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Original Research Paper

Exploring the genetic variability, heritability, gene action for yield related traits and ToLCNDV resistance on F_3 and F_4 generations in cucumber [*Cucumis sativus* L.]

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ABSTRACT

Cucumber is traditionally cultivated in India and is recognized as a primary centre of origin, belonging to the gourd family, Cucurbitaceae. The study focused on assessing genetic variability in F_3 and F_4 cucumber populations and examining correlations among various characters including ToLCNDV resistance. In both F_3 and F_4 generations, per cent disease index, fruit weight and vine length exhibited high heritability and genetic advance as per cent of mean. In F_4 generation, yield per plant, fruit girth, fruit length, number of branches and number of fruits per plant also showed high heritability and genetic advance as per cent of mean. Yield related traits *viz.*, sex ratio, number of fruits per vine, yield per plant and vine length exhibited complementary gene action. Days to first harvest and crop duration demonstrated negatively skewed distribution suggesting duplicate gene action and rapid genetic gain under selection. Leptokurtic distribution in yield per plant and associated traits implied the involvement of few genes for genetic inheritance of the above traits. Significant positive associations were found between yield per plant and number of fruits per plant, fruit weight and number of branches per plant suggesting potential early selection for these characters to enhance overall yield.

Keywords: Gene action, heritability, kurtosis, skewness, variability

INTRODUCTION

Cucumber (2n=2x=14) is an important vine crop belonging to the family Cucurbitaceae, with wide spread commercial cultivation across the country. Cucumber originated in India, adapted and thrived well over various continents (Gotz et al., 2022). It ranks as the third most frequently grown fruit vegetable crop globally. Cucumber holds a prominent position among cultivated vegetable crop followed by tomato and onion. The global production of cucumber exceeded 94 million MT during 2022. This crop is widely recognized as a premium vegetable for fresh consumption on a global scale, also it is valued for its abundant supply of vitamins, minerals, antioxidants, low-calorie food offering excellent hydration with 90% water as the main composition.

In general, genetic variability arises from genetic differences generated through gene recombination. It is crucial in identifying superior genotypes for rapid advancements in yield and related traits. Genotypic and phenotypic coefficient of variation reveal the nature of variability in the breeding population, while heritability estimates the transmission magnitude of traits from parents to progenies. Correlation coefficients assess the proportion of relationships. Genetic advance and heritability help to determine the environmental effects on characters and the extent to which improvement is feasible after selection (Sultana et al., 2015). Therefore, research was aimed to explore the genetic variability, examine correlations among various traits including ToLCNDV resistance in F_3 and F_4 populations of cucumber.

MATERIALS AND METHODS

The field experiment was conducted at the college orchard, Department of Vegetable Science, Tamil Nadu Agricultural University, Coimbatore 641003, Tamil Nadu during February-March 2023 (F_3 population) and July-August 2023 (F_4 population). The F_3 and F_4 cucumber populations were derived from the parental cross combination of DC 70 (R) x

Table 1 : Characteristics of parent cucumber genotypes used in the current study

Genotype	Source	Fruit Colour	Salient Features
DC-70	IARI, New Delhi	Light green	Monoecious, resistant to LCD and downy mildew, fruits 13-16 cm long, black spine. Resistant to ToLCNDV.
DC-773	IARI, New Delhi	Dark green	Monoecious, fruits 40-43 cm long, white spine and susceptible to ToLCNDV.

DC 773 (S) (Table 1). Thirteen parameters observed on each individual plant were recorded for quantitative characters related to yield and yield associated traits. The research work consisted 85 progenies and their parents for each population. Phenotypic and genotypic coefficient of variation were assessed as suggested by Butron & Devane (1953). Heritability was determined as per Singh & Chaudhary (1985) and genetic advance as per cent of mean was estimated as per Johnson et al. (1995).

Disease scoring

Symptom assessment on progenies resulting from the cross DC 70 x DC 773 (Table 1), evaluating their susceptibility to ToLCNDV disease on 45 days after planting under natural condition. The scoring relied on visual observation using a standardized phenotypic scale as per Lopez et al. (2015). The per cent disease index (PDI) of ToLCNDV, following formula outlined by Saez et al. (2021).

$$\text{Per cent disease index} = \frac{\text{Sum of all numerical ratings}}{\text{Total number of plants observed}} \times \frac{100}{\text{Maximum disease grade}}$$

Statistical analysis

The correlation between yield and its characteristics was determined by correlation coefficient as recommended by Spearman (1904) and correlogram computed by using R software. Skewness (K3) and Kurtosis (K4) representing third and fourth-degree statistics, respectively, were calculated (Snedecor & Cochran, 1967) by assistance of SPSS statistical software to comprehend the distribution characteristics of various traits.

RESULTS AND DISCUSSION

The present research demonstrated that phenotypic coefficient of variation (PCV) was highest in PDI (F_3:322.34%; F_4:243.77%) followed by yield per plant (F_3:30.33%; F_4:28.85%) and vine length (F_3:28.29%; F_4:27.84%). These findings align with results of Singh et al. (2022). Moderate values of PCV were observed for node at first female flower appearance (F_4:18.98%) and number of branches per plant (F_3:19.96%; F_4:18.71%) (Table 2). Results inferred that PCV were relatively higher than GCV for most characters, suggesting that the characters were fewer persuaded by the environment. Traits with the highest values of PCV and GCV indicate a high level of variability, while those with low PCV and GCV values suggest low genetic variability (Upadhyay et al., 2019).

Genotypic coefficient of variation (GCV) is a measure of potent genetic variability for a trait. The highest GCV values were identified for per cent disease index (F_3:322.34%; F_4:243.61%) followed by yield per plant (F_4:28.79%) and fruit weight (F_3:20.05%; F_4:20.56%) (Table 2) which aligns with the findings of Singh et al. (2022).

Moderate GCV values were recorded in yield per plant (F_3:15.99%), fruit girth (F_3:12.57%) and number of fruits per vine (F_3:14.74%) coherent with the results of Khan et al. (2023). The lowest GCV values were recorded for traits such as node at the first female flower appearance (F_3:6.78%; F_4:18.93%), days to first harvest (F_3:3.13%; F_4:5.91%) as presented in Table 2. The calculation of genetic coefficient of variation serves as a measure of level of genetic variation existing for various desirable traits.

Heritability serves as a reliable indicator of inheritance of the characters to their offspring from parents. In F_4 generations, the highest heritability was observed for most traits, such as PDI (F_3:100.00%; F_4:99.87%), sex ratio (F_4:98.81%) and yield per plant (F_4:99.57%). These results align with earlier observations made by Ahmed et al. (2022). The high heritability values for all traits suggests that these characters were predominantly under genetic control, indicating minimal environmental influence.

It is important to note that the total genotypic variance comprises both additive genetic variance and non-additive variance. In F_3 generation, certain traits

Table 2 : Co-efficient of variation, heritability, genetic advance, mean, skewness and kurtosis for various yield and yield attributing traits in F_3 and F_4 generations of a cross DC 70 X DC773

Trait	Mean		Skewness		Kurtosis		CV (%)		PCV (%)		GCV (%)		Heritability (%)		Genetic advance		Genetic advance as per cent of mean	
	F_3	F_4	F_3	F_4	F_3	F_4	F_3	F_4	F_3	F_4	F_3	F_4	F_3	F_4	F_3	F_4	F_3	F_4
X1	5.52	5.72	0.36	-0.14	-0.58	-0.96	24.05	18.98	24.05	18.98	6.78	18.93	7.94	99.41	0.22	2.22	3.93	38.87
X2	3.71	4.32	0.68	0.00	0.20	-0.96	19.96	18.71	19.96	18.71	11.09	18.63	30.88	99.08	0.47	1.65	12.70	38.19
X3	23.15	23.04	0.01	0.35	-1.42	0.24	15.80	17.99	15.80	17.99	7.25	17.77	21.09	97.52	1.59	8.33	6.86	36.14
X4	7.34	8.02	-0.24	-0.34	-1.21	-0.73	22.80	21.10	22.80	21.10	14.74	21.00	41.77	99.08	1.44	3.45	19.62	43.07
X5	48.14	48.43	-0.14	-0.20	-1.08	-1.21	6.57	6.14	6.57	6.14	3.13	5.91	22.64	92.71	1.48	5.68	3.06	11.72
X6	13.37	13.55	0.30	0.18	-1.29	-0.77	24.72	21.34	24.72	21.34	12.57	21.27	25.85	99.35	1.76	5.92	13.16	43.67
X7	38.97	39.42	-0.18	-0.29	-1.25	-1.11	8.03	7.48	8.03	7.48	4.19	7.12	27.22	90.60	1.75	5.50	4.50	13.96
X8	84.06	84.35	-0.08	-0.06	-1.26	-1.22	8.24	6.66	8.24	6.66	3.33	6.37	16.33	91.39	2.33	10.58	2.77	12.55
X9	210.97	210.24	-0.83	-0.80	0.30	0.37	20.93	20.64	20.93	20.64	20.05	20.56	91.76	99.26	83.46	88.72	39.56	42.20
X10	2.77	2.96	0.62	0.45	0.21	-0.07	23.39	23.94	23.39	23.94	16.53	23.80	49.93	98.81	0.67	1.44	24.06	48.73
X11	3.20	8.06	3.16	2.20	8.91	3.36	322.34	243.77	322.34	243.77	322.34	243.61	100.0	99.87	21.26	40.42	664.02	501.51
X12	164.98	165.61	0.77	0.76	-0.08	-0.14	28.29	27.84	28.29	27.84	27.40	27.75	93.77	99.35	90.17	94.37	54.65	56.99
X13	1.55	1.68	0.02	0.22	-0.47	-0.03	30.33	28.85	30.33	28.85	15.99	28.79	27.80	99.57	0.27	0.99	17.37	59.19

X1-node at first female flower appearance, X2-number of branches/plant, X3-fruit length, X4-number of fruits/plant, X5-days to first harvest, X6-fruit girth, X7-number of days for first female flower appearance, X8-crop duration, X9-fruit weight, X10-sex ratio, X11-per cent disease index, X12-vine length, X13-yield/plant

displayed moderate heritability for sex ratio (49.93%), number of branches per plant (30.88%) and number of fruits per vine (41.77%) as also observed by Singh *et al*. (2022). The lowest heritability in F_3 generation was recorded for yield per plant (27.80%) and fruit length (21.09%) as shown in Table 2.

Genetic advance as per cent of mean exhibited the highest values for certain traits such as per cent disease index (F_3:664.02%; F_4:501.51%) followed by yield per plant (F_4:59.19%) and vine length (F_3:54.65%; F_4:56.99%). These findings are aligning with the results reported by Singh et al. (2022).

Yield per plant (F_3:0.017, F_4:0.220) and vine length (F_3:0.771, F_4:0.762) exhibited positively skewed leptokurtic distribution, while, PDI (F_3:3.156, F_4:2.204) displayed platykurtic distribution in both generations (Table 2). This suggests that participation of a reasonably smaller number of segregating genes has mainly diminishing effect on the inheritance of these characters. These findings align with earlier studies (Singh et al., 2022). Distribution curves for number of fruits per vine, fruit weight and yield per plant were depicted as Fig. 2(A), 2(B) and 2(C) in F_3 and F_4 generations.

Days to first harvest (F_3:-0.137, F_4:-0.342) and crop duration (F_3:-0.075, F_4:-0.0285) exhibited negatively skewed leptokurtic distribution in F_3 and F_4 generations. This distribution indicates the involvement of a smaller number of dominant genes with incremental outcomes and coefficient of skewness significantly fluctuates from zero, determining the occurrence of duplicate gene interaction in the inheritance of these characters (Roy, 2000).

Node at first female flower appearance (F_3:0.364, F_4:-0.065) and number of branches per plant (F_3: 0.676, F_4: -0.137) exhibited positively skewed distribution in F_3 generation and negatively skewed distribution in F_4 generation (Table 2). This negatively skewed platykurtic distribution indicates the participation of a large number of genes with accelerating effects.

Number of fruits per vine (F_4:0.351) showed positively skewed leptokurtic distribution and negatively skewed leptokurtic distribution in (F_3:-0.236) generations. Since selection will be made in F_4 generation in future, negatively skewed platykurtic distribution indicates duplicate gene action together with polygenes.

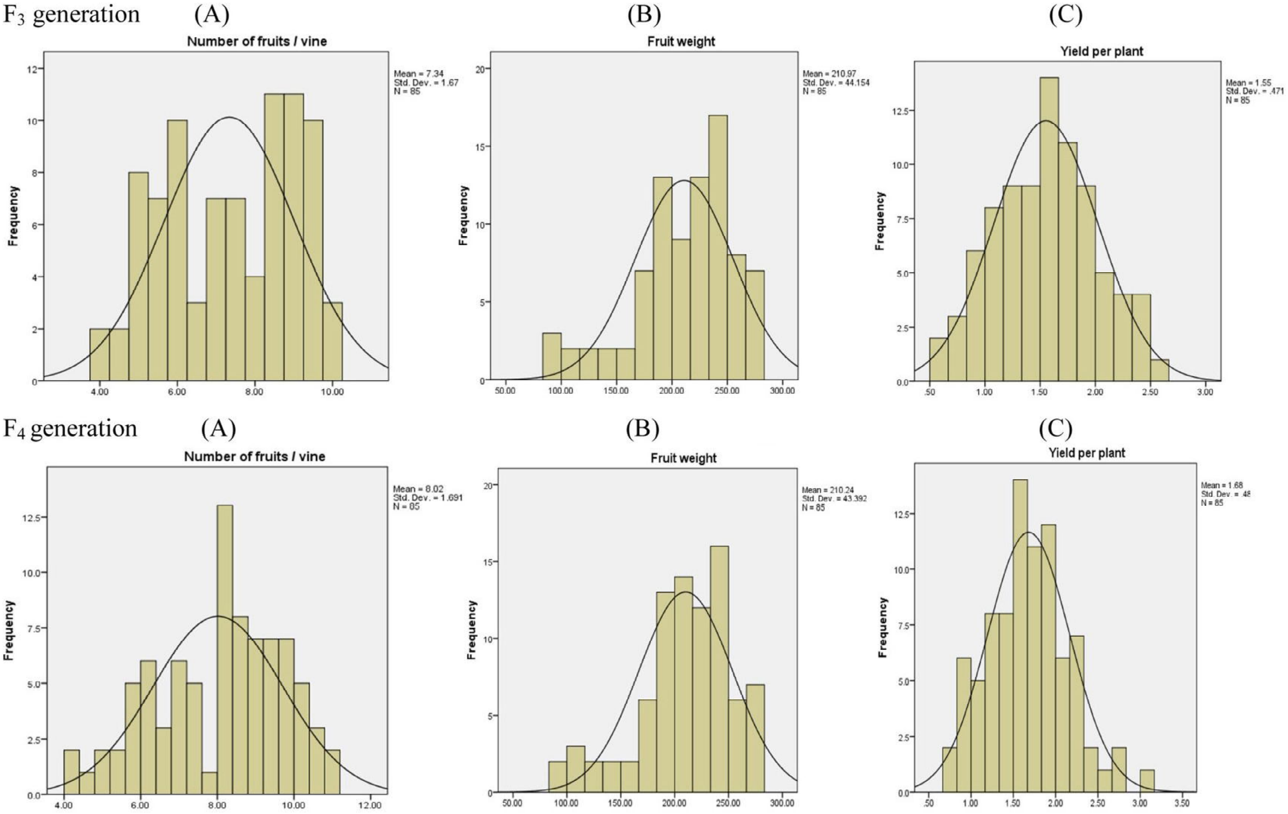


Fig. 2 : Distribution of quantitative traits (A) number of fruits per vine (B) fruit weight (C) yield per plant in F_3 and F_4 generations of a cross DC 70 x DC 773 in cucumber

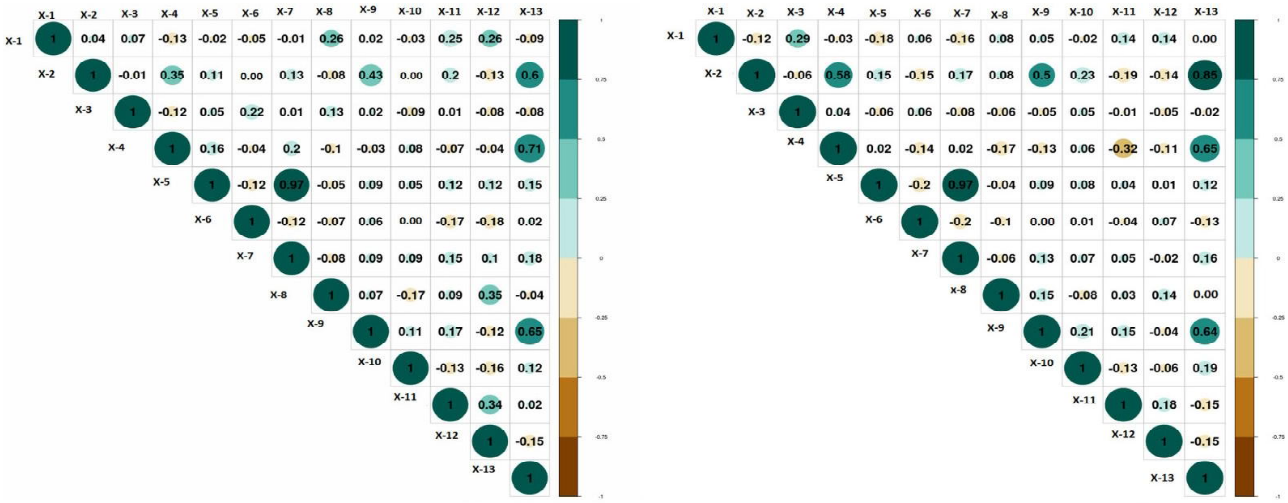
In this study, positive and significant associations were observed between yield per plant and several traits at both F_3 and F_4 generations (Fig. 1) including number of fruits per plant (F_3:0.707; F_4:0.647) and fruit weight (F_3:0.650; F_4:0.641). These results suggest that selection for these traits, which exhibit a positive relationship, can lead to improved cucumber yield. PDI (F4:0.023) and days to first harvest (F_3:0.152; F_4:0.125) (Fig 1) exhibited positive associations with yield per plant. Conversely, negative associations were found between yield per plant and node at first female flower appearance (F_3: -0.086; F_4: -0.001) and fruit length (F_3:-0.077; F_4:-0.017). PDI (-0.148) showed a negative association with yield in F_3 generation. These results are similar with results of Bhaiya et al. (2020).

Examining the correlation among yield components, it was observed that node at first female flower appearance exhibited positive and significant associations with crop duration (F_3:0.260), PDI (F_3:0.247) and vine length (F_3:0.261). Fruit length (F_3:0.069) and fruit girth (F_4:0.057) showed positive associations (Fig 1).

Number of branches per plant exhibited positive and significant associations with number of fruits per vine (F_3:0.350; F_4:0.583) and fruit weight (F_3:0.431; F_4:0.501). Days to first harvest (F_3:0.111; F_4:0.151), sex ratio (F_3:0.165) and crop duration (F_4:0.076) registered positive associations with yield. Number of fruits per plant (F_4:0.035) and fruit weight (F_3:0.019) showed positive associations with yield. Bhaiya et al. (2020) reported a positive and significant correlation of fruit length with number of fruits per plant.

Number of fruits per vine exhibited positive and significant associations with number of days for first female flower appearance (F_3:0.195). Negative associations were found with crop duration (F_3:-0.045; F_4:0.035). The number of days for first female flower appearance exhibited negative associations with crop duration (F_3:-0.083; F_4:-0.059) and vine length (-0.016). Bhaiya *et al.* (2020) reported a positive and significant correlation of the days to the anthesis of first female flower with days taken to fruit harvest

Crop duration exhibited positive and significant associations with vine length (F_3:0.349). Fruit weight (F_3:0.072; F_4:0.148) and PDI (F_3:0.094; F_4:0.032).



F_3 generation

	X-1	X-2	X-3	X-4	X-5	X-6	X-7	X-8	X-9	X-10	X-11	X-12	X-13
X-1	1	0.04	0.07	-0.13	-0.02	-0.05	-0.01	0.26	0.02	-0.03	0.25	0.26	-0.09
X-2		1	-0.01	0.35	0.11	0.00	0.13	-0.08	0.43	0.00	0.2	-0.13	0.6
X-3			1	-0.12	0.05	0.22	0.01	0.13	0.02	-0.09	0.01	-0.08	-0.08
X-4				1	0.16	-0.04	0.2	-0.1	-0.03	0.08	-0.07	-0.04	0.71
X-5					1	-0.12	0.97	-0.05	0.09	0.05	0.12	0.12	0.15
X-6						1	-0.12	-0.07	0.06	0.00	-0.17	-0.18	0.02
X-7							1	-0.08	0.09	0.09	0.15	0.1	0.18
X-8								1	0.07	-0.17	0.09	0.35	-0.04
X-9									1	0.11	0.17	-0.12	0.65
X-10										1	-0.13	-0.16	0.12
X-11											1	0.34	0.02
X-12												1	-0.15
X-13													1

F_4 generation

	X-1	X-2	X-3	X-4	X-5	X-6	X-7	X-8	X-9	X-10	X-11	X-12	X-13
X-1	1	-0.12	0.29	-0.03	-0.18	0.06	-0.16	0.08	0.05	-0.02	0.14	0.14	0.00
X-2		1	-0.06	0.58	0.15	-0.15	0.17	0.08	0.5	0.23	-0.19	-0.14	0.85
X-3			1	0.04	-0.06	0.06	-0.08	-0.06	-0.05	0.05	-0.01	-0.05	-0.02
X-4				1	0.02	-0.14	0.02	-0.17	-0.13	0.06	-0.32	-0.11	0.65
X-5					1	-0.2	0.97	-0.04	0.09	0.08	0.04	0.01	0.12
X-6						1	-0.2	-0.1	0.00	0.01	-0.04	0.07	-0.13
X-7							1	-0.06	0.13	0.07	0.05	-0.02	0.16
X-8								1	0.15	-0.08	0.03	0.14	0.00
X-9									1	0.21	0.15	-0.04	0.64
X-10										1	-0.13	-0.06	0.19
X-11											1	0.18	-0.15
X-12												1	-0.15
X-13													1

Fig. 1 : Correlogram depicting the simple genotypic correlation among yield and yield attributing traits in F_3 and F_4 generations

Fruit weight exhibited positive and significant associations with sex ratio (F_4:0.211). Fruit weight (F_3:0.108) and PDI (F_3:0.169; F_4:0.150) showed positive correlations (Fig. 1). Fruit weight showed significant and positive correlations with total fruit yield. The findings are consistent with the results of Hauke et al. (2011) in their studies on determining relationships between different horticultural traits in cucumber genotypes. PDI exhibited positive associations with vine length (0.340; 0.184) in F_3 & F_4 generations, respectively.

CONCLUSION

All examined traits displayed significance suggesting the presence of genetic variability and heritability that can be harnessed in crop improvement programs. The estimates of moderate to high PCV and GCV for PDI, yield per plant, number of fruits per vine, vine length, fruit girth and fruit weight indicated substantial variability, offering ample opportunities for enhancement through selection. Yield attributing traits exhibited high heritability and GAM suggesting significance of additive gene action in their inheritance. A highly significant positive correlation between number of fruits per plant and yield per plant was observed indicating that direct selection based on these features would enhance fruit yield. The present study highlights the importance of natural screening of F_3 and F_4 cucumber populations for ToLCNDV resistance and it will facilitate breeding resistance against ToLCNDV.

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