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Genetic Divergence Studies in Cucumber (*Cucumis sativus* L.) Genotypes for Yield and Quality

J. Phani kumar[1*], Sadarunnisa Syed[2], P. Syam Sundar Reddy[3], L. Mukunda Lakshmi[4] and D. Srinivasa Reddy[5]

College of Horticulture, Anantharajupeta, Dr.YSR Horticultural University, Venkataramannagudem-516105, India

**Corresponding author*

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A B S T R A C T

The present study was carried out during Late *kharif*, 2016 at College of Horticulture, Anantharajupeta. The experiment was conducted with an objective to identify divergent genotypes to be used as donor parents in crop improvement. Thirty-two genotypes along with two checks were evaluated in a randomized block design with three replications and the data on 25 yield and yield attributing traits were recorded. The analysis of variance revealed significant differences among all genotypes indicating the presence of sufficient amount of variability for the characters studied. Wide range of variability was observed for number of fruits per plant, fruit weight, fruit yield per plant, powdery mildew incidence and aphid infestation, indicating the scope for selection of suitable initial breeding material for further breeding programme. The genotypes belong to the clusters VI and III, when the D^2 analysis was carried out for 24 characters which partitioned the thirty-two genotypes into 6 clusters, which are genetically divergent and hybridization between these genotypes will likely produce desirable segregants. The characters like primary branches per plant, days to first male flowering, days to first female flowering, days to 50% male flowering, days to 50% female flowering, days to first fruit harvest, days to last harvest, number of seeds per fruit, TSS, carotenoids, acidity, ascorbic acid and fruit yield per vine recorded high heritability in conjunction with high genetic advance as percent of mean, suggests the predominant role of additive genetic component in governing of these traits and improvement of these traits through simple selection can be employed in cucumber. The genotypes exhibited high variability for most of the traits like plant growth characters, fruit characters, quality and seed characters. On the basis of mean performance of the genotypes studied, in terms of earliness, yield and quality traits, the genotypes *viz*., A10 (JS 541367), A12 (JB 595504), A22 (IC 321367) and A30 (IC 550207) were found superior and were identified as promising lines for further crop improvement in cucumber.

Introduction

Cucumber, *Cucumis sativus* L. (2n=14) is one of the most important cucurbitaceous vegetable crops grown widely in tropical and sub-tropical parts of the world, which is native to the Indian subcontinent (Sebastian *et al*., 2010). Cucumber is a warm season crop which

is grown extensively throughout the year in southern states of India. In plains of northern India, it is grown in summer and rainy season, but it does not tolerate cold injury (Rastogi, 1998). In the recent past, cucumber has shown tremendous potential and has gained importance as a high value vegetable crop under protected cultivation. It is highly cross-pollinated crop and usually monoecious in nature. Other sex forms *viz.*, androecious, gynoecious, hermaphrodite and andromonoecious can be encountered in cucumber (Bailey, 1969).

The scope of improvement of any crop depends upon the magnitude of genetic variability present in the available germplasm. Greater the variability in the available germplasm, better would be the chances of selecting superior genotypes (Simmonds, 1962). In cucumber too, fruits vary in shape, size, colour, maturity and taste. Before starting any breeding programme, genetic variability must be available in the parental material. Further, phenotypic variability being controlled by environmental factors may not prove effective in crop improvement. Therefore, it is necessary to partition the phenotypic variations into its genetic and environmental components, because in the total variability, not only the heritable genetic components but also genetic advance is important, as it predicts the extent of advancement to next generation through selection.

While selecting for yield, one should take into account the improvement of yield contributing traits, provided that the association of such traits with yield is known. Moreover, correlation and path coefficient analysis have been of immense help in selecting suitable plant type. So, in order to identify the desirable genotypes, there is an urgent need to assess the existing variability for higher yield and quality under specific conditions. Hence, the present investigation was chosen to evaluate the genotypes for better parent for hybridization programme.

Materials and Methods

The present investigation was carried out during Late *kharif*, 2016 at College of Horticulture, Anantharajupeta, Dr. Y.S.R. Horticultural University, Andhra Pradesh. This location is at an elevation of 162 m (531 feet) above mean sea level lying between the $13^0$59' North latitude and $79^0$19' East longitude. The total rainfall during growing season was 255 mm. The maximum and minimum temperatures ranged from 28.14^{0}C to 35.71^{0}C and 18.57 ^{0}C to 27.57^{0}C respectively. The relative humidity during the period of crop growth ranged between 33.14 to 99.71 %.

Planting material

The experiment was laid-out under a shade net in a randomized block design replicated thrice. In each replication, each genotype was grown in a single row of 6 m length with a spacing of 75 x 60 cm accommodating 10 plants in a replication. The experimental material (Table. 1) comprised of a set of 32 genotypes (30 accessions and 2 checks). Thirty genotypes were obtained from NBPGR, Regional Station, Thrissur and Jodhpur. Two genotypes *viz*., Multistar RZ F1 and ICPCHI served as checks.

The recommended fertilizer dose of N: P_2O_5:K_2O was applied at the time of field preparation at the rate of 400, 315 and 100 Kg ha^{-1} as calcium ammonium nitrate, single superphosphate, and muriate of potash, respectively. Seeds were sown in protrays initially, there after transplanted to beds on 15th day. Observations were recorded on vine length, No. of primary branches per plant, inter nodal length, No. of nodes per vine, node

number at which first female flower appearance, days to first male & female flowering, days to 50% male & female flowering, days to first & last fruit harvest, fruit length, diameter, weight, No. of seeds per fruit, 100 seed weight, TSS, Carotenoid content, acidity, ascorbic acid, yield per plant, powdery mildew & aphid incidence in 10 random plants per treatment.

Grouping of the genotypes into different clusters was done by using Torcher's method as described by Rao (1952). The criterion used in clustering by this method is that any two variables belonging to the same cluster should at least on an average show a smaller D^2 value among themselves than those belonging to two different clusters. For this purpose, D^2 values of all the possible combinations in each genotype was arranged in increasing order of the magnitude in a tabular form as described by Singh and Choudhary (1985).

Statistical analysis

Genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), broad sense heritability, genetic advance and genetic gain were computed as per standard formulas.

Analysis of variance

The data for different characters were statistically analysed on the basis of the model described by Panse and Sukhatme (1961).

$Yij = u + gi + rj + eij$
Where,
Yji = Phenotypic observation in i^{th} genotype and j^{th} replication, u= General mean
gi= Effect of i^{th} genotype
rj = Effect of j^{th} replication
ejj = Random error associated with i^{th} genotype and j^{th} replication.

Genetic variance

It is the variance contributed by genetic causes or the genetic occurrence of difference among the individuals due to their genetic makeup. It was calculated by using the formula given by Al-Jibouri, 1958.

$$Vg = \frac{MSV - V_3}{r} = \frac{b' - c'}{r}$$

Where,
Vg = Genotypic variance,
MSV= Mean square for varieties,
VE = Error mean square and
r= Number of replication

Phenotypic variance

It is the sum of variance contributed by genetic causes and environmental factors and was computed as formula given by Al-Jibouri, 1958.

$Vp = Vg + Ve$
Where,
Vp = Phenotypic variance, Vg = Genotypic variance and Ve = Error variance.

Genotypic coefficient of variation (GCV)

The magnitude of genetic variation existing in a character was estimated by the formula given by Burton (1952).

$$GCV = \frac{\sqrt{Vg}}{\bar{x}} X100$$

Where,
Vg= Genotypic variance and
$\bar{x}$ = General mean of the character understudy.

Phenotypic coefficient of variation (PCV)

The magnitude of phenotypic variation existing in a character was estimated by the formula given by Burton (1952).

$$PCV = \frac{\sqrt{V_p}}{\bar{x}} X100$$

Where,
Vp = Phenotypic variance and
$\bar{x}$ =General mean of the character under study.

Heritability [h^2 broad sense]

Heritability in the broad sense refers to the proportion of genotypic variance to the total variance observed in total population. Heritability (h^2) in broad sense was calculated according to the formula given by Allard (1960).

$$h^2 = {}^{v_g}/_{v_p} X100$$

Where,
h^2 = Heritability (broad sense)
Vg = Genotypic variance and
Vp = Phenotypic variance

Genetic advance (GA)

This was estimated as per the formula proposed by Johnson et al., (1955).

$GA = K \times h^2_{bs} \times \sigma_p$

Where
K = Selection differential at 5% selection intensity which accounts to a constant value 2.06 (Lush, 1949).
h^2 (b) =Heritability in broad sense
σ_p=Phenotypic standard deviation

Results and Discussion

The analysis of variance indicated highly significant differences among the genotypes for all the traits studied (Table. 2). The results revealed that the values of PCV were higher than the GCV values but the difference between PCV and GCV were very low indicating these characters are less influenced by environment.

The study of genetic parameters in 32 cucumber genotypes revealed the presence of large amount of variation (Fig. 1). Maximum amount of variability was recorded for characters *viz.,* total yield per plant (1.67 to 6.49 kg), average fruit weight (203.67 to 1088.13 g), fruit length (4.74 to 26.69 cm) presented in Table 2 indicating the scope for selection of suitable initial breeding material for further improvement. The results are in accordance with the reports of Kumar *et al.,* (2011) in cucumber.

The estimates of PCV and GCV were high (> 20%) for characters (Table 3) such as number of primary branches per plant (36.91%, 36.40%), node number at which first female flower appears (36.78%, 23.92%), fruit length (45.60%, 29.23%), fruit weight (36.13%, 23.72%), number of seeds per fruit (30.06%, 28.32%), 100 seed weight (42.58%, 40.01%), total soluble solids (24.64%, 23.61%), carotenoids (66.91%, 62.09%), acidity (48.84%, 46.39%), ascorbic acid (25.16%, 23.84), aphid incidence (122.11%, 119.51%), powdery mildew incidence (53.17%, 51.83%) and fruit yield per vine (38.45%, 36.04%). High PCV and GCV values indicate large amount of variation and consequently more scope for their improvement through selection. The higher the GCV, the more will be the chance for exploitation of that particular character in a selection programme. These findings are in agreement with Veena *et al.,* (2012).

Heritability

The estimates of heritability (Table 4.10) were high (>60%) for vine length (60.66%), number of primary branches per plant (97.2%), days to first male flowering (89.9%), days to first female flowering (92.4%), days to 50% male flowering (95.9%), days to 50% female flowering (89.2%), days to first fruit harvest (95.7%), days to last fruit harvest (95.1%), number of seeds per fruit (88.8%), total soluble solids (91.8%), carotenoids (86.1%), acidity (90.2%), ascorbic acid (89.8%), aphid

incidence (95.8%), powdery mildew incidence (95.0%) and fruit yield per vine (87.8%). Similar findings were reported by Tomar *et al.,* 2008 in cucumber. As per the above results, it can be concluded that direct selection based on these characters will be promising.

The estimates for genetic advance as percent of mean (Table. 3) were high (>20%) for number of primary branches per plant (73.93%), days to first male flowering (23.67%), days to first female flowering (22.34%), days to 50% male flowering (23.22%), days to 50% female flowering (24.07%), days to first fruit harvest (22.52%), days to last fruit harvest (21.12%), inter nodal length (21.90%), node number at which first female flower appears (32.04%), fruit length (38.59%), fruit diameter (24.41%), fruit weight (32.07%), number of seeds per fruit (54.97%), 100 seed weight (77.44%), total soluble solids (46.60%), carotenoids (118.69%), acidity (90.78%), ascorbic acid (46.52%), aphid incidence (240.96%), powdery mildew incidence (104.09%) and fruit yield per vine (69.57%). Characters showing high value of GAM indicate the role of additive gene action and hence selection is more effective for such characters. These findings are agreement with Chikezie *et al.,* 2015 in cucumber.

Johnson *et al.,* (1955) reported that high heritability along with high genetic gain was more efficient and dependable in predicting the improvement through selection. Characters like primary branches per plant, days to first male flowering, days to first female flowering, days to 50% male flowering, days to 50% female flowering, days to first fruit harvest, days to last harvest, number of seeds per fruit, TSS, carotenoids, acidity, ascorbic acid and fruit yield per vine recorded high heritability accompanied with high genetic advance. Thus, the expression of these traits is predominantly governed by additive gene effects and therefore selection based on phenotypic performance will be useful to improve these characters in future as suggested by Chandrashekhar *et al.,* (2006).

The characters *viz.,* number of primary branches per plant, number of seeds per fruit, carotenoids, TSS, acidity, ascorbic acid and fruit yield were observed with high genetic variability, high heritability in conjunction with high genetic advance as percent mean indicating the predominance of additive gene action on the expression of these traits and hence direct selection will be rewarding for improvement of these traits in cucumber.

Genetic divergence

The genetic diversity for 32 genotypes of cucumber were assessed quantitatively for yield, yield related attributes, aphid and powdery mildew incidence by employing Mahalonobis D^2 statistics. Tocher's method (Rao, 1952) was used to group 32 cucumber genotypes into six clusters by treating estimated D^2 values as the square of the generalized distance.

The intra and inter cluster D^2 values among 6 clusters were presented given in Table 4. The inter cluster D^2 value is the main criterion for selection of genotypes. The genotypes belonging to cluster VI and V (622.52), followed by cluster IV and III (591.45) are genetically more divergent and selection of parents from these diverse clusters for hybridization programme would help in achieving novel recombinants in cucumber.

A wide range of variation was registered in the cluster means for most of the characters studied. Cluster VI ranked first with respect to the desirable characters viz., number of fruits per plant, fruit length fruit diameter and fruit yield per vine.

Table 1 List of cucumber genotypes along with their sources

Table 1. **List of cucumber genotypes along with their sources**

S. No	Genotypes	Accession No	Source/Place
1.	A1	SKY 613476	NBPGR, Thrissur, Kerala
2.	A2	SKY 613477	NBPGR, Thrissur, Kerala
3.	A3	SKY 613479	NBPGR, Thrissur, Kerala
4.	A4	SKY 613480	NBPGR, Thrissur, Kerala
5.	A5	SKY 613481	NBPGR, Thrissur, Kerala
6.	A6	SKY 613484	NBPGR, Thrissur, Kerala
7.	A7	SKY 613485	NBPGR, Thrissur, Kerala
8.	A8	KP613474	NBPGR, Thrissur, Kerala
9.	A9	JJK 595518	NBPGR, Thrissur, Kerala
10.	A10	JS541367	NBPGR, Thrissur, Kerala
11.	A11	JR469517	NBPGR, Thrissur, Kerala
12.	A12	JB595504	NBPGR, Thrissur, Kerala
13.	A13	JB613462	NBPGR, Thrissur, Kerala
14.	A14	JB613488	NBPGR, Thrissur, Kerala
15.	A15	JB595508A	NBPGR, Thrissur, Kerala
16.	A16	JB613470	NBPGR, Thrissur, Kerala
17.	A17	JB595510	NBPGR, Thrissur, Kerala
18.	A18	JB618083	NBPGR, Thrissur, Kerala
19.	A19	JB595512	NBPGR, Thrissur, Kerala
20.	A20	JB 618084	NBPGR, Thrissur, Kerala
21.	A21	IC 567558-2	NBPGR, Jodhpur, Rajasthan
22.	A22	IC 321367	NBPGR, Jodhpur, Rajasthan
23.	A23	IC 567558-3	NBPGR, Jodhpur, Rajasthan
24.	A24	IC 321370	NBPGR, Jodhpur, Rajasthan
25.	A25	IC 567558-4	NBPGR, Jodhpur, Rajasthan
26.	A26	IC 321375	NBPGR, Jodhpur, Rajasthan
27.	A27	IC 567558-1	NBPGR, Jodhpur, Rajasthan
28.	A28	IC 567558-5	NBPGR, Jodhpur, Rajasthan
29.	A29	IC 321379	NBPGR, Jodhpur, Rajasthan
30.	A30	IC 550207	NBPGR, Jodhpur, Rajasthan
31.	A31	ICPCHI	F1 Hybrid
32.	A32	Multistar RZ F1	RijkZwaan

Table.2 Analysis of variance for various horticultural traits in cucumber

	Source of variance					
S. No	**Parameters**		**Genotypes**	**Replications**	**Errors**	**Total**
		df	31	2	62	95
1.	Vine Length (cm)		63.54**	5.61	21.38	90.53
2.	Number of primary branches per plant		6.60**	0.00	0.06	6.67
3.	Inter nodal length (cm)		21.52**	0.23	4.84	26.59
4.	Number of nodes per vine		6.81**	2.21*	1.76	10.78
5.	Node number at which first female flower appears		13.68**	0.32	4.28	18.28
6.	Days to first male flowering		108.13**	1.61	3.90	113.63
7.	Days to first female flowering		110.49**	7.53	2.94	120.95
8.	Days to 50% male flowering		103.92**	0.15	1.45	105.52
9.	Days to 50% female flowering		110.47**	11.83	4.30	126.59
10.	Days to first fruit harvest		164.12**	0.64	2.39	167.15
11.	Days to last fruit harvest		212.08**	0.01	3.57	215.66
12.	Number of fruits per plant		1.39**	0.08	0.42	1.89
13.	Fruit length (cm)		128.33**	2.19*	41.51	172.03
14.	Fruit diameter (cm)		6.12**	1.22*	1.64	8.98
15.	Fruit weight (gm)		92588.98**	10179.93**	28302.40	131071.3
16.	Number of seeds per fruit		17336.29**	407.19**	700.82	18444.30
17.	100 Seed weight (gm)		1.84**	0.05	0.08	1.97
18.	TSS (^{0}Brix)		1.49**	0.01	0.04	1.54
19.	Carotenoids (µg/100 gm)		0.02**	0.00	0.00	0.03
20.	Acidity (%)		0.07**	0.01	0.00	0.08
21.	Ascorbic Acid (mg/100 gm fresh fruit weight)		1.54**	0.00	0.06	1.60
22.	Aphids incidence		1273.6**	47.58	183.06	1297.3
23.	Powdery mildew incidence		2112.00**	4.63	36.11	2152.73
24.	Fruit yield (kg/vine)		4.22**	0.17	0.19	4.57
****Significant at 5% level, *significant at 1% level**						

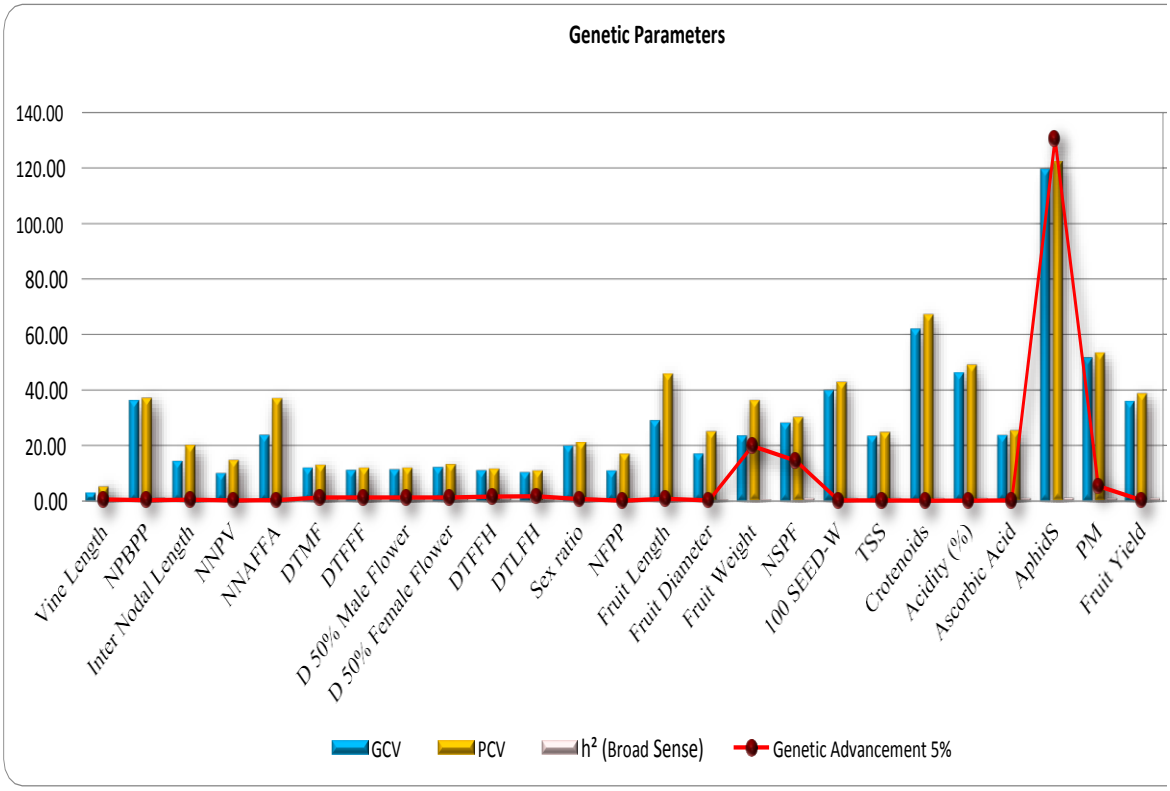
Table.3 Estimates of variability, heritability and genetic advance as percent of mean for 24 characters in cucumber

S. No	Parameters	General Mean	Variance		Coefficient of variation		Heritability (Broad sense %)	Genetic advance @ 5%	GAM @ 5%
			Genotypic (rg)	**Phenotypic (rp)**	**Genotypic %**	**Phenotypic %**			
1	Vine Length (cm)	214.45	58.5	64.5	6.35	5.15	60.66	26.5	**12.35**
2	Number of primary branches per plant	4.06	2.18	2.24	36.40	36.91	97.2	3.00	**73.93**
3	Inter nodal length (cm)	16.21	5.56	10.40	14.54	19.89	53.5	3.55	**21.90**
4	Number of nodes per vine	12.79	1.68	3.44	10.14	14.51	48.8	1.87	**14.59**
5	Node no. at which first female flower appears	7.40	3.14	7.41	23.92	36.78	42.3	2.37	**32.04**
6	Days to first male flowering	48.64	34.74	38.64	12.12	12.78	89.9	11.51	**23.67**
7	Days to first female flowering	53.08	35.85	38.79	11.28	11.73	92.4	11.86	**22.34**
8	Days to 50% male flowering	50.77	34.15	35.61	11.51	11.75	95.9	11.79	**23.22**
9	Days to 50% female flowering	48.08	35.39	39.69	12.37	13.10	89.2	11.57	**24.07**
10	Days to first fruit harvest	65.71	53.91	56.30	11.17	11.42	95.7	14.80	**22.52**
11	Days to last fruit harvest	79.32	69.50	73.07	10.51	10.78	95.1	16.75	**21.12**
12	Number of fruits per plant	5.12	0.32	0.75	11.12	16.85	43.5	0.77	**15.11**
13	Fruit length (cm)	18.41	28.94	70.45	29.23	45.60	41.1	7.10	**38.59**
14	Fruit diameter (cm)	7.12	1.49	3.13	17.17	24.87	47.6	1.74	**24.41**
15	Fruit weight (gm)	617.20	21428.86	49731.26	23.72	36.13	43.1	197.95	**32.07**
16	Number of seeds per fruit	262.96	5545.16	6245.98	28.32	30.06	88.8	144.54	**54.97**
17	100 Seed weight (gm)	1.92	0.59	0.67	40.01	42.58	88.3	1.48	**77.44**
18	TSS (0Brix)	2.94	0.48	0.52	23.61	24.64	91.8	1.37	**46.60**
19	Carotenoids micro gm/100 gm	0.14	0.01	0.01	62.09	66.91	86.1	0.17	**118.69**
20	Acidity (%)	0.33	0.02	0.03	46.39	48.84	90.2	0.30	**90.78**
21	Ascorbic Acid (mg/100 gm fresh fruit weigh)	2.95	0.49	0.55	23.84	25.16	89.8	1.37	**46.52**
22	Aphids incidence	541.30	418500.84	436873.91	119.51	122.11	95.8	1304.32	**240.96**
23	Powdery mildew incidence	50.75	691.96	728.07	51.83	53.17	95.0	52.83	**104.09**
24	**Fruit yield (kg/vine)**	**3.22**	**1.34**	**1.53**	**36.04**	**38.45**	**87.8**	**2.24**	**69.57**

Table.4 Average intra and inter cluster D2 values of cucumber genotypes

Table. 4 Average intra and inter cluster D2 values of cucumber genotypes						
Cluster	**I**	**II**	**III**	**IV**	**V**	VI
I	88.25 (9.39)	196.98 (14.03)	454.74 (21.32)	187.69 (13.70)	452.50 (21.27)	**517.70 (22.75)**
II		125.73 (11.21)	258.77 (16.09)	289.84 (17.02)	298.35 (17.27)	**404.27 (20.11)**
III			60.34 (7.77)	591.45 (24.32)	518.64 (22.77)	**415.66 (20.39)**
IV				180.69 (13.44)	507.42 (22.53)	**453.65 (21.30)**
V					0.00 (0.00)	**622.52 (24.95)**
VI						**0.00 (0.00)**

Fig.1 Phenotypic and genotypic coefficient of variation, Heritability, genetic advance for different characters in cucumber



The same cluster also recorded lower mean value for powdery mildew incidence. Cluster III ranked first for earliness characters like days to first female flowering, days to 50% female flowering and days to first fruit harvest, besides having ideal quality characters like maximum cluster mean value for carotenoids. Hence genotypes belonging to the clusters VI and III are amenable for exploitation in future crop improvement of cucumber.

In conclusion, cucumber genotypes exhibited high variability for most of the traits like plant growth characters, fruit characters, quality and seed characters. On the basis of mean performance of the genotypes studied, in terms of earliness, yield and quality traits, the genotypes *viz.,* A10 (JS 541367), A12 (JB 595504), A22 (IC 321367) and A30 (IC 550207) were found superior and were identified as promising lines for further crop improvement in cucumber. These genotypes belong to the clusters VI and III which are genetically divergent and hybridization between these genotypes will likely produce desirable segregants.

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