



RESEARCH ARTICLE

Genetic variability, correlation, path analysis and genetic divergence for yield traits in cucumber (*Cucumis sativus* L.)

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Abstract

Twenty cucumber (*Cucumis sativus* L.) genotypes were evaluated during the summer of 2022 at the Horticultural Research Centre, Sardar Vallabhbhai Patel University of Agriculture and Technology, Meerut, Uttar Pradesh, to estimate genetic variability and selection parameters for 16 quantitative traits. The experiment was laid out in a randomised block design (RBD) with three replications at 90 × 60 cm spacing. Analysis of variance (ANOVA) revealed highly significant differences among genotypes for all traits, indicating the presence of substantial variability. High genotypic and phenotypic coefficients of variation were recorded for average fruit weight, fruit yield per hectare, vine length and number of fruits per plant, while all traits exhibited high heritability coupled with moderate to high genetic advance as percent of mean, suggesting the predominance of additive gene action. Fruit yield per hectare showed highly significant and positive correlations with fruit yield per plot, fruit diameter, number of fruits per plant, average fruit weight, number of leaves per plant, fruit length and vine length at both genotypic and phenotypic levels, whereas days to first male and female flower anthesis and days to first fruit harvest were negatively associated. Genotypic path analysis revealed high positive direct effects of fruit diameter, fruit yield per plot, days to first male and female flower anthesis, vine length, node number to first male and female flower anthesis, number of fruits per plant and average fruit weight on fruit yield per hectare. Mahalanobis D² analysis grouped the genotypes into five clusters, with maximum inter-cluster distance between clusters III and V, indicating high genetic divergence and suggesting that crosses between these clusters may produce superior segregants for yield and related traits.

Keywords: correlation; cucumber; genetic divergence; genetic variability; heritability; path analysis

Introduction

Cucumber (*Cucumis sativus* L.) belongs to the family Cucurbitaceae, which comprises approximately 90 genera and about 750 species (1). The genus *Cucumis* consists of 32 annual and perennial species that are broadly classified into two distinct groups based on geographical origin and chromosome number, namely the African group (2n: 24) and the Asiatic group (2n: 14) (2). The African group includes melon (*Cucumis melo* L.), whereas the Asiatic group encompasses cucumber (*C. sativus*) and its putative progenitor, *C. sativus* var. *hardwickii* (3). Cucumber is widely consumed worldwide, both as a fresh vegetable and in processed forms such as sliced or pickled fruits. Considerable intraspecific variability has been reported in cucumber for traits related to growth habit, maturity, yield and fruit characteristics including shape, size, colour, spines and vine architecture, providing substantial scope for genetic improvement. Globally, cucumbers are grown on about 3.49 Mha with a production of 158.14 Mt and a productivity of 55.68 t ha⁻¹ (4), while in India they occupy 1.09 Mha with 16.64 Mt production, contributing substantially to the

national vegetable basket (5). The crop is mainly grown for tender fruits, which are consumed fresh as salad, cooked as vegetable or used for pickling and valued for high water content (≈ 95 %) and appreciable levels of vitamins, minerals and bioactive compounds with diuretic, laxative and medicinal properties (6, 7).

Despite being a crop of Indian origin endowed with wide variability, productivity of cucumber in India (about 13.6 t ha⁻¹) remains lower than that of advanced countries, necessitating genetic improvement for higher yield and better quality (8). Yield is a complex quantitative trait influenced by several component characters and their interactions and its improvement requires information on the magnitude of genetic variability, heritability, genetic advance, inter-character correlations and causal relationships through path analysis (9, 10). Vavilov emphasised the importance of wide variability for effective selection, while other studies highlighted the combined use of heritability and genetic advance in predicting response to selection (11, 12). Correlation analysis provides the nature and strength of association among traits, whereas path coefficient analysis partitions these

correlations into direct and indirect effects, thereby clarifying the cause–effect relationships. Furthermore, Mahalanobis D² statistic allows quantification of genetic divergence among genotypes and facilitates identification of diverse parents for heterosis breeding and broad-based segregating populations (13).

Several studies have examined variability and trait associations in cucumber; however, information on combined evaluation of genetic variability, trait association and genetic divergence among diverse genotypes under North Indian conditions remains limited. Considering the need to enhance yield and associated traits in cucumber, the present study was undertaken with the objectives: (i) to estimate genetic variability, heritability and genetic advance for quantitative traits, (ii) to assess correlation and path coefficients for yield and its components and (iii) to evaluate genetic divergence among cucumber genotypes using D² statistics.

Materials and methods

Plant material

The experimental material comprised 20 genotypes of cucumber, including released varieties and indigenous collections, obtained from the Division of Vegetable Science, ICAR-Indian Agricultural Research Institute, New Delhi. The list and description of the genotypes are provided in Table S1.

Experimental site and design

The experiment was conducted during summer 2022 at the Horticultural Research Centre, College of Horticulture, Sardar Vallabhbhai Patel University of Agriculture and Technology, Meerut, Uttar Pradesh. The site is located at 29.01° N latitude, 77.75° E longitude and 237 m above mean sea level. The climate of the region is subtropical with hot dry summers (maximum temperature 40–45 °C) and cool winters (8–10 °C), receiving about 750 mm annual rainfall, 85 % of which occurs during monsoon. The trial was laid out in a randomised block design (RBD) with three replications. Each genotype was planted in a plot of 1.8 m × 1.8 m at 90 cm × 60 cm spacing, resulting in 60 plots in total recommended agronomic practices were followed.

Crop management practices

A fertiliser dose of 100: 60: 60 kg N: P₂O₅: K₂O ha⁻¹ was applied. Half of the nitrogen (N) and the full dose of phosphorus (P) and potassium (K) were applied at basal at the time of field preparation, while the remaining N was applied in two equal splits at vine development and flowering stages. Irrigation was provided immediately after sowing and subsequently at 5–7 days interval depending upon soil moisture conditions and weather. Proper drainage was maintained to avoid water stagnation.

For pest management, need-based plant protection measures were adopted. Spraying of neem-based formulations and recommended insecticides was carried out for the management of major insect pests such as fruit fly and red pumpkin beetle. Preventive fungicidal sprays were also applied to manage powdery mildew and downy mildew whenever required.

Traits recorded

Observations were recorded on 16 quantitative traits node number to first male flower anthesis, node number to first female flower anthesis, number of primary branches per plant, number of

leaves per plant, vine length (cm), days to first fruit harvest, fruit length (cm), fruit diameter (cm), number of fruits per plant, average fruit weight (g) and total soluble solids (°Brix) from five randomly selected plants per plot per genotype, except for days to germination traits, days to first male flower anthesis, days to first female flower anthesis, fruit yield per plot (kg) and fruit yield per hectare (kg) recorded on a plot basis.

Fruit yield recorded on a plot basis (kg plot⁻¹) was converted into hectare yield (kg ha⁻¹) using the following formula:

$$\text{Yield (Kg ha}^{-1}\text{)} = \frac{\text{Yield per plot (Kg)} \times 10000}{\text{Net plot area (m}^2\text{)}}$$

Selection intensity was maintained at 5 %, indicating that only the top 5 % superior genotypes based on the performance of target traits were considered for selection and further evaluation.

Statistical analysis

Analysis of variance (ANOVA) for RBD was carried using the linear model $Y_{ij} : \mu + t_i + b_j + e_{ij}$, where Y_{ij} is the observation of the i -th genotype in the j -th replication, μ the overall mean, t_i the effect of the i -th genotype, b_j the effect of the j -th replication and e_{ij} the experimental error (14). Phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were calculated (15).

$$\text{GCV (\%)} = \left[\frac{\sqrt{\sigma^2_g}}{\bar{x}} \right] \times 100 \quad (\text{Eq. 1})$$

$$\text{PCV (\%)} = \left[\frac{\sqrt{\sigma^2_p}}{\bar{x}} \right] \times 100 \quad (\text{Eq. 2})$$

where, PCV is the phenotypic coefficient of variation and GCV is the genotypic coefficient of variation and $\bar{x}$ is the population means of the characters.

Heritability broad sense (bs) was calculated as per the following formula (16).

$$H^2 = \left(\frac{\sigma^2_g}{\sigma^2_p} \right) \times 100 \quad (\text{Eq. 3})$$

where, H^2 is the heritability in broad sense, σ^2_g is the genotypic coefficient of variance and σ^2_p is the phenotypic coefficient of variance.

Classifications were done as: > 80 % high, 60–80 % medium and < 60 % low (17). Genetic advance and genetic advance over percent mean were estimated as per the following formula (18, 19).

$$\text{GA} = K \times \sigma_p \times H^2 \quad (\text{Eq. 4})$$

$$\text{GAM} = \left(\frac{\text{GA}}{\bar{x}} \right) \times 100 \quad (\text{Eq. 5})$$

The correlation and path coefficients were calculated as per the following formula (20, 21).

$$r_{xy} = \frac{\text{MSPt}}{(\text{MSt}_x \text{MSt}_y)^{1/2}} \quad (\text{Eq. 6})$$

where, r_{xy} is the correlation between attributes x and y , MSPt is mean sum of products of genotypes, MSt_x is mean square of treatments for variable x and MSt_y is mean square of treatments for variable y .

$$R^2 = b'_1 r_{1y} + b'_2 r_{2y} + b'_3 r_{3y} + \dots \quad (\text{Eq. 7})$$

$$\text{Residual effect} = 1 - R^2 \quad (\text{Eq. 8})$$

where, $b'1, b'2, b'3 \dots$: standardised partial regression of $x_1, x_2, x_3 \dots$ and $r_{1y}, r_{2y}, r_{3y}, \dots$: correlation coefficient between $x_1, x_2, x_3 \dots$ and y .

Genetic divergence among genotypes was quantified using Mahalanobis D^2 statistic (22) and genotypes were grouped into clusters using Tocher's method; cluster means, intra and inter-cluster distances and per cent contribution of traits to total divergence were computed (23). All analyses were performed using OPSTAT software (24).

Results and discussion

Mean performance of genotypes

Analysis of variance for the 20 cucumber genotypes revealed highly significant differences among genotypes for all 16 traits, while replication effects were non-significant for most traits, demonstrating adequate experimental precision (Table 1). Significant variation for days to germination, flowering traits, vegetative traits and yield components provides a broad scope for effective selection and genetic improvement, in agreement with earlier reports in cucumber. Similar observations of significant analysis of variance of all traits were also reported in previous studies (25, 26).

Descriptive analysis of 16 quantitative traits across 20 cucumber genotypes revealed substantial phenotypic variability (Table S2). Days to germination ranged from Pusa Barkha (5.81 days) to DC 83 (8.17 days), with a mean of 6.98 days. Flowering behaviour showed wide variation, as node number to first male and female flower anthesis varied from Swarna Poorna (4.07 and 8.21 nodes, respectively) to Pusa Barkha (7.09 and 12.37 nodes), with means of 5.46 and 10.11 nodes, respectively. Days to first male and female flower anthesis ranged from 32.43 and 42.45 days in Pusa Barkha to 39.84 and 53.53 days in Swarna Poorna, respectively.

Vegetative growth also varied considerably among genotypes. The number of primary branches per plant ranged from 3.56 in Barsha Rani to 6.74 in Swarna Poorna, the number of leaves per plant from 24.40 in Swarna Poorna to 44.78 in Pusa Barkha and vine length from 127.19 cm in Swarna Poorna to 270.49 cm in Pusa Barkha, reflecting strong vegetative vigour in Pusa Barkha. Days to first fruit harvest varied from Pusa Barkha (50.28 days) to Swarna Poorna (59.41 days), with a mean of 53.68 days. Fruit traits showed significant variation, as fruit length ranged from Punjab Barsati (9.67 cm) to DC 43 (18.66 cm) and fruit diameter from Agro 1 (1.98 cm) to DC 43 (3.21 cm), with respective means of 14.41 and 2.49 cm. Yield attributes also differed widely,

with number of fruits per plant ranging from Pusa Uday (5.99) to DC 43 (13.65), average fruit weight from Beet Alfa (86.88 g) to WBC 38-2 (268.39 g) and fruit yield per plot from Swarna Poorna (5.41 kg) to WBC 1 (8.63 kg). Fruit yield per hectare ranged from Pusa Uday (4011.74 kg ha⁻¹) to Pusa Barkha (8981.13 kg ha⁻¹), followed by WBC 1 (8567.22 kg ha⁻¹) and Meenakshi (8186.41 kg ha⁻¹), with a mean of 6387.63 kg ha⁻¹ while total soluble solids ranging from Pohari Barshati (2.51 °Brix) to Barsha Rani (4.63 °Brix).

These results collectively identify Pusa Barkha as a standout genotype for earliness, vigour and superior yield, WBC-1 and Meenakshi for high yield and fruit size, DC-43 and Pohari Barshati for prolific fruiting and Barsha Rani for elevated TSS alongside good productivity, thereby providing a robust foundation for targeted genetic improvement in cucumber. Similar observations for mean performance were also reported in previous studies (27–31).

Genetic variability heritability and genetic advance

Estimates of GCV, PCV, heritability and genetic advantage (GA) % for 16 traits are presented in Table 2. High GCV and PCV (> 20 %) were recorded for average fruit weight (32.17 and 32.21 %), fruit yield per hectare (22.62 and 22.72 %), vine length (21.14 and 21.27 %) and number of fruits per plant (20.38 and 20.48 %), suggesting substantial genetic variability and good prospects for selection for these traits. Similar high observations for GCV and PCV for fruit yield per hectare were also reported in earlier research (31, 32). Moderate GCV and PCV (10–20 %) were observed for number of primary branches per plant (19.86 and 20.01 %), fruit length (16.41 and 16.55 %), total soluble solids (16.39 and 16.54 %), number of leaves per plant (16.00 and 16.24 %), fruit yield per plot (13.85 and 14.00 %), node number to first male flower anthesis (13.64 and 13.88 %), fruit diameter (12.88 and 13.05 %) and node number to first female flower anthesis (12.20 and 12.40 %). Low GCV and PCV (< 10 %) were found for days to germination (8.56 and 8.87 %), days to first female flower anthesis (5.81 and 6.54 %), days to first male flower anthesis (5.50 and 6.16 %) and days to first fruit harvest (4.78 and 5.20 %), indicating comparatively narrower genetic base for these traits were also studied in earlier research (33–36).

Broad-sense heritability estimates were high for most traits. It is an indicator of character transmission from parents to offspring. High heritability (> 80 %) was observed for traits for days to first female flower anthesis to 99.72 % for average fruit weight, with fruit yield per hectare (99.08 %), number of fruits per plant (99.04 %), vine length (98.84 %) and number of primary branches per plant (98.51 %) also exhibiting very high values (Table 3). High heritability coupled with high GA % (> 20 %) was recorded for average fruit weight (66.18 %), fruit yield per hectare (46.37 %), vine

Table 1. Analysis of variance for 16 quantitative traits in cucumber genotypes

Source of variation	DF	DG	NNMFA	NNMFeA	DMFA	DFeA	PB	LP	VL	DFH	FL	FD	NFP	AFW	TSS	FYPP	FY
Repl	2	0.005	0.010	0.015	1.07	0.61	0.010	0.28	0.05	0.03	0.02	0.020	0.01	1.44	0.005	0.015	604.4
Treat	19	1.098**	1.686**	4.613**	12.64**	23.60**	3.206**	104.10*	5096.54*	20.94**	16.87**	0.312**	13.26**	7944.31*	1.271**	2.729**	6280064.9**
Error	38	0.026	0.019	0.049	1.00	1.93	0.016	1.03	19.85	1.20	0.096	0.003	0.042	7.44	0.008	0.020	19400.5
Total	59	0.370	0.555	1.517	4.75	8.86	1.043	34.20	1654.04	7.52	5.49	0.102	4.30	2563.18	0.414	0.892	2034909.5

DF: days to flower; DG: days to germination; NNMFA: node number to first male flower anthesis; NNMFeA: node number to first female flower anthesis; DMFA: days to first male flower anthesis; DFeA: days to first female flower anthesis; PB: number of primary branches per plant; LP: number of leaves per plant; VL: vine length (cm); DFH: days to first fruit harvest; FL: fruit length (cm); FD: fruit diameter (cm); NFP: number of fruits per plant; AFW: average fruit weight (g); TSS: total soluble solids (%); FYPP: fruit yield per plot (kg); FY: fruit yield (kg ha⁻¹).

Table 2. Estimates of genetic variability parameters for 16 traits in cucumber genotypes

Trait	Mean	Range	GCV (%)	PCV (%)	Heritability (%)	GA	GA % mean
DG	6.98	5.81–8.17	8.56	8.87	93.29	1.19	17.04
NNMFA	5.46	4.07–7.09	13.64	13.88	96.69	1.51	27.64
NNMFeA	10.11	8.21–12.37	12.20	12.40	96.90	2.50	24.74
DMFA	35.85	32.43–39.84	5.50	6.16	79.52	3.62	10.09
DFeA	46.24	42.45–53.53	5.81	6.54	78.91	4.92	10.64
PB	5.19	3.56–6.74	19.86	20.01	98.51	2.11	40.61
LP	36.63	24.40–44.78	16.00	16.24	97.08	11.90	32.48
VL	194.58	127.19–270.49	21.14	21.27	98.84	84.25	43.30
DFH	53.68	50.28–59.41	4.78	5.20	84.55	4.86	9.05
FL	14.41	9.67–18.66	16.41	16.55	98.32	4.83	33.51
FD	2.49	1.98–3.21	12.88	13.05	97.36	0.65	26.18
NFP	10.30	5.99–13.65	20.38	20.48	99.04	4.30	41.78
AFW	159.89	86.88–268.39	32.17	32.21	99.72	105.81	66.18
TSS	3.96	2.51–4.63	16.39	16.54	98.24	1.33	33.47
FYPP	6.86	5.41–8.63	13.85	14.00	97.84	1.94	28.22
FY	6387.63	4011.74–8981.13	22.62	22.72	99.08	2962.15	46.37

GCV: genotypic coefficient of variation; PCV: phenotypic coefficient of variation; GA: genetic advance; GA % mean: genetic advance as percentage of mean; DG: days to germination; NNMFA: node number to first male flower anthesis; NNMFeA: node number to first female flower anthesis; DMFA: days to first male flower anthesis; DFeA: days to first female flower anthesis; PB: number of primary branches per plant; LP: number of leaves per plant; VL: vine length (cm); DFH: days to first fruit harvest; FL: fruit length (cm); FD: fruit diameter (cm); NFP: number of fruits per plant; AFW: average fruit weight (g); TSS: total soluble solids (%); FYPP: fruit yield per plot (kg); FY: fruit yield (kg ha⁻¹).

Table 3. Genotypic direct and indirect effects of different traits on fruit yield per hectare in cucumber

Traits	DG	NNMF	NNFF	DMF	DFF	PB	LP	VL	DFH	FL	FD	NFP	AFW	TSS	FYH	r(FYP)
DG	0.064	0.024	0.018	-0.086	-0.044	-0.317	-0.008	0.041	0.026	0.130	0.258	-0.007	-0.003	0.006	-0.339	-0.235
NNMF	-0.012	-0.131	-0.073	0.364	0.223	-0.095	0.004	-0.023	-0.157	-0.147	-0.227	-0.020	0.001	0.015	0.398	0.119
NNFF	-0.011	-0.087	-0.109	0.319	0.103	-0.123	0.008	-0.028	-0.074	-0.198	0.195	-0.000	-0.001	-0.019	0.030	0.002
DMF	0.008	0.071	0.052	-0.666	-0.388	0.235	-0.021	0.096	0.264	-0.001	0.648	0.007	-0.004	-0.026	-0.571	-0.295*
DFF	0.007	0.072	0.028	-0.635	-0.407	0.152	-0.025	0.093	0.304	-0.092	0.886	0.018	-0.005	-0.027	-0.883	-0.513**
PB	-0.028	0.017	0.018	-0.211	-0.083	0.741	-0.019	0.030	0.022	-0.105	0.043	0.023	-0.004	-0.023	-0.599	-0.177
LP	-0.009	-0.011	-0.016	0.261	0.191	-0.263	0.054	-0.159	-0.110	0.081	-0.327	-0.017	0.008	-0.030	0.924	0.578**
VL	-0.015	-0.017	-0.018	0.360	0.213	-0.126	0.048	-0.178	-0.145	0.038	-0.382	-0.010	0.006	-0.018	0.773	0.529**
DFH	0.006	0.069	0.027	-0.593	-0.417	0.054	-0.020	0.087	0.296	-0.050	0.821	0.012	-0.003	-0.033	-0.582	-0.324*
FL	0.019	0.043	0.048	0.001	0.083	-0.173	0.010	-0.015	-0.033	0.449	-0.816	-0.022	0.005	-0.013	0.825	0.410**
FD	-0.013	-0.022	0.016	0.326	0.272	-0.024	0.013	-0.051	-0.184	0.277	-1.325	-0.034	0.007	0.013	1.377	0.649**
NFP	0.007	-0.043	-0.000	0.075	0.121	-0.276	0.015	-0.028	-0.059	0.163	-0.720	-0.062	0.004	0.013	1.360	0.571**
AFW	-0.014	-0.007	0.012	0.180	0.155	-0.208	0.031	-0.074	-0.059	0.184	-0.729	-0.020	0.013	-0.055	1.227	0.636**
TSS	0.002	-0.011	0.011	0.093	0.059	-0.090	-0.009	0.017	-0.052	-0.032	-0.091	-0.004	-0.004	0.187	-0.014	0.062
FYH	-0.012	-0.029	-0.002	0.214	0.202	-0.250	0.028	-0.078	-0.097	0.209	-1.027	-0.047	0.009	-0.002	1.776	0.895**

DG: days to germination; NNMFA: node number to first male flower anthesis; NNMFeA: node number to first female flower anthesis; DMFA: days to first male flower anthesis; DFeA: days to first female flower anthesis; PB: number of primary branches per plant; LP: number of leaves per plant; VL: vine length (cm); DFH: days to first fruit harvest; FL: fruit length (cm); FD: fruit diameter (cm); NFP: number of fruits per plant; AFW: average fruit weight (g); TSS: total soluble solids (%); FYPP: fruit yield per plot (kg); FY: fruit yield (kg ha⁻¹).

length (43.30 %), number of fruits per plant (41.78 %), number of primary branches per plant (40.61 %), fruit length (33.51 %), total soluble solids (33.47 %), number of leaves per plant (32.48 %), fruit yield per plot (28.22 %), node number to first male flower anthesis (27.64 %) and node number to first female flower anthesis (24.74 %), indicating predominance of additive gene action and effectiveness of direct selection for these traits. Moderate GA % (10–20 %) was observed for days to germination (17.04 %), days to first female flower anthesis (10.64 %) and days to first male flower anthesis (10.09 %), whereas days to first fruit harvest showed low GA % (9.05 %), suggesting relatively slower response to selection. Similar observations for high genetic advance estimates for fruit weight, fruit yield per hectare and total soluble solids were reported earlier (36, 37).

The combination of high GCV, high heritability and high GA % for average fruit weight, fruit yield per hectare, vine length and fruits per plant suggests that these traits are largely governed by additive gene effects and are amenable to improvement through simple phenotypic selection in early generations, similar to previous findings in cucumber and other cucurbits reported in the thesis. Conversely, lower GA % for days-related traits despite high heritability implies possible involvement of non-additive gene action or greater environmental influence, warranting progeny

testing for stable improvement.

Correlation analysis among yield and yield-related traits

Genotypic and phenotypic correlation coefficients among the 16 traits are presented in Table 4. In general, genotypic correlations were higher in magnitude than their corresponding phenotypic correlations, indicating that environmental effects tended to mask the true genetic associations among traits. At the genotypic level, fruit yield per hectare exhibited highly significant and positive correlations with fruit yield per plot (0.895 kg), fruit diameter (0.775 cm), number of fruits per plant (0.766), average fruit weight (0.691 g), number of leaves per plant (0.520), fruit length (0.465 cm) and vine length (0.435 cm), suggesting that these traits are the principal contributors to yield and that simultaneous improvement in these traits is feasible (Fig. 1, Table 4). Positive and non-significant associations were observed with node number to first male flower anthesis (0.224) and node number to first female flower anthesis (0.017), whereas number of primary branches per plant (-0.337) and days to first female flower anthesis (-0.497) showed negative and highly significant correlations with fruit yield per hectare. Days to first male flower anthesis (-0.322) and days to first fruit harvest (-0.328) were negatively and significantly associated with yield, while days to

Table 4. Genotypic (above diagonal) and phenotypic (below diagonal) correlation coefficients among sixteen traits in cucumber genotypes

Traits	DG	NNMFA	NNMFeA	DMFA	DFeA	PB	LP	VL	DFH	FL	FD	NFP	AFW	TSS	FYPP	FY
DG	1	-0.186	-0.167	0.129	0.108	-0.428**	-0.142	-0.231	0.088	0.289*	-0.195	0.115	-0.214	0.032	-0.235	-0.191
NNMFA	-0.200	1	0.667**	-0.546**	-0.548**	-0.129	0.080	0.128	-0.530**	-0.328*	0.171	0.325*	0.053	0.080	0.119	0.224
NNMFeA	-0.145	0.623**	1	-0.479**	-0.254	-0.166	0.141	0.160	-0.250	-0.442**	-0.147	0.001	-0.106	-0.103	0.002	0.017
DMFA	0.062	-0.446**	-0.470**	1	0.954**	0.317*	-0.393**	-0.540**	0.890**	-0.002	-0.489**	-0.112	-0.271*	-0.140	-0.295*	-0.322*
DFeA	0.119	-0.517**	-0.178	0.627**	1	0.205	-0.470**	-0.523**	1.026**	-0.204	-0.669**	-0.297*	-0.382**	-0.144	-0.513**	-0.497**
PB	-0.411**	-0.122	-0.172	0.293*	0.151	1	-0.355**	-0.169	0.073	-0.234	-0.033	-0.373**	-0.281*	-0.121	-0.177	-0.337**
LP	-0.137	0.078	0.140	-0.362**	-0.401**	-0.357**	1	0.890**	-0.373**	0.180	0.247	0.275*	0.572**	-0.159	0.578**	0.520**
VL	-0.220	0.121	0.158	-0.474**	-0.467**	-0.164	0.860**	1	-0.488**	0.085	0.288*	0.158	0.418**	-0.097	0.529**	0.435**
DFH	0.074	-0.475**	-0.231	0.736**	0.846**	0.059	-0.327*	-0.468**	1	-0.112	-0.620**	-0.199	-0.200	-0.176	-0.324*	-0.328*
FL	0.282*	-0.322*	-0.430**	-0.023	-0.170	-0.229	0.171	0.087	-0.131	1	0.616**	0.363**	0.409**	-0.071	0.410**	0.465**
FD	-0.194	0.172	-0.148	-0.404**	-0.616**	-0.031	0.244	0.278*	-0.544**	0.591**	1	0.543**	0.550**	0.069	0.649**	0.775**
NFP	0.118	0.314*	0.007	-0.115	-0.244	-0.372**	0.270*	0.158	-0.195	0.361**	0.524**	1	0.318*	0.071	0.571**	0.766**
AFW	-0.214	0.056	-0.108	-0.228	-0.349**	-0.276*	0.558**	0.415**	-0.179	0.404**	0.544**	0.313*	1	-0.296*	0.636**	0.691**
TSS	0.044	0.068	-0.093	-0.141	-0.117	-0.121	-0.151	-0.096	-0.168	-0.066	0.061	0.075	-0.297*	1	0.062	-0.008
FYPP	-0.246	0.124	-0.006	-0.247	-0.460**	-0.173	0.558**	0.521**	-0.293*	0.400**	0.639**	0.555**	0.632**	0.048	1	0.895**
FY	-0.159	0.209	0.023	-0.305*	-0.429**	-0.333**	0.511**	0.431**	-0.301*	0.461**	0.758**	0.761**	0.684**	-0.003	0.873**	1

DG: days to germination; NNMFA: node number to first male flower anthesis; NNMFeA: node number to first female flower anthesis; DMFA: days to first male flower anthesis; DFeA: days to first female flower anthesis; PB: number of primary branches per plant; LP: number of leaves per plant; VL: vine length (cm); DFH: days to first fruit harvest; FL: fruit length (cm); FD: fruit diameter (cm); NFP: number of fruits per plant; AFW: average fruit weight (g); TSS: total soluble solids (%); FYPP: fruit yield per plot (kg); FY: fruit yield (kg ha⁻¹).

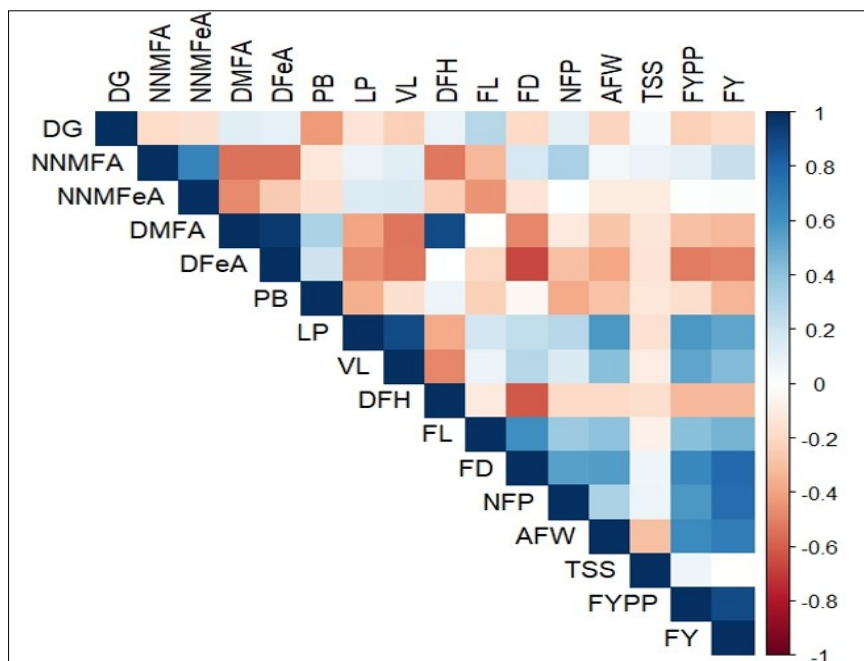


Fig. 1. Genotypic correlation corrplot for 16 traits.

germination (-0.191) and total soluble solids (-0.008) had negative, non-significant relationships.

At the phenotypic level, fruit yield per hectare also showed highly significant positive correlations with fruit yield per plot (0.873 kg), number of fruits per plant (0.761), fruit diameter (0.758 cm), average fruit weight (0.684), number of leaves per plant (0.511), fruit length (0.461 cm) and vine length (0.431 cm), confirming their importance in selection for yield (Table 4). Node number to first male flower anthesis (0.209) and node number to first female flower anthesis (0.023) were positively but non-significantly associated with yield, whereas number of primary branches per plant (-0.333) and days to first female flower anthesis (-0.429) exhibited negative and highly significant correlations and days to first male flower anthesis (-0.305) and days to first fruit harvest (-0.301) showed negative and significant associations (Fig. 2).

These findings indicate that selection for higher fruit yield per hectare can be effectively based on increasing fruit yield per plot, fruit diameter, number of fruits per plant, average fruit weight, vine length, fruit length and number of leaves per plant, while simultaneously reducing days to first male and female flowering and days to first fruit harvest. The negative association of yield with late flowering and harvest suggests that earliness is advantageous for yield in the studied environment, as discussed in earlier studies (38–40). However, correlation analysis alone does not establish causal relationships among traits; therefore, path coefficient analysis was performed to partition correlations into direct and indirect effects.

Path coefficient analysis of yield and its component traits

Genotypic and phenotypic path coefficients of different traits towards fruit yield per hectare are presented in Tables 3 and 5. At the genotypic level, the highest positive direct effect on fruit yield

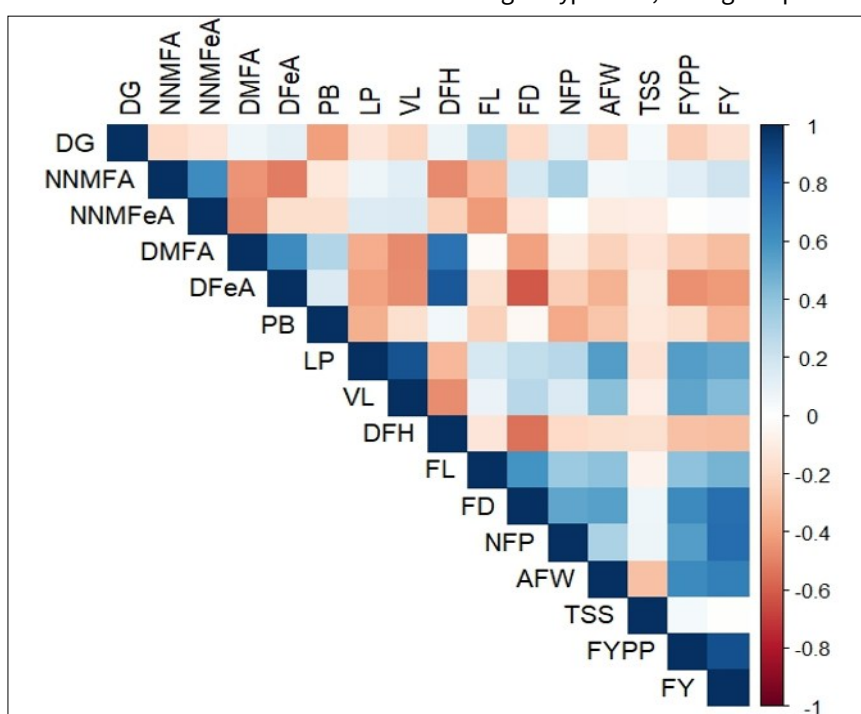


Fig. 2. Phenotypic correlation corrplot for 16 traits.

per hectare was exerted by fruit diameter (0.740 cm), followed by fruit yield per plot (0.531 kg), days to first male flower anthesis (0.344), days to first female flower anthesis (0.246), vine length (0.091 cm), node number to first male flower anthesis (0.070), node number to first female flower anthesis (0.062), number of fruits per plant (0.054) and average fruit weight (0.005 g) (Table 6). Negative direct effects were observed for number of leaves per plant (-0.010), days to germination (-0.037), total soluble solids (-0.095), days to first fruit harvest (-0.162), fruit length (-0.242) and number of primary branches per plant (-0.398).

The strong positive genotypic correlation of fruit yield per hectare with fruit diameter (0.775) was mainly due to its large positive direct effect (0.740) and substantial positive indirect effects via fruit yield per plot and number of fruits per plant, indicating that fruit diameter can be used as a reliable selection criterion. Similarly, fruit yield per plot showed a high direct effect (0.531) along with strong positive correlation (0.895) with fruit yield per hectare, suggesting that selection based on plot yield would effectively enhance yield per hectare. The positive correlations of number of fruits per plant and average fruit weight with yield were also largely explained by their direct or indirect effects through fruit diameter and fruit yield per plot.

At the phenotypic level, the pattern of direct and indirect effects was generally similar to the genotypic level, although magnitudes were slightly lower, as indicated by the relatively small residual effects at both levels, implying that the major yield-contributing traits were included in the analysis (Table 4). The high positive direct effects of fruit diameter, fruit yield per plot, number of fruits per plant and average fruit weight, together with their significant positive correlations with yield, confirm that

simultaneous improvement of these traits would be most effective for enhancing fruit yield in cucumber (25, 26). Traits with high negative direct effects, such as number of primary branches per plant, days to first fruit harvest and fruit length, should be carefully considered in selection indices to avoid undesirable indirect effects.

Genetic divergence among cucumber genotypes

Mahalanobis D^2 analysis grouped the 20 genotypes into five distinct clusters (Fig. 3, Table 5). Cluster I comprised five genotypes (Barsha Rani, WBC-1, DC-83, DC-43, Meenakshi), cluster II also contained five genotypes, cluster III had two genotypes, cluster IV five genotypes and cluster V three genotypes, indicating considerable genetic diversity among the materials. Cluster showed that cluster III recorded the highest mean values for several important characters, including fewer days to germination (6.42), higher node number to first male flower anthesis (6.66), higher node number to first female flower anthesis (11.86), greater vine length (248.13 cm), higher number of leaves per plant (44.71), more fruits per plant (12.99), greater fruit length (11.80 cm), higher total soluble solids (4.41 °Brix), higher fruit yield per plot (7.72 kg) and highest fruit yield per hectare (8022.79 kg ha⁻¹). Cluster I recorded high mean fruit diameter (2.83 cm), total soluble solids (4.46 °Brix) and fruit yield per hectare (7537.75 kg ha⁻¹), while cluster II was superior for average fruit weight (199.44 g) (Table 7).

Average intra- and inter-cluster distances are presented in Table 6. The maximum inter-cluster D^2 distance (7.268) was observed between clusters III and V, followed by clusters I and V (6.104), indicating that genotypes in these cluster pairs are highly divergent and may produce transgressive segregants when intercrossed. The minimum inter-cluster distance (3.014) occurred

Table 5. Phenotypic direct and indirect effects of different traits on fruit yield per hectare in cucumber

Traits	DG	NNMF	NNFF	DMF	DFF	PB	LP	VL	DFH	FL	FD	NFP	AFW	TSS	FYH	r(FYP)
DG	-0.0479	0.0219	-0.0113	0.0023	-0.0467	-0.1068	0.0039	-0.0253	0.0102	0.0560	0.0894	-0.0100	-0.0133	0.0068	-0.1753	-0.246
NNMF	0.0096	-0.1093	0.0487	-0.0165	0.2022	-0.0316	-0.0022	0.0140	-0.0652	-0.0640	-0.0794	-0.0266	0.0035	0.0106	0.2307	0.124
NNFF	0.0069	-0.0681	0.0782	-0.0174	0.0698	-0.0447	-0.0040	0.0182	-0.0317	-0.0853	0.0683	-0.0006	-0.0067	-0.0144	0.0250	-0.006
DMF	-0.0030	0.0488	-0.0367	0.0370	-0.2453	0.0760	0.0103	-0.0547	0.1010	-0.0045	0.1864	0.0098	-0.0142	-0.0219	-0.3361	-0.247
DFF	-0.0057	0.0566	-0.0140	0.0232	-0.3910	0.0391	0.0114	-0.0539	0.1161	-0.0339	0.2840	0.0207	-0.0217	-0.0181	-0.4732	-0.460**
PB	0.0197	0.0133	-0.0135	0.0108	-0.0589	0.2595	0.0101	-0.0189	0.0082	-0.0454	0.0142	0.0315	-0.0171	-0.0188	-0.3677	-0.173
LP	0.0065	-0.0085	0.0110	-0.0134	0.1567	-0.0927	-0.0284	0.0992	-0.0449	0.0339	-0.1124	-0.0229	0.0346	-0.0234	0.5631	0.558**
VL	0.0105	-0.0132	0.0123	-0.0175	0.1827	-0.0426	-0.0244	0.1153	-0.0642	0.0173	-0.1281	-0.0134	0.0257	-0.0149	0.4752	0.521**
DFH	-0.0036	0.0519	-0.0181	0.0272	-0.3308	0.0154	0.0093	-0.0539	0.1373	-0.0261	0.2506	0.0165	-0.0111	-0.0260	-0.3319	-0.293*
FL	-0.0135	0.0353	-0.0336	-0.0008	0.0667	-0.0593	-0.0049	0.0101	-0.0180	0.1986	-0.2725	-0.0306	0.0250	-0.0103	0.5079	0.400**
FD	0.0093	-0.0188	-0.0116	-0.0150	0.2410	-0.0080	-0.0069	0.0321	-0.0746	0.1174	-0.4609	-0.0444	0.0337	0.0095	0.8358	0.639**
NFP	-0.0057	-0.0343	0.0006	-0.0043	0.0955	-0.0966	-0.0077	0.0182	-0.0267	0.0718	-0.2415	-0.0847	0.0194	0.0117	0.8397	0.555**
AFW	0.0103	-0.0061	-0.0084	-0.0085	0.1366	-0.0716	-0.0159	0.0479	-0.0245	0.0802	-0.2509	-0.0265	0.0620	-0.0461	0.7538	0.632**
TSS	-0.0021	-0.0075	-0.0073	-0.0052	0.0457	-0.0315	0.0043	-0.0111	-0.0230	-0.0132	-0.0281	-0.0064	-0.0184	0.1550	-0.0028	0.048
FYH	0.0076	-0.0229	0.0018	-0.0113	0.1678	-0.0865	-0.0145	0.0497	-0.0413	0.0915	-0.3493	-0.0645	0.0424	-0.0004	1.1027	0.873**

DG: days to germination; NNMF: node number to first male flower anthesis; NNMFa: node number to first female flower anthesis; DMFA: days to first male flower anthesis; DFeA: days to first female flower anthesis; PB: number of primary branches per plant; LP: number of leaves per plant; VL: vine length (cm); DFH: days to first fruit harvest; FL: fruit length (cm); FD: fruit diameter (cm); NFP: number of fruits per plant; AFW: average fruit weight (g); TSS: total soluble solids (%); FYPP: fruit yield per plot (kg); FY: fruit yield (kg ha⁻¹).

Table 6. Average intra- and inter-cluster Mahalanobis D^2 distances among cucumber genotypes

Clusters	I	II	III	IV	V
I	2.759				
II	3.014	2.764			
III	4.419	4.570	2.507		
IV	4.421	4.009	4.802	2.429	
V	6.104	4.759	7.268	4.128	2.857

Table 7. Distribution of cucumber genotypes into clusters based on Mahalanobis D^2 analysis

Cluster	No. of genotypes	Genotypes
I	5	Barsha Rani, WBC-1, DC-83, DC-43, Meenakshi
II	5	WBC-38-2, WBC-39-2, Panipat Local, Kalyanpur All Green, Pohari Barshati
III	2	Stay Green-2, Pusa Barkha
IV	5	Pusa Uday, Punjab Barsati, WBC-72, Bala Patta, Beet Alfa
V	3	Poinsett, Swarna Poorna, Agro-1

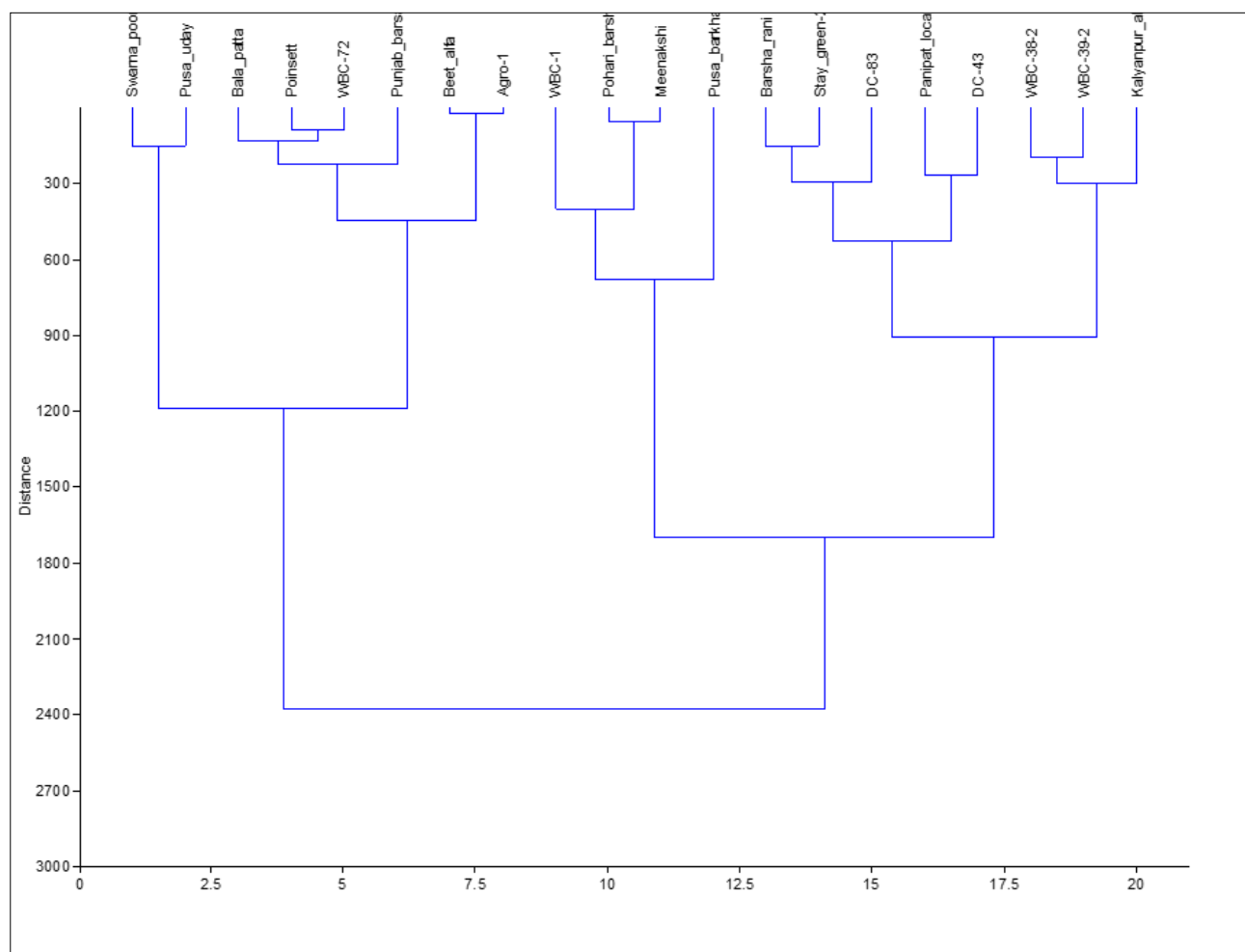


Fig. 3. Dendrogram for 20 cucumber genotypes.

between clusters I and II, suggesting close genetic relationship among genotypes of these clusters. Maximum intra-cluster distance was recorded for cluster V (2.857), followed by cluster II (2.764), cluster I (2.759) and cluster III (2.507), whereas cluster IV had the lowest intra-cluster distance (2.429), reflecting comparatively homogeneous genotypes within cluster IV.

The high inter-cluster distances involving clusters III and V and the favourable cluster means for yield and its components suggest that crosses between genotypes belonging to these clusters would be most rewarding for generating high-yielding and diverse segregants. In particular, Pusa Barkha and WBC-1, which showed superior mean performance for fruit yield and related traits and genotypes from cluster V with desirable earliness or specific attributes may be utilised as parents in hybridisation programmes. These results corroborate the importance of combining information on mean performance, variability parameters, association analysis and genetic divergence in planning effective breeding strategies in cucumber (40–42).

Conclusion

The present study revealed substantial genetic variability among the evaluated cucumber (*Cucumis sativus*) genotypes for important growth, yield and fruit quality traits. High heritability combined with high genetic advance for traits such as average fruit weight, fruit yield per hectare, vine length and number of fruits per plant suggests the predominance of additive gene effects and highlights the potential for effective phenotypic

selection. Fruit yield per hectare showed strong positive associations and high positive direct effects with fruit diameter, fruit yield per plot, number of fruits per plant, average fruit weight, vine length, fruit length and number of leaves per plant, suggesting that simultaneous improvement of these traits would be most efficient for yield enhancement. Genetic divergence analysis grouped the genotypes into five clusters with maximum inter-cluster distance between clusters III and V, indicating that crosses between highly divergent and high performing genotypes, particularly those in clusters III and V, can be exploited to develop superior high yielding varieties of cucumber. Based on the overall evaluation of the cultivars and their associated traits, Pusa Barkha and WBC-1 were identified as superior with respect to yield-contributing characters. Among the evaluated cultivars, Pusa Barkha also recorded the minimum number of days to germination, indicating early establishment. DC-43 was found to be superior, exhibiting the maximum fruit diameter and fruit length. These promising cultivars may therefore be effectively utilised in future cucumber breeding and varietal improvement programmes aimed at enhancing yield and associated traits.

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Authors' contributions

VT, SS¹, KAR and DBS carried out conceptualisation, data curation, formal analysis, writing original draft, review and editing. BS and HK carried out investigation, methodology, resources, supervision and validation. JS, Y and SS² carried out software use, supervision, validation and visualisation. All authors read and approved the final manuscript [SS¹ stands for Sudhanshu Singh and SS² stands for Supriya Singh].

Compliance with ethical standards

Conflict of interest: Authors do not have any conflict of interest to declare.

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Declaration of generative AI and AI-assisted technologies in the writing process

During the preparation of this work, the authors used QuillBot and Grammarly for grammar correction. After using QuillBot and Grammarly, the authors reviewed and edited the content as needed and take full responsibility for the content of the publication.

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