflorescence count appears to be physiologically fundamental, while including both branching and non-branching genotypes in the stock.

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