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Understanding genetic variability and traits association in cucumber utilizing diverse sex types under open field conditions

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Abstract

Gynoecious and parthenocarpic sex types in cucumber are often overlooked in studies assessing genetic variability and the interrelationships among key horticultural traits. In this study, we evaluated 16 diverse cucumber lines—representing gynoecious, parthenocarpic, predominantly gynoecious, and monoecious genotypes—to characterize genetic variation and quantify associations among 11 yield and quality related traits. Variability, correlation, and path coefficient analyses revealed moderate to high genotypic and phenotypic coefficients of variation, heritability and genetic gain for fruit yield, node number to the first female flower, fruit number per plant, ascorbic acid content, fruit length and fruit weight. Additionally, correlation and path analysis demonstrated that fruit number per plant, fruit weight, ascorbic acid content, total soluble solids, days to first fruit harvest and node number to the first female flower exerted positive and direct effects on fruit yield at both phenotypic and genotypic levels. These traits, therefore, represent key targets for direct selection to enhance yield and quality in cucumber breeding programs.

Keywords: *Cucumis sativus* L., correlation, path coefficient, heritability, genetic gain

Key findings: The study identified substantial genetic variability with moderate to high heritability and genetic gain for major yield-related traits, particularly fruit yield, fruit number per plant, fruit weight, and ascorbic acid content. Correlation and path coefficient analyses confirmed that fruit number per plant and fruit weight were the strongest direct contributors to fruit yield at both phenotypic and genotypic levels, highlighting these traits as the most effective selection criteria for genetic improvement.

1. Introduction

Cucumber (*Cucumis sativus* L.), a vegetable having high medicinal, nutritional and economic wealth, belongs to the family Cucurbitaceae with chromosomal number $2n=14$ and is thought to have originated in India, southern Asia (Papadopoulos et al. 1994). It has been cultivated for at least three millennia (Ullah et al. 2012). It is a cross-pollinated crop and exhibits a significant degree of heterosis for yield, making it an ideal candidate for hybrid breeding programs (Weiss et al 2025a). After watermelon, it is the most widely cultivated cucurbit species. Cucumbers are grown over approximately 111 thousand hectares in India, yielding production annually of 1638 thousand metric tons (NHB 2020). It is diuretic in nature and helps to remove waste from the body in the form of uric acid. It has cooling properties, which reduce the heat content of our body and it also prevents constipation (Weiss et al. 2025b). Cucumber seed oil aids in brain development as it contains a flavonol called “fisetin”; promotes body smoothness, removes dark circles and dark spots due to the presence of ascorbic acid and caffeic acid (Kumar and Peter 2020). Cucumber cultivation in India is largely done in open fields, with the majority of cultivated cultivars being monoecious and grown between the summer and rainy season. Besides, most studies on cucumber variability, association, and

path coefficient analysis of horticultural traits were conducted using monoecious lines, ignoring parthenocarpic and gynoeceious lines. Gynoeceious lines can be exploited to improve the yield character, which is the ultimate goal of any breeding programme. These lines produce only pistillate flowers at all the flowering nodes, which increases their yield. In addition, parthenocarpic gynoeceious lines yield higher yields than commercially cultivated varieties, as parthenocarpic varieties do not need pollination to form fruit sets, and every node produces female flowers. Therefore, the present research used gynoeceious, predominantly gynoeceious, and parthenocarpic lines along with monoecious lines to study the genetic variability and heritability in inbred lines.

In India, researchers use various locally collected and newly introduced germplasm to develop varieties with better combinations of traits, high yield potential, and broad adaptability. However, even with numerous germplasm accessions, their proper use in breeding programs is limited when fundamental genetic information is lacking. Effective selection requires sufficient variation in the breeding material and heritability. Firstly, genetic enhancement on a population basis, in conjunction with the implementation of suitable selection methodologies and the augmentation of genetic improvement rates, is imperative for breeding. Secondly, the enhancement of the mean genetic value within a population or the elevation of the mean phenotypic value as a consequence of selection within a population, assuming that the environmental effect remains constant, is required. Thirdly, the concept of heritability is employed. The genetic enhancement of any breeding population for yield and quality is predominantly contingent on the extent of available genetic variability. The heritability of a genetic trait plays a crucial role in determining how a population will respond to selection. The high genetic advancement and heritability create the most effective conditions for selecting specific traits. Understanding the genetic variability of the characteristics that contribute to yield and quality and the relationships between them is a prerequisite for any successful breeding program. The basic idea of studying genetic variability is determining the amount and nature of variability in the breeding population, which will help decide the successful breeding programme (Gatti et al. 2005). For this purpose, these diverse cucumber lines were evaluated for the selection of desirable characters. The genetic gain can be accurately predicted by estimating heritability with genetic advance. The ease with which traits can be passed on from parents to their progeny is often determined by heritability, while the actual gain anticipated throughout the selection process is determined by genetic gain (Ogunniyan et al. 2015). According to Johnson et al. 1955 heritability estimates would not be useful without genetic advance estimation. A high heritability means low environmental effect on observed variance (Songsri et al. 2008, Eid 2009). The genetic advance is the difference between the initial parental population and mean genotypic values of the selected plants. High genetic advance and heritability for a given character suggest that additive gene activity governs it, making it the ideal situation for selection (Tazeen et al. 2009, Shukla et al 2006).

Path coefficient and correlation analysis are also critical biometric tools successfully used to measure direct and indirect causes of association and yield association with other characters, respectively (Falconer 1981). Breeders spend less time on the selection process when they use path coefficient analysis, which offers a selection criterion (Deway and Lu 1959, Qaizar et al. 1991). Therefore, correlations and path coefficient analysis would provide a better understanding of cause and effect association among different characters and be beneficial in selecting yield traits for genetic improvement of positively associated quantitative traits (Idehen et al. 2021, Lnu et al. 2025). In India, till date, limited studies have been done on cucumber to evaluate association studies and direct and indirect effects of these associations for horticultural traits by utilizing gynoeceious, parthenocarpic, predominantly gynoeceious, and monoecious lines.

Considering these facts, the present study was conducted with the aim of understanding the variability among genotypes and to find out the path coefficient and correlation between various traits contributing to yield and quality so that breeding programmes can be successfully planned.

2. Materials and methods

2.1. Experimental location and climate conditions

The present research was performed at Punjab Agricultural University, Ludhiana, from 2020 to 21. Ludhiana has a subtropical climate at 30°54' N latitude, 75°48' E longitude, and 247 m above sea level. Winters (mid-December to mid-February) are chilly with occasional frost, while summers (April to June) are hot with dry breezes. Rainfall in the area averages 700 mm per year, mainly during the July-mid-September monsoon season.

2.2. Plant material

The materials used in the experiment included 16 diverse parents, including gynoeceious, predominantly gynoeceious, parthenocarpic and monoecious. Table 1 describes the parental lines used in the study. The parental lines viz. AVCU-1303, AVCU-1205, AVCU-1302, AVCU-1202, AVCU-1203, AVCU-1206 were procured from the AVRDC-The World Vegetable Center, Taiwan by following the import procedure. The variety “Pusa Uday” was developed by ICAR- Indian Agricultural Research Institute, New Delhi, India and the seeds of this variety were collected from IARI, New Delhi. The lines of PAU viz. Punjab Naveen, PBRK-11, Punjab Kheera-1, CMVR-1, PMC-1 and 25-16 VNR were developed by single plant selection from segregating material. The lines Swarna Ageti and Swarna Sheetal were collected from Horticulture and Agro-Forestry Research Programme, Ranchi, India. The gynoeceious line “GY-14” was collected from the University of Wisconsin, USA.

Table 1. List of parental lines with salient characteristics

Plant material	Sex type	Suitable for cultivation	Fruit types	Source
Lines				
25-16-VNR	Predominately gynoeceious	Open field conditions only	Picking type	PAU
Punjab Kheera-1 (PK-1)	Parthenocarpic and Gynoeceious	Poly-net house only	Beit alpha type and seedless.	PAU
PBRK- 11	Parthenocarpic and Predominately gynoeceious	Both poly-net and open field	Slicing type and seedless.	PAU
GY-14	Gynoeceious	Open field conditions only	Picking type	UW
AVCU-1303	Gynoeceious	Open field conditions only	Picking type	AVRDC
Testers				
Punjab Naveen	Monoecious	Open field conditions only	Picking type	PAU
PMC-1	Monoecious	Open field conditions only	Slicing type	PAU
AVCU-1205	Monoecious	Open field conditions only	Picking type	AVRDC
AVCU-1203	Monoecious	Open field conditions only	Picking type	AVRDC
AVCU-1202	Monoecious	Open field conditions only	Picking type	AVRDC
AVCU-1206	Monoecious	Open field conditions only	Picking type	AVRDC
AVCU-1302	Monoecious	Open field conditions only	Picking type	AVRDC
Swarna Sheetal	Monoecious	Open field conditions only	Slicing type	HARP
Swarna Ageti	Monoecious	Open field conditions only	Slicing type	HARP
CMVR-1	Monoecious	Open field conditions only	Picking type	PAU
Pusa Uday	Monoecious	Open field conditions only	Slicing type	IARI

2.3. Experimental method

Parental line seeds were planted in pro-trays during 1st week of January 2021. The pro-trays were covered with a polythene sheet to prevent frost damage to the seedlings. Later, these seedlings were transplanted on raised beds that were 1.5 meters wide and planted 30 cm apart on one side of the raised bed. Silver-black plastic mulch was used to cover the beds for weed control. At sowing, 40 kg of N, 20 kg of P₂O₅, and 20 kg of K₂O per acre were placed 15 cm from the bed mark (Anonymous 2022). After transplanting, irrigation was given right away, and thereafter, it was applied every three to five days depending on the temperature. One month after transplanting, 20 kg N per acre was used in furrows on the side where seedling was transplanted, and then the soil was turned over the beds.

Three replications of the experiment, each with ten plants, were carried out using Randomised Complete Block Design (RCBD). Data was collected from randomly selected five plants per replication.

2.4. Observation Recording

The observations were taken from five plants per plot and mean was estimated regarding fruit diameter (measured by Vernier calliper), fruit length (measured by scale), fruit weight (measured by weighing balance), fruit yield per plant, number of fruits per plant, days to first fruit picking, node at which first female flower appears and quality traits viz. TSS (measured by digital refractometer), flesh to seed cavity ratio, water content and ascorbic acid. The formula for calculating the flesh-to-seed cavity (F/C) = $(P \times E) / (P' \times E')$, where P and E stand for the fruit's polar and equatorial diameters and P' and E' for the fruit cavity. Using the formula Ascorbic acid = $(V \times S \times D \times 100) / (W \times A)$, where V is the volume of dye used, S is the dye standardisation, D is dye factor, W is weight of sample, and A is aliquot taken, the ascorbic acid concentration was then determined as mg/100g fresh weight. The water content (%) was computed using formula: Water content (%) = $[(\text{Fresh weight} - \text{Dry weight}) / \text{Fresh weight}] \times 100$.

2.5. Statistical analysis

The variation which occurs between the individuals of a population is commonly expressed in terms of variance. The phenotypic variance represents the overall variation observed in a genotype and is equivalent to the sum of variance stemming from genetic factors, environmental influences and the interactions between genotype and environment. The traits which showed genotypic variation significantly were obtained from the Mean Squares as below:

$$\sigma^2 g = \frac{Mg - Me}{r}$$

$$\sigma^2 p = \sigma^2 g + \sigma^2 e$$

where,

$\sigma^2 g$ = Genotypic Variance; $\sigma^2 p$ = Phenotypic Variance; $\sigma^2 e$ = Environmental Variance

Coefficient of Variation, CV (%) = $\frac{\sigma}{\bar{x}} \times 100$

Where,

σ = Standard deviation

$\bar{x}$ = Grand mean

The coefficients of variation for genotype, phenotype, and environment were determined employing the method of Burton and De Vane (1953), following the details provided below:

Genotypic coefficient of variation (GCV)% = $\sigma p / \bar{x} \times 100$

Phenotypic coefficient of variation (PCV)% = $\sigma g / \bar{x} \times 100$

Environmental coefficient of variation (ECV)% = $\sigma e / \bar{x} \times 100$

Where,

σ_g = Genotypic standard deviation

σ_p = Phenotypic standard deviation

σ_e = Environment standard deviation

$\bar{x}$ = Grand mean

The range of PCV and GCV was classified as high (>30%), moderate (15-30%) and low (<15%). Broad sense heritability is defined as the proportion of genotypic variance to overall phenotypic variance, and it was computed using the formula provided by Burton and De Vane (1953) and Johnson *et al* (1955).

$$\text{Heritability} = \frac{\sigma_g^2}{\sigma_p^2}$$

Where,

$$\begin{aligned}\sigma_g^2 &= \text{Genotypic variance;} \\ \sigma_p^2 &= \text{Phenotypic variance}\end{aligned}$$

Heritability serves as a strong measure of how traits are passed down from parents to their offspring. The range of heritability (H) was categorised as high (>80%), moderate (50-80%) and low (<50%) (Lnu et al 2025).

Genetic advance, also known as genetic gain, refers to the difference between the average genotypic values of selected lines and the average genotypic values of the parent populations. The effectiveness of genetic advance relies on three key factors: the amount of genetic variability in the base population, the heritability of the trait being assessed, and the intensity of selection. The expected genetic advance (GA) achieved through selecting 5% of the most superior individuals was computed according to the methods outlined by Burton and De Vane 1953 and Johnson et al. 1955.

$$GA = k \cdot \sigma_p \cdot H^2$$

Where,

$$\begin{aligned}k &= 2.06 \text{ (selection differential at 5\% selection index)} \\ \sigma_p &= \text{Phenotypic standard deviation} \\ H^2 &= \text{Heritability (broad sense)}\end{aligned}$$

$$\text{Genetic advance as percent of mean} = \frac{GA}{\text{Grand mean}} \times 100$$

The range of genetic gain over mean percent was categorised as high (>50%), moderate (25-50%) and low (<25%) as proposed by Sharma 1994.

Genotypic and phenotypic correlations were calculated based on the analysis of variance and covariance for all observations (Al-Jibouri et al. 1958).

$$\text{Phenotypic Correlation coefficient } (rp_{12}) = \frac{\sigma_{p12}}{\sqrt{\sigma^2_{p1} \times \sigma^2_{p2}}}$$

where,

$$\begin{aligned}\sigma_{p12} &= \text{Phenotypic Covariance between the observations, } X_1 \text{ and } X_2 \\ \sigma^2_{p1} &= \text{Phenotypic Variance of observation } X_1 \\ \sigma^2_{p2} &= \text{Phenotypic Variance of observation } X_2\end{aligned}$$

$$\text{Genotypic Correlation coefficient } (rg_{12}) = \frac{\sigma_{g12}}{\sqrt{\sigma^2_{g1} \times \sigma^2_{g2}}}$$

where,

$$\begin{aligned}\sigma_{g12} &= \text{Genotypic Covariance between the observations, } X_1 \text{ and } X_2 \\ \sigma^2_{g1} &= \text{Genotypic Variance of observation } X_1 \\ \sigma^2_{g2} &= \text{Genotypic Variance of observation } X_2\end{aligned}$$

To evaluate the significance level, the genotypic correlation coefficient was assessed using the 'r' value at n-2 degrees of freedom (Fisher and Yates 1963), with 'n' representing the total number of genotypes and 'r' indicating the number of replications.

The VIF, tolerance values with multi-collinearity interpretation was done by using R software. The path co-efficient analysis was conducted as suggested by Dewey and Lu 1959. The analysis was carried out using computer software programme Windostat Version 9.3.

3. Results

3.1. Variability

The extent of variability in terms of phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability (broad sense), and genetic gain as mean % are depicted in Table 2.

3.1 Phenotypic coefficient of variation (%) and Genotypic coefficient of variation (%)

The phenotypic coefficient of variation of different characters varied from 0.66 to 31.58% (Table 2). A high magnitude of phenotypic coefficient of variation was recorded for fruit yield (31.58%). The moderate level of phenotypic coefficient of variation was recorded for node number of first female flower (29.51%), fruit number per plant (23.21%), ascorbic acid (23.05%), fruit weight (17.40%), and fruit length (15.38%). The low level of PCV was found for TSS (14.79%), flesh to seed cavity ratio (11.32%), fruit diameter (7.14%), days to first fruit picking (5.78%), and water content (0.66%).

While genotypic coefficient of variation ranges from 30.70 to 0.56% (Table 2). The high value of the GCV was recorded for fruit yield (30.70%). The moderate level of GCV was observed for node number of first female flower (28.64%), ascorbic acid (22.98%), fruit number per plant (22.13%), fruit weight (16.57%), and fruit length (15.13%). The low level of GCV was observed for TSS (14.43%), flesh to seed cavity ratio (11.27%), fruit diameter (6.96%), days to first fruit picking (5.28%), and water content (0.56%).

3.2. Heritability

Heritability (broad sense) of different characters ranged from 0.35 to 99.44% (Table 2). High heritability was found for ascorbic acid (99.44%) followed by flesh to seed cavity ratio (99.09%), fruit length (96.71%), total soluble solids (95.19%), fruit diameter (95.08%), fruit yield (94.52%), node number of first female flower (94.17%), number of fruits per plant (90.90%), fruit weight (90.68%) and days to first fruit picking (83.34). A moderate heritability value was found for water content (72.23%).

3.3. Genetic gain

The genetic gain of different characters varied from 0.98 to 61.48% (Table 2). Higher gene gain was found for fruit yield (61.48%) and node number of the first female flower (57.26%). The moderate level of genetic gain was observed for ascorbic acid (47.21%), fruit number per plant (43.47%), fruit weight (32.51%), fruit length (30.64%), and total soluble solids (28.99%). The lower value of genetic gain was found for flesh to seed cavity ratio (23.11%), fruit diameter (13.98%), days to first fruit picking (9.92%), and water content (0.98%).

Table 2. Components of variance, heritability (broad sense), and genetic advance of yield and quality traits

Trait	Mean	CV	GCV	PCV	H ² (b.s.)	GA	GA (as % mean)
Fruit yield	1.40	7.39	30.70	31.58	94.52	0.86	61.48
Fruit number per plant	8.77	7.00	22.13	23.21	90.90	3.81	43.47
Fruit weight	176.90	5.31	16.57	17.40	90.68	57.50	32.51
Fruit length	15.24	2.79	15.13	15.38	96.71	4.67	30.64
Fruit diameter	4.47	1.58	6.96	7.14	95.08	0.62	13.98
Node number of first female flower	3.64	7.13	28.64	29.51	94.17	2.08	57.26
Days to first fruit picking	52.11	2.36	5.28	5.78	83.34	5.17	9.92
Total soluble solids	3.21	3.24	14.43	14.79	95.19	0.93	28.99
Flesh to seed cavity ratio	1.76	1.08	11.27	11.32	99.09	0.41	23.11
Water content	97.18	0.35	0.56	0.66	72.23	0.95	0.98
Ascorbic acid	3.21	1.72	22.98	23.05	99.44	1.52	47.21

CV= Coefficient of variation, PCV= Phenotypic coefficient of variation; GCV= Genotypic coefficient of variation (GCV), H^2 (b.s) = heritability (broad sense); GA= Genetic advance; GA (as% mean) = Genetic advance as mean percentage

3.4. Correlation studies

The correlation matrices among various traits were calculated at genotypic and phenotypic level, as shown in Figures 1 and 2. In most cases, genotypic correlation coefficient values were higher than their corresponding phenotypic correlation coefficient values, indicating that genotypic correlations were more accurate and unaffected by environmental factors.

The correlation study revealed that fruit yield had significantly higher and positive correlation with number of fruits per plant, fruit weight, fruit length, node number of first female flower, days to first fruit picking, TSS, and ascorbic acid at both phenotypic and genotypic levels. As a result, selection based on these traits has the potential to increase yield. However, fruit yield was negatively correlated with flesh to seed cavity ratio and water content at both genotypic and phenotypic level and there is no need to go for selection of these traits for yield improvement. Fruit diameter showed a positive but insignificant correlation with yield; therefore, these cannot be considered yield-determining traits.

Fruit number per plant had a positive and significant correlation with fruit length, node number of first female flower, and days to first fruit picking at genotypic and phenotypic level both. Significant positive correlation was also observed for fruit weight with fruit length, fruit diameter, TSS, flesh to seed cavity ratio, and ascorbic acid. Fruit length had a significant and positive association with fruit diameter, days to first fruit picking, TSS, and ascorbic acid. There was significant and negative correlation of fruit diameter with days to first fruit picking both at phenotypic and genotypic level. The significant and positive correlation of node number of first female flower was observed with days to first fruit picking highlighting the importance of these traits for identifying early maturing genotypes while negative and significant association with flesh to seed cavity ratio and water content. Flesh to seed cavity ratio had a positive and significant correlation with ascorbic while a significant and negative association with water content both at genotypic and phenotypic level.

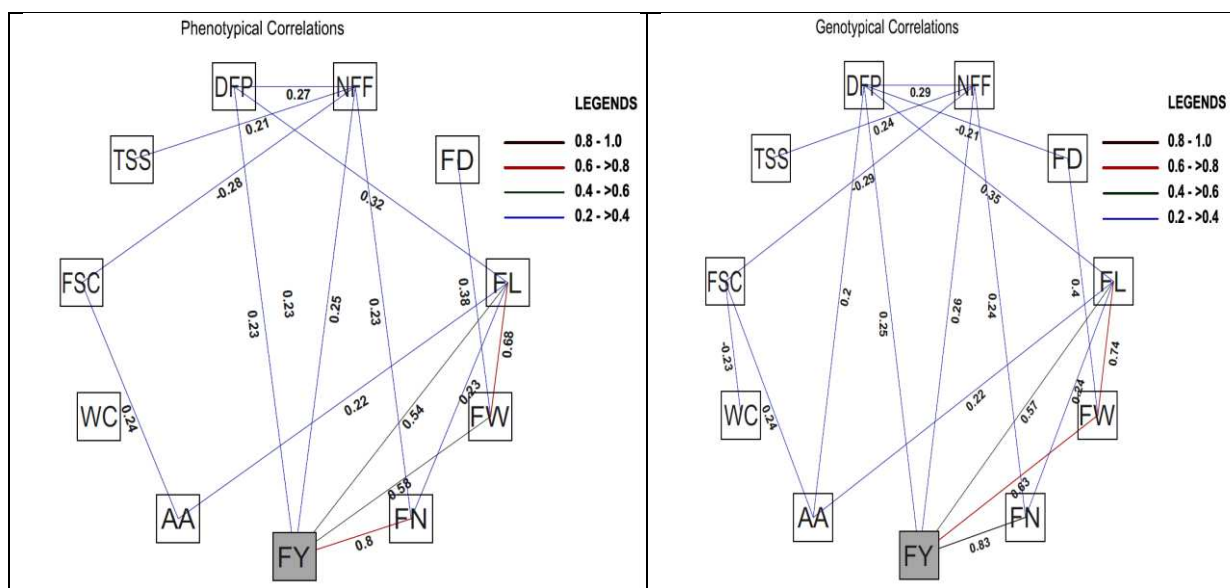


Fig 1. Phenotypic and Genotypic correlation among 11 different yield and quality traits (FY: Fruit yield per plant, FW: Fruit weight, FN: Number of fruits per plant, FL: Fruit length, FD: Fruit diameter, NFF: Node at which first female flower appears, DFP: Days to first fruit picking and quality traits viz. TSS: Total soluble solids, FSC: Flesh to seed cavity ratio, WC: Water content, and AA: Ascorbic acid)

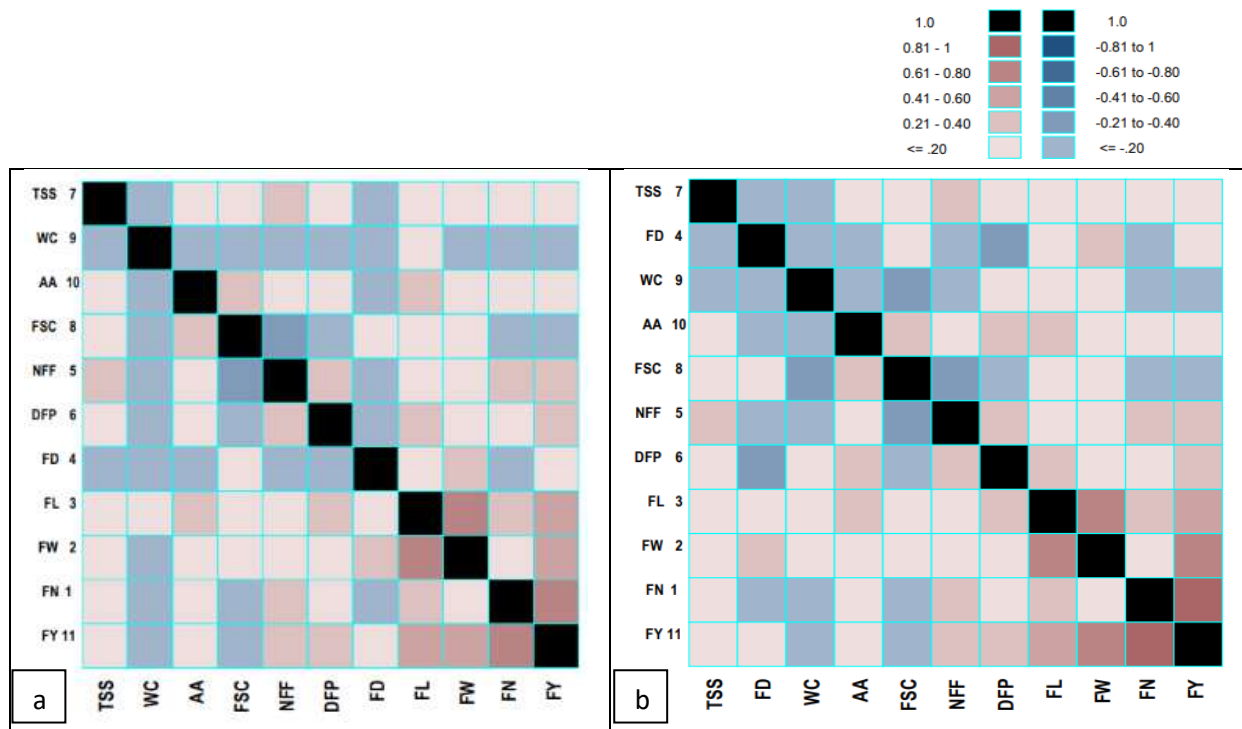


Fig 2. Correlation diagram among 11 yield and quality traits in cucumber (a) Shaded phenotypic correlation matrix (b) Shaded genotypic correlation matrix. (FY: Fruit yield per plant, FW: Fruit weight, FN: Number of fruits per plant, FL: Fruit length, FD: Fruit diameter, NFF: Node at which first female flower appears, DFP: Days to first fruit picking, and quality traits viz. TSS: Total soluble solids, FSC: Flesh to seed cavity ratio, WC: Water content, and AA: Ascorbic acid)

3.5. Path Coefficient Analysis

Prior to path coefficient analysis, multi-collinearity among the predictor traits was assessed using the variance inflation factor (VIF) and tolerance statistics. All predictor traits exhibited VIF values below 5.0 and tolerance values above 0.20, indicating that severe multi-collinearity was not present among the traits included in the path analysis (Table 3). Therefore, the path coefficients could be interpreted without substantial concern regarding inflated variance caused by multi-collinearity.

Table 3. VIF, tolerance values with multi-collinearity interpretation

Variable	R_squared	VIF	Tolerance	Interpretation
Fruit yield	0.883823	8.607522	0.116177	Moderate multi-collinearity
Fruit number per plant	0.815504	5.420183	0.184496	Moderate multi-collinearity
Fruit weight	0.753301	4.053516	0.246699	No serious multi-collinearity
Fruit length	0.559591	2.270617	0.440409	No serious multi-collinearity
Node number of first female flower	0.253426	1.339452	0.746574	No serious multi-collinearity
Flesh to seed cavity ratio	0.232766	1.303384	0.767234	No serious multi-collinearity
Fruit diameter	0.228983	1.296987	0.771017	No serious multi-collinearity
Days to first fruit picking	0.227851	1.295087	0.772149	No serious multi-collinearity
Ascorbic acid	0.146554	1.171721	0.853446	No serious multi-collinearity
Water content	0.093742	1.103438	0.906258	No serious multi-collinearity
TSS	0.085871	1.093937	0.914129	No serious multi-collinearity

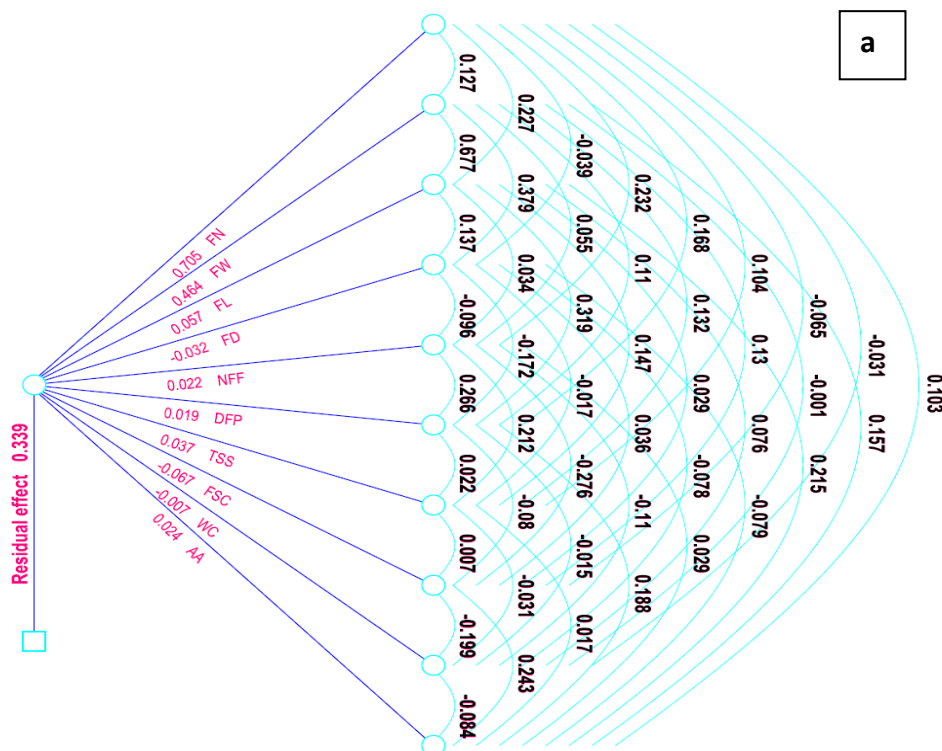
The estimates of path coefficient analysis at both genotypic and phenotypic levels, showing direct and indirect effects of traits on yield has been provided in Figure 3. The fruit yield was considered a

dependent variable which depends on the independent variable, viz., number of fruits per plant, fruit length, fruit diameter, fruit weight, node at which first female flower appears, days to first fruit picking, flesh to seed cavity ratio, water content, TSS, and ascorbic acid.

The path coefficient analysis at phenotypic level indicated that number of fruits per plant (0.706), fruit weight (0.464), fruit length (0.057), TSS (0.037), ascorbic acid (0.024), node number of first female flower (0.022), days to first fruit picking (0.019) had direct and positive effect on fruit yield. Among all characters, the number of fruits per plant, fruit weight, and fruit length showed the higher positive impact on fruit yield. However, fruit diameter, water content, and flesh-to-seed cavity ratio negatively affected yield.

Similarly, path coefficient analysis at the genotypic level showed that the number of fruits per plant (0.737), fruit weight (0.585), days to first fruit picking (0.034), ascorbic acid (0.018), TSS (0.022), and node number of first female flower (0.002) had direct positive effects on yield. Fruit length, diameter, water content, and flesh-to-seed cavity ratio showed a negative and direct effect.

The residual effect in path coefficient analysis measures the influence of other independent factors on the dependent variable that was excluded from the research. In the current study, residual effects at the genotypic level were only 0.186 and 0.339 at the phenotypic level. This suggests that most potential yield-influencing variables were included in the survey to support the goal, but some proportions still need to be included to obtain more conclusive results.



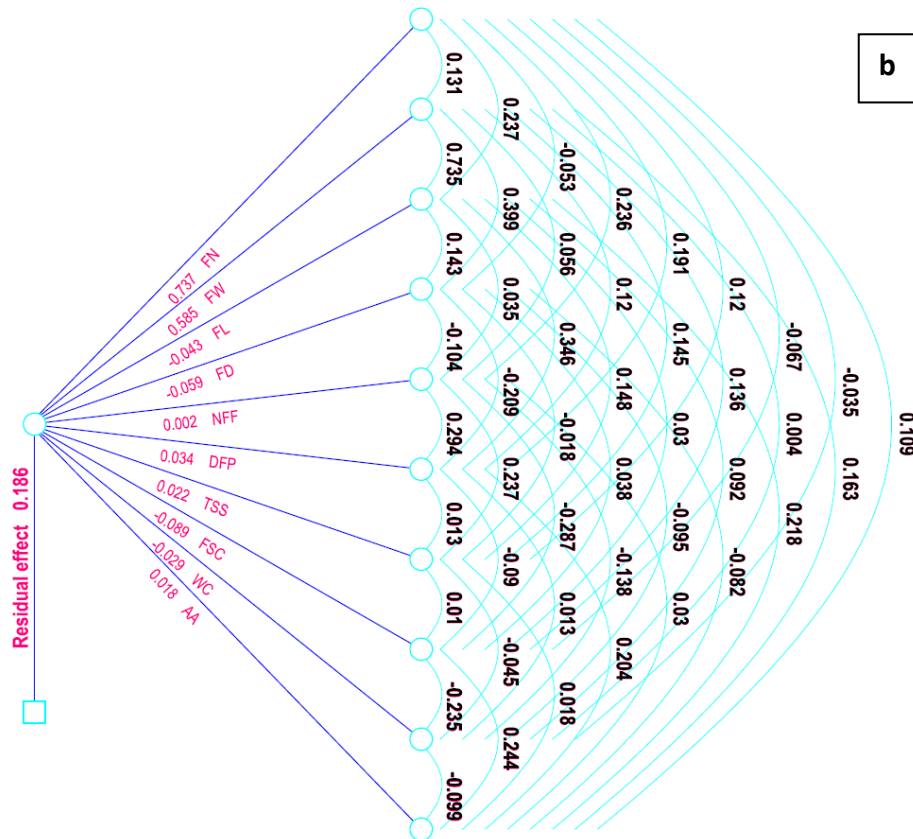


Fig. 3 Path coefficient diagram presenting direct and indirect effect on fruit yield (a) Phenotypic path diagram for yield (b) Genotypic path diagram for yield; Phenotypic Residual effect (P): 0.339; Genotypic Residual effect (G): 0.186; (FY: Fruit yield per plant, FW: Fruit weight, FN: Number of fruits per plant, FL: Fruit length, FD: Fruit diameter, NFF: Node at which first female flower appears, DFP: Days to first fruit picking and quality traits viz. TSS: Total soluble solids, FSC: Flesh to seed cavity ratio, WC: Water content, and AA: Ascorbic acid)

4. Discussion

4.1. Phenotypic and genotypic coefficient of variation

In any crop, genetic variability is a crucial component of selection. Genetic variance and environment effects cannot be accurately determined solely from phenotypic variability, and mean variance based on phenotypic expression provides a rudimentary picture of the genotypic variability. Thus, phenotypic variation is separated into environmental and heritable components. The genotypic and phenotypic coefficient of variation can be used to study the nature of variability. In the present study, the phenotypic variation coefficient was more significant than the genotypic variation coefficient for all of the traits studied, signifying that the environment considerably influences the expression of these features (Shah et al. 2018, Dhall et al. 2023, Gruda et al 2025). Higher PCV and GCV suggest the presence of high genetic variability among traits, while those showing lower GCV and PCV indicate limited genetic variation among the characters. Several breeding methods can improve the traits showing high PCV and GCV. Our study showed high to moderate GCV and PCV for fruit yield, node number of first female flower, fruit number per plant, ascorbic acid, fruit weight, and length. Kaur et al. 2024 also reported high PCV and GCV for yield and the node at which the first female flower appears. Kumari et al. 2024 obtained similar results and found high PCV and GCV for TSS, number of fruits per plant, fruit length and the node number at which the first female flower appears. Dhall et al. 2023 and Pushpalatha et al. 2016 observed high PCV and GCV for fruit yield, length,

number of fruits per plant, and weight. Kandasamy 2017 and Bhagwat et al. 2018 observed high GCV and PCV for number of fruits per plant and fruit yield.

4.2. Heritability and Genetic Gain

Heritability refers to the precision with which a genotype may be identified based on its phenotypic performance. Heritability information alone may not be helpful for a selection of characters, but heritability analysis combined with genetic advance is more reliable (Johnson et al 1955). The present study reported high to moderate genetic gain over mean and high heritability in traits like fruit yield, node number of first female flower, ascorbic acid, fruit number, fruit weight, fruit length, and total soluble solids. So, for these traits, selection is easy and reliable. Similarly, high heritability and genetic gain for above characteristics were observed by Shah et al. 2018, Singathiya et al. 2025, Kandasamy 2017, Pradhan et al. 2018, Tripathi et al. 2021, Chaudhary et al. 2015 and Veena et al. 2013. At the same time, low genetic advance and heritability showed that these attributes are inherited through non-additive gene action and improvement from this simple selection may not yield desirable results due to the genotype's small range of phenotypic variation. However, these traits could be improved through recombinant breeding.

4.3. Correlation studies

The correlation coefficient is a statistical metric that determines degree of positive or negative link between various plant traits, assisting in finding character from which selection can be done for crop improvement. Breeders used correlation coefficient studies to find a strong link between fruit yield and other traits that increase production. In cucumber crop improvement, knowledge of degree of association between fruit yield and yield contributing traits is of great importance because many genes control the fruit yield, have low heritability, and are influenced by the environment, which makes it challenging to improve. Selecting yield directly is less effective than selecting traits that contribute indirectly to yield. So, to improve yield, other contributing traits were selected, which have high heritability and good correlation with yield. The correlation between a specific trait and yield is caused by direct effect of that trait and the indirect effects of other characteristics. The correlation study between plant traits is critical for plant breeders because it measures the degree of association between fruit yield and other yield-contributing variables. This will help indirectly select genotypes for increasing yield (Machikowa & Laosuwan 2011). The presence of a genuine relationship is revealed by genotypic correlation, not by phenotypic correlation, as they are affected by environmental factors. Significant phenotypic association is useless without significant genotypic correlation. Significant genotypic correlation with non-significant phenotypic association revealed the presence of accurate correlation, but ecological factors mask it. Our correlation study showed that fruit yield per plant had a highly significant and positive correlation with the number of fruits per plant, fruit weight, fruit length, node number of the first female flower, days to first fruit picking, TSS, and ascorbic acid. Thapliyal et al. 2023 observed that the fruit weight and number of fruits per plant positively and significantly correlated with fruit yield. Similar results align with the research conducted by Dhall 2019, Dhall 2021, Golabadi et al. 2013, Dhall et al. 2024, Kumar et al. 2011, Kaur et al. 2023, Nandi et al. 2019, Rao et al. 2004 and Prasad and Singh 1992 who found significantly positive correlation between fruit yield and characteristics like fruit length, diameter, weight and fruits number. Days to first fruit picking and node number at which first female flower appears showed positive correlation with fruit yield, indicating higher yield in early maturing varieties. In contrast, late-maturing varieties showed lower yield. This suggests that choosing such traits will boost fruit yield. Verma 2003 observed significantly positive correlation between days to first female flower anthesis and days to first fruit picking at genotypic and phenotypic level.

4.4. Path coefficient analysis

No doubt, correlation does not give a clear picture of the extent and nature of the contribution by several independent variables. Selecting characters which have direct and indirect effect on fruit yield may be helped by the path coefficient study, which divides correlation into direct and indirect effects. Therefore, the study of phenotypic and genotypic correlation and path coefficient would be beneficial for formulating breeding methods that aim for development of elite genotypes through selection in the advanced generations. If the relationship between fruit yield and trait is due to the

trait's direct effect, then direct selection of that trait can be done for crop improvement. At the same time, the indirect impact of the character suggests that indirect selection will improve yield (Veena et al. 2013).

It was interpreted that the number of fruits, fruit weight, TSS, ascorbic acid, node number at which the first female flower appears, and days to first fruit picking positively and directly impacted yield at phenotypic and genotypic level. Hence, selecting these traits can be beneficial for improving yield. Similar results for path coefficient were obtained in cucumber by Kumar et al. [45], Keshari et al. 2020, Sharma et al. 2018 and Lnu et al. 2025 for fruit diameter, fruit length, fruit weight, and fruit number, which had positive phenotypic and genotypic effects on fruit yield. The inclusion of diverse sex types provides new insights for improving yield particularly through the use of parthenocarpic and gynoeocious lines extending beyond findings from previous variability and correlation studies using monoecious lines. However, this study was conducted at a single location and within one growing season, which may limit the generalizability of the findings across diverse environmental conditions. Genotype $\times$ environment interactions are known to influence trait expression in cucumber; therefore, the results presented here should be interpreted as environment-specific rather than universally applicable.

5. Conclusions

This study found a notable variation in cucumber genetic materials. The fruit yield, node number of first female flower, number of fruits, ascorbic acid, fruit weight, and fruit length showed high to moderate GCV and PCV, highlighting the existence of higher variability and helpful for crop improvement through selection. The high to moderate value of heritability and genetic gain was found in fruit yield, number of fruits per plant, fruit weight, fruit length, node number of first female flower, ascorbic acid and total soluble solids signifying additive gene action importance for inheritance of these characters and phenotypic selection can be done for improvement. The number of fruits, fruit weight, TSS, ascorbic acid, node number of first female flower, and days to first fruit picking all exhibited positive and direct effect on fruit yield at genotypic and phenotypic level, as per correlation and path correlation study. Thus, it can be concluded that crop improvement in cucumber can be achieved by directly selecting these traits. However, broader application in breeding programs requires validation across multiple environments and growing seasons.

Declarations

Author contributions: Conceptualization, P.K, R.K.D.; methodology, P.K., R.K.D.; validation, P.K., R.K.D.; data recording, P.K., P.Sin.; formal analysis, P.K., P.Sin., G.K.; software, P.K., P.Sam.; investigation, R.K.D.; resources, R.K.D.; writing—original draft preparation, P.K.; writing—review and editing, R.K.D.; visualization, P.K, R.K.D.; supervision, R.K.D.; project administration, R.K.D.

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Dual publication: The results, data and figures presented in this manuscript have not been published before and are not being submitted to any other journal.

Ethics and consent to participate

This research did not involve human or animal subjects, and any sensitive personal data. The germplasm used in the present study were developed/maintained by the breeder (Dr. Rajinder Kumar Dhall) at Punjab Agricultural University, Ludhiana, Punjab, India. All the guidelines were followed as per the University research ethics for development, characterisation and documentation of germplasm accessions. The proper breeding procedure was followed during field experiments and its details were

mentioned in material and methods section. Punjab Agricultural University, Ludhiana, Punjab, India has been established in 1962 by an act of legislature and is the custodian of crop biodiversity. As a faculty member of the University and Principal Olericulturist at Vegetable Science department, Corresponding author (RKD) is fully authorised to develop, conserve and characterise the germplasm for breeding improved varieties. All the authors have read and approved the manuscript and all the authors are aware of its submission to the Journal.

Permissions to collect the seeds: The appropriate permissions for collection of seeds have been taken for import of germplasm using country guidelines.

Source of the seeds used in your study: The full names of the sources of each of the germplasm/seeds used in your study have been mentioned in the material and method section.

Consent to Publish: The authors declare that no individual data or image of other publication has been used in the manuscript. Therefore, there is no need to take consent for publication.

Declaration by the corresponding author: The corresponding author confirms having read and accepted the editorial policies of Discover Agriculture and submits this manuscript in accordance with these policies. The present study does not use any clinical trials

Authorization to use third-party material: All figures and tables included in this manuscript were created by the author and have not been published elsewhere. No third-party material has been used.

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