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Genetic variability, heritability and performance evaluation of an F_2 population in cucumber (*Cucumis sativus* L.) for yield and component traits

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Abstract

Developing high-yielding and stable crop varieties is paramount for global food security. A comprehensive investigation was conducted to evaluate genetic variability, heritability and genetic advance for twenty quantitative traits in an F_2 segregating population of cucumber (*Cucumis sativus* L.). The field experiment, executed during the summer season 2024-25, involved 20 F_2 progenies along with two standard checks. The experiment was conducted in randomized block design with two replications. The analysis of variance (ANOVA) revealed highly significant differences ($p<0.01$) among all genotypes for all characters studied. This confirmed the presence of substantial amount of genetic variability, which is the fundamental prerequisite for effective crop improvement. Mean performance analysis successfully identified superior progenies, with the cross EC-1041436 × SP recording the highest fruit yield per hectare (167.07 q/ha). The progeny IC-410682 × SP was particularly found outstanding, exhibiting the highest number of fruits per vine (13.00), maximum fruit weight (190.17 g) and the highest yield per vine (2.45 kg). High estimates of heritability coupled with high genetic advance as a percentage of the mean were observed for critical economic traits, including yield per hectare (h^2b = 81.58%, GAM = 32.42%), yield per plot (h^2b = 90.54%, GAM = 36.33%), yield per vine (h^2b = 88.70%, GAM = 37.36%), and number of fruits per vine (h^2b = 83.50%, GAM = 27.31%). This suitable combination strongly signifies the predominance of additive gene action in the inheritance of the traits, suggesting that direct phenotypic selection would be a highly effective and rewarding strategy for achieving significant genetic gains for yield and yield attributes.

Keywords: Genetic variability, cucumber, *Cucumis sativus*, F_2 population, heritability, genetic advance, mean performance

Introduction

Cucumber (*Cucumis sativus* L.) is a globally significant vegetable crop of the family Cucurbitaceae, cultivated extensively for its tender fruits. It is consumed as fresh in salads, cooked or processed into pickles. Its economic importance and consumer demand necessitate continuous efforts toward developing high-yielding varieties with improved quality and resilience to biotic and abiotic stresses (Bhandari *et al*., 2022) [2]. The success of any crop improvement program is fundamentally dependent on the magnitude of genetic variability and nature of gene action in the inheritance of those traits present in the base population, as this variation serves as the raw material for selection (Allard, 1960; Ullah *et al*., 2021) [1, 15].
The F_2 generation of a cross is a critical stage in breeding, as it exhibits the maximum genetic segregation and recombination, offering an unparalleled opportunity for selection of desirable transgressive segragants that may surpass the performance of both parents (Bhardwaj *et al*., 2021) [3].

The overall phenotypic variability observed in a population is a composite of genetic and environmental effects. To devise an effective and efficient selection strategy, it is imperative to partition this total variability into its heritable (genetic) and non-heritable (environmental) components. This is achieved through the estimation of key genetic parameters. The genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) quantify the extent of genetic and total variability, respectively. The magnitude of the difference between PCV and GCV provides an indication of the environmental influence on a trait's expression (Kumar *et al*., 2023) [9].

Broad-sense heritability (h^2b) measures the proportion of phenotypic variation that is genetically controlled, thus indicating the reliability of selection based on the phenotype. However, heritability alone does not predict the quantum of genetic gain expected from selection. When high heritability is coupled with high genetic advance as a percentage of the mean (GAM), it strongly suggests the prevalence of additive gene effects, which are fixable and respond effectively to simple selection methods, leading to rapid genetic improvement in subsequent generations (Johnson *et al.*, 1955; Reddy *et al.*, 2023) [8, 12]. Conversely, high heritability with low GAM often indicates the presence of non-additive gene action (dominance and epistasis), which is better exploited through hybridization rather than simple selection (Pradhan *et al.*, 2021) [11].

Therefore, this study was designed to systematically evaluate an F_2 cucumber population to (1) Assess the mean performance of diverse progenies for various agro-morphological traits and (2) Estimate the key genetic parameters to elucidate the nature of gene action and guide the selection of superior genotypes for the development of high- yielding cucumber varieties.

Materials and Methods

The field investigation was conducted at the experimental farm of the Department of Horticulture, College of Agriculture, Vasantrao Naik Marathwada Krishi Vidyapeeth, Parbhani, India, which is situated in the dry sub-humid western plateau agro-climatic zone. The experimental material consisted of 22 cucumber genotypes, including 20 F_2 progenies derived from a line × tester mating design and two standard commercial varieties, Gypsy and Himangi, as checks. The trial was established in a randomized block design (RBD) with two replications during the summer season of 2024-25. Sowing was done on February 19, 2025, maintaining a spacing of 1.5 m between rows and 60 cm between plants. The recommended package of practices, including a fertilizer dose of 120:60:60 kg NPK/ha and need-based plant protection measures, was followed to ensure optimal crop growth.

Data were meticulously recorded on five randomly selected plants per plot for twenty quantitative characters: Days to 1st female flower appearance, Node at 1st male flower appearance, Node at 1st female flower appearance, Days to 50% flowering, Number of nodes per vine (at 30, 45, and 60 days), Internode length (cm) (at 30, 45, and 60 days), Vine length (cm), Days to first harvest, Fruit length (cm), Fruit diameter (cm), Fruit weight (g), Number of fruits per vine, Yield per vine (kg), Yield per plot (kg), Yield per hectare (q) and 100 Seed weight (g).

The collected data were subjected to statistical analysis. Analysis of variance (ANOVA) was performed to test the significance of differences among the genotypes. Mean values, range and critical difference (CD) were computed. The genetic parameters including GCV and PCV were calculated as per Burton and De Vane (1953) [5], while h^2b and GAM were estimated following the methods of Johnson *et al.* (1955) [8].

Results and Discussion

The ANOVA (Table 1) revealed highly significant differences ($p<0.01$) among the 22 genotypes for all twenty agro-morphological characters studied. This is a critical finding, as it confirms the existence of a substantial reservoir of genetic variability within the F_2 population. This variability is the essential raw material for plant breeders to make effective selections and achieve genetic improvement in cucumber (Singh *et al.*, 2022; Gireesh *et al.*, 2021) [14, 7]. The presence of such significant diversity is a prerequisite for any breeding program aiming to develop new cultivars with improved traits.

Table 1: Analysis of variance (ANOVA) for different characters in F_2 population of cucumber

Trait	Mean sum of squares (MSS)		
	Replication	**Genotypes**	**Error**
Days to first female flower appearance	16.824	15.702**	5.247
Node at which 1st male flower appearance	0.079	0.216**	0.059
Node at which 1st female flower appearance	0.124	0.605**	0.079
Days to 50% flowering	4.479	8.412**	2.116
Number of nodes per vine at 30 days	0.424	0.726**	0.147
Number of nodes per vine at 45 days	0.124	0.894*	0.328
Number of nodes per vine at 60 days	0.257	1.713**	0.408
Internode length at 30 days (cm)	0.252	0.787**	0.116
Internode length at 45 days (cm)	0.094	1.112**	0.388
Internode length at 60 days (cm)	1.221	1.377*	0.545
Vine length (cm)	143.064	336.795*	154.122
Days to first harvest	0.124	25.25**	7.789
Fruit length (cm)	2.745	2.419**	0.716
Fruit diameter (cm)	0.016	0.072*	0.033
Fruit weight (g)	138.141	234.399**	62.802
Number of fruits per vine	0.731	5.005**	0.45
Yield per vine (kg)	0.003	0.236**	0.014
Yield per plot (kg)	12.36	40254.114**	1,997.68
Yield per hectare (q)	138.344	1041.219**	105.618
100 Seed weight (g)	1.372	2.683**	0.538

* Significance at the 5% level, ** Significance at the 1% level

The mean performance and descriptive statistics for all traits (Table 2) showed a wide range of variation, highlighting the effectiveness of hybridization in creating diverse segregants. For the ultimate economic trait, yield per hectare, the values ranged from 95.33 q/ha to 167.07 q/ha. The cross EC-1041436 × SP was found highest yielder (167.07 q/ha), followed by IC-410682 × SS (165.48 q/ha). These progenies significantly out-yielded the population mean (124.12 q/ha) and the checks, demonstrating their potential for commercial release after further evaluation. The identification of such high-performing genotypes is consistent with similar evaluation studies in cucumber (Yadav *et al.*, 2023; Kumar *et al.*, 2022) [16, 10]. For earliness, an economically important trait, the cross IC-538126 × SS was found earliest for days to first female flower appearance (32.67 days). The progeny IC-410682 × SP proved to be exceptionally promising, excelling in multiple key yield components: it recorded the highest number of fruits per vine (13.00), maximum fruit weight (190.17 g), and the highest yield per vine (2.45 kg). The superior performance of this cross in multiple traits underscores its value as a genetic resource for developing elite cucumber lines with a balanced plant ideotype.

The estimates of GCV, PCV, heritability and genetic advance are crucial for predicting the response to selection (Table 3). A favorable combination of high heritability and high GAM was observed for several key economic traits. These included yield per hectare (h^2b=81.58%, GAM = 32.42%), yield per plot (h^2b=90.54%, GAM = 36.33%), yield per vine (h^2b=88.70%, GAM = 37.36%), and number of fruits per vine (h^2b=83.50%, GAM=27.31%). This combination is a strong indicator of predominant additive gene action, meaning the variation is primarily due to the cumulative effects of heritable genes. This suggests that simple phenotypic selection would be highly effective in achieving rapid and significant genetic gains for these traits. This conclusion is strongly supported by recent findings in cucumber (Bhoi *et al.*, 2022; Reddy *et al.*, 2023; Sharma & Kumar, 2022) [4, 12, 13]. Node at 1st female flower appearance also showed high heritability (77.02%) and high GAM (23.60%), making it a reliable trait for indirect selection for earliness. In contrast, traits like fruit weight and vine length showed moderate heritability with lower GAM, suggesting the involvement of non-additive gene action, which would be better exploited through hybrid breeding (Choudhary *et al.*, 2021) [6].

Table 2: Mean performance and descriptive statistics for yield and its component traits in F_2 population of cucumber

Crosses	DFFA	NAWMF	DFM	FL (cm)	FD (cm)	FW (g)	FPV	YPV (kg)	YP Plot (kg)	Ypha (q)	HSW (g)
EC-888549xSP	33.83	3.34	44.00	16.33	3.83	175.67	12.67	2.20	967.17	150.42	21.50
EC-1041463xSP	38.33	3.34	49.50	14.00	3.42	167.34	9.00	1.50	659.67	110.00	21.00
EC-1041436xSP	35.17	4.17	44.50	16.17	3.75	182.50	12.50	2.28	980.67	167.07	21.67
IC-410682xSP	36.17	3.17	42.34	16.17	3.83	190.17	13.00	2.45	984.50	159.87	23.17
IC-538126xSP	39.00	3.50	52.50	13.00	3.33	166.67	9.50	1.58	695.00	115.86	23.00
EC-888594xSS	35.33	3.50	53.00	14.00	3.25	161.50	9.67	1.56	684.50	114.15	22.50
IC-410682xSS	34.83	3.50	44.17	16.17	4.00	177.00	12.84	2.26	992.67	165.48	20.84
IC-538126xSS	32.67	3.50	49.33	13.17	3.42	147.00	9.50	1.40	612.34	102.17	22.28
Gypsy (Check)	40.00	3.50	46.00	14.84	3.59	168.17	12.17	2.04	896.50	149.47	21.33
Himangi (Check)	37.00	3.67	44.50	14.50	3.42	172.00	12.83	2.12	931.00	155.22	22.84
Mean	36.83	3.54	48.78	14.13	3.50	165.77	10.40	1.73	746.17	124.12	21.90
Min	32.67	3.17	42.34	13.00	3.25	143.50	8.50	1.30	572.00	95.33	18.83
Max	41.50	4.50	54.33	16.33	4.00	190.17	13.00	2.45	992.67	167.07	24.33
CD @ 5%	4.76	0.50	5.80	1.76	0.38	16.48	1.40	0.25	92.95	21.37	1.53

(DFFA=Days to first female flower appearance, NAWMF=Node at 1st male flower, DFM=Days to first harvest, FL=Fruit length, FD=Fruit diameter, FW=Fruit weight, FPV=Fruits per vine, YPV=Yield per vine, YPPlot=Yield per plot, Ypha=Yield per hectare, HSW=100 seed weight)

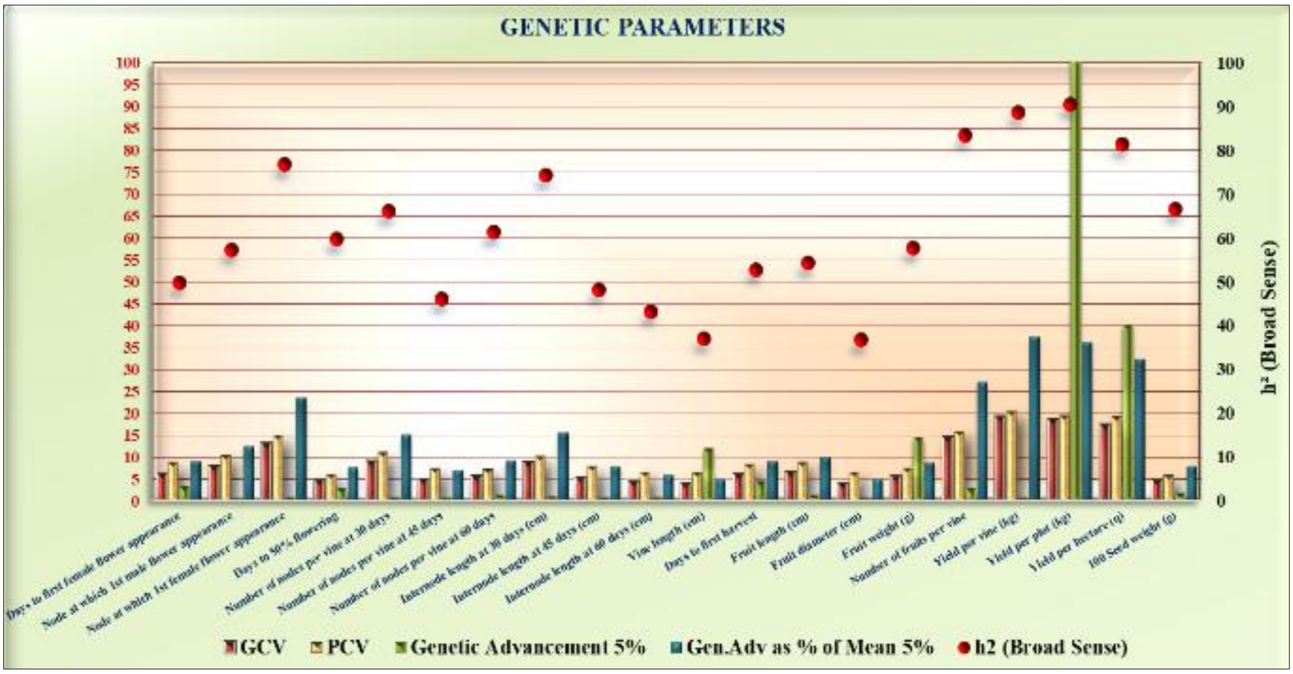

Fig 1: Grouped bar chart of genetic parameters for twenty quantitative traits in cucumber

Table 3: Estimates of genetic parameters for yield and its component traits in F_2 Population of Cucumber

Traits	GCV (%)	PCV (%)	h^2b (%)	GAM (%)
Days to first female flower appearance	6.21	8.79	49.91	9.04
Node at which 1st male flower appearance	7.93	10.47	57.35	12.38
Node at which 1st female flower appearance	13.05	14.87	77.02	23.60
Days to 50% flowering	4.76	6.15	59.81	7.58
Number of nodes per vine at 30 days	9.00	11.06	66.24	15.09
Number of nodes per vine at 60 days	5.69	7.25	61.52	9.19
Vine length (cm)	3.95	6.47	37.21	4.96
Days to first harvest	6.06	8.33	52.85	9.07
Fruit length (cm)	6.53	8.86	54.31	9.91
Fruit diameter (cm)	3.97	6.55	36.81	4.97
Fruit weight (g)	5.59	7.35	57.74	8.75
Number of fruits per vine	14.51	15.88	83.50	27.31
Yield per vine (kg)	19.26	20.45	88.70	37.36
Yield per plot (kg)	18.54	19.48	90.54	36.33
Yield per hectare (q)	17.43	19.29	81.58	32.42
100 Seed weight (g)	4.73	5.80	66.62	7.95

Conclusion

The present study successfully identified substantial genetic variability in the F_2 cucumber population, providing a robust foundation for a successful breeding program. The predominance of additive gene action for key economic traits like yield per hectare, number of fruits per vine, and yield per vine was conclusively established. This indicates that direct phenotypic selection will be a highly rewarding for isolation of transgressive segregants. Mean performance evaluation identified several superior progenies, with EC-1041436 × SP as the highest yielder and IC- 410682 × SP showing exceptional promise with a desirable combination of high fruit number and weight. These top-performing segregants are valuable genetic resources that should be advanced through pedigree selection to develop high-yielding, homozygous inbred lines for future utilization in developing elite cucumber hybrids.

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