

## Original Research Article

# Assessment of Genetic Variation and Genetic Divergence in Cucumber (*Cucumis sativus* L.)

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## ABSTRACT

The present investigation was carried out at Vegetable Research Farm, Dr. Rajendra Prasad Central Agricultural University, Pusa, Samastipur, Bihar in a randomized block design comprising three replications during kharif season 2019 to assess genetic variability parameters as well as genetic divergence in cucumber. Twenty-two genotypes along thirteen traits were studied. The investigation revealed that the analysis of variance exhibited significant variation amongst the twenty-two genotypes for the thirteen quantifiable traits signifying a wide range of variability. The phenotypic coefficient of variation was slightly higher than the equivalent genotypic coefficient of variation which implies the role of genotypes in the manifestation of studied thirteen traits. The high heritability attached with high genetic advance as percent of mean were detected for node number at which first female flower appeared, fruit length, fruit diameter, inter nodal length, average fruit weight, fruit yield per plant, number of primary branches per plant and vine length at final harvest. Selection on these studied traits in an early generation will be effective in crop improvement program. The placement of genotypes in five different clusters with respect to Mahalanobis  $D^2$  statistic. Among the five various clusters a maximum inter-cluster distance was exhibited between cluster number IV and cluster number V trailed by cluster number II and cluster number V. Since a maximum cluster mean of yield contributing traits such as number of primary branches per plant, fruit diameter, average fruit weight and number of fruit per plant was observed in cluster number II as well as high cluster distance found in cluster number II and cluster number V. thus, inter crossing among the genotypes belonging to cluster number II and cluster number V was signifying to develop high yielding recombinants.

### Keywords

Cucumber,  
Genetic variability,  
Phenotypic  
coefficient of  
variation,  
Genotypic  
coefficient of  
variation,  
Heritability,  
Genetic advance,  
Mahalanobis  $D^2$

## Introduction

Cucumber is one of India's most commercial growing vegetable crops (Dhaliwal, 2017), is part of the cucurbitaceous family (Lower and Edward, 1986). Its chromosome number ( $2n$ ) is 14. In context to preference, it is grown all over the world, in Asia utmost fourth

important vegetable crop next to Tomato, Cabbage then Onion whereas, the second most grown cucurbit after watermelon (Wehner, 2007). It is a greatest economic and dietic vital crop. It is cultivated for tender fruit that provided as raw or salad (Arunkumar *et al.*, 2011), cooked as a vegetable, in immature stage as pickling.

Cucumber has 95 % of water content (Ene *et al.*, 2016) which makes diuretic and it possessing a deep cooling effect. Its fruits are used as astringent and antipyretic. Cucumber fruit juice is valuable in the treatment of hyperacidity in gastric and duodenum ulcers and also a good laxative for constipation (Ernestina, 2001).

Genetic variability is an important part of crop improvement, being it is in cultivation since from long back, cucumber crop with its cross-pollinated character which exhibits the large variation for the diverse quantitative as well as qualitative characters (Rawahi *et al.*, 2011).

The scope for ameliorating of any crop hinge on the amount of genetic variability in geographical availability of the genotypes. Higher the extent of changeability healthier would be the probabilities of selection of greater genotypes (Bhagwat *et al.*, 2018). Due to the continuous production of cross-pollinated crop vast difference existed for fruit as well as vegetative traits. So, fruit is varying viz., shape, colour, size, maturity and taste.

Starting with any breeding program genetic variability must be in parental material (Gaikwad *et al.*, 2011). Phenotypic variability being controlled by environmental components may not prove influential in crop improvement. Heritability is a reasonable measure for the transfer of traits to offspring (Arunkumar *et al.*, 2011). Heritability denotes precisely with a genotype that can be identified by the assistance of its phenotypic performance. Heritability (broad sense) belonging to mutual additive as well as non-additive properties (Shah *et al.*, 2017). Genetic advance is also important so, it predicts the extent of advancement to the next-generation via the selection. For selection of yield, yield improvement

characters provide the association of such characters with yield is known (Veni *et al.*, 2013).

Genetic diversity estimation is rewarding criterion in quantifying the extent of divergence in the genotypic level of biological population (Punitha *et al.*, 2012). To examine the extent of influence of unlike apparatuses to overall divergence both at intra-cluster as well as inter-cluster levels (Jatasra and Paroda, 1978). To detect divergent parents cluster analysis is carried out for hybridization program to recognize foreseeable crossing and to obtain meaningful constellation of collected genotypes for the heterosis exploitation, selection of utmost suitable important parents will be rewarding (Shah *et al.*, 2018).

### **Materials and Methods**

The current study was carried out at Vegetable Research Farm, Dr. Rajendra Prasad Central Agricultural University, Pusa, Samastipur, Bihar during kharif season 2019. The materials for study had twenty-two genotypes of cucumber such as Punjab Naveen, Kanpur Local, Kalyanpur Long Green, Barsati Local, Barsa Rani, Pusa Uday, DC-821, Mirpur Local, Baropata, PCUC-8, Pusa Barkha, Swarna Ageti, Barsati-012, Japanese Green Long, Mahatana Kheera-M-40, Cucumber Summer Long-45, Swarna seeds, DC-78, Raja (Golden), Phule Subhangi, Dev Kamal and Seven Star. The studied genotypes were statistically placed out in the field using Randomized Block Design (RBD) together with three replications. The planting spacing was 100cm×60cm. Before the sowing of seeds pure as well as vigorous seeds of each genotypes stood placid then the water soaking of seeds for twelve hours to get better germination. The seeds were sown in the field directly along filled with soil and

well rotten farm yard manure after that watering was done to maintain soil moisture. Only one healthy seedling was retained per hill after the emergence of the seedlings thereby keeping 10 plants per plot in each replication of the genotypes. In a field investigation, entire population study rather difficult to study the entire population. Thus, randomly five plant were selected from each replication along with tagged that specific selected plant for observation records.

The genotypes were gathered from the IARI New Delhi, IIVR Varanasi as well as CSAUAT Kanpur. All the cultural practices followed in order with almost care as well as attention. The observations were marked on vine length at final harvesting/VL (cm), number of primary branches per plant/NPB, inter nodal length/INL (cm), node number at which first female flower appeared/NNFF, appearance of first male flower/FMF (days), appearance of first female flower/FFF (days), days to first fruit harvesting/DFH, number of fruits per plant/NF/P, fruit length/FL (cm), fruit diameter/FD (cm), average fruit weight/AFW (g), shelf life/SL and fruit yield per plant/FY/P (kg). Statistical analysis such as analysis of variance for individual traits was done as per Panse and Sukhatme (1967), Components of variance, heritability, genetic advance and genetic divergence were estimated as per Burton and Devane (1953), Falconer (1981), Johnson *et al.*, (1955) and Mahalanobis, P.C. (1936) respectively.

## Results and Discussion

The current investigation, twenty-two diverse genotype of cucumber were studied in terms of yield and yield attribute traits. The analysis of variance clearly showed the highly significant variation among the twenty-two genotypes for studied traits. Thus, it specified the sufficient variability in the resources studied, which could be utilized in further

breeding program. Interestingly, the degree of the mean sum of squares indices such as vine length at final harvest, average fruit weight, fruit length, node number at which first female flower appearance and days to first fruit harvest were comparatively higher than the other studied traits. Thus, it exhibited the presence of considerable extent of variability in the genotypes can be utilized in further crop upgrading program through selection of superior genotypes by the plant breeders. These finding is in accord with Ahirawar and Singh, 2018; Karthick *et al.*, 2019; Bartaula *et al.*, 2019. The phenotypic variances for thirteen traits under study were higher than the genotypic variances (Deepa *et al.*, 2018; Karthick *et al.*, 2019). This possibly will be due to the non-genetic influence which played vital role in the pointer of these thirteen characters. The maximum variability (phenotypic and genotypic variance) exhibited by the traits such as vine length at final harvest (1909.49 and 1165.90), average fruit weight (970.89 and 697.89) and fruit length (9.39 and 8.05). These finding is confirmation with Shah *et al.*, 2018; Bartaula *et al.*, 2019. It is exciting to reported that the differences between genotypic coefficient of variance and phenotypic coefficient of variance values were minimum for the characters such as node number at which first female flower appearance (0.84) followed by fruit length (1.21), average fruit weight (2.24), inter nodal length (2.26) and fruit diameter (2.99) exhibited a least influence of environment and additive gene effects indicating genotypes can be improved and selected for studied characters for fruit yield improvement. These discoveries are confirmation with Karthik *et al.*, (2019).

The information of heritability was helpful in reporting merits and demerits of a precise trait as it empowers the plant breeder to resolve the course of selection procedures to be followed under a given situation.

(Ahirawar and Singh, 2018). In the existing studies the characters such as node number at which first female flower appearance, fruit diameter, fruit length, inter nodal length, vine length at final harvest, fruit yield per plant and average fruit weight have recorded high heritability coupled with high genetic advance as percent of mean. Hence, direct selection can be done through these characters for future improvement of genotypes for crop improvement of fruit yield per plant. whereas moderate to low genetic gain was studied for appearance of first female flower and days to first harvest. These results are confirmation with Pal *et al.*, 2016; Ahirawar and Singh, 2018; Kumar *et al.*, 2018.

The high heritability coupled with high genetic advance indicated, the variation was mostly due to additive gene effects. It indicates that if studied characters are subjected to any selection scheme for exploiting fixable genetic variance, a wide adopted genotype can be developed. (Bartaula *et al.*, 2019).

Mahalanobis  $D^2$  statistic is an exclusive tool for classifying genetically diverse parents based on quantitative traits which could be optimally utilized in hybridization program (Mahalanobis, 1936; Rao, 1952). In the present investigation, twenty-two genotypes (including check) were grouped into five clusters on the basis of  $D^2$  statistics and ward minimum variance method. The cluster number I comprise seven genotypes which is highest number of genotypes followed by cluster number III had five genotypes, cluster number II and cluster number V had four genotypes whereas, cluster number IV had two genotypes. Similar studied based on  $D^2$  statistics. These finding is accordance with Yadav *et al.*, 2005; Punitha *et al.*, 2012.

Different clusters comprise unique feature for different characters under study. The cluster

number II had maximum average value for vine length at final harvest (259.08), number of primary branches (10.00), shelf life (4.70), fruit length (22.17), fruit diameter (5.91), number of fruits per plant (9.50), average fruit weight (238.09) and yield per plant (2.26). The cluster number II have been utilized as parent for development for high yield in crop improvement. Whereas, cluster number V had maximum inter nodal length (9.96), node number at which first female flower appearance (10.69), appearance of first male flower (32.46), appearance of first female flower (41.61) and days to first fruit harvest (52.45). The cluster number IV had minimum vine length (179.93) and inter nodal length (7.43) thus it may be utilized as parent for dwarfness. Whereas cluster number IV had minimum mean for node at first female flower (4.68), appearance of first female flower (37.53), appearance of first male flower (28.68) and days to first fruit harvest (47.85) so, this might be select as parent for earliness of the crop improvement. cluster number V had maximum number of node number of first female flower, appearance of first male flower, appearance of first female flower and days to first fruit harvest suitable for late flowering, but cluster number II had maximum mean value for number of fruits per plant (9.50), fruit diameter (5.91) and fruit length (22.17) may be use further selection program for high yield. The cluster number V had minimum average fruit weight (183.21) and yield per plant (1.67) may select as parents for further hybridization to achieve maximum yield of the crop. For better keeping quality we go for cluster number II because it has high mean for the shelf life. Selection of genotypes based on cluster mean for better exploitation of genetic potential. These finding is validation with Kanwar and Rana, 2006; Manohar and Murthy, 2011; Punitha *et al.*, 2012; Hasan *et al.*, 2015; Kumar *et al.*, 2019; Sharma *et al.*, 2018 (Table 1–6).

**Table.1** Analysis of variance for thirteen characters in cucumber

Sl. No.	Characters	Mean sum of square		
		Replication (df = 2)	Treatment (df = 21)	Error (df = 42)
1.	Vine length at final harvesting (cm)	646.9	4241.31**	743.58
2.	Number of primary branches per plant	0.047	4.14**	0.695
3.	Inter nodal length (cm)	1.92	5.50**	0.54
4.	Node number at which first female flower appeared	0.11	13.33**	0.25
5.	Appearance of first male flower (days)	4.00	10.04**	3.67
6.	Appearance of first female flower (days)	2.26	9.92*	5.02
7.	Days to first fruit harvesting	14.42	12.10*	6.31
8.	Number of fruits per plant	1.40	2.13**	0.53
9.	Fruit length (cm)	3.35	25.51**	1.33
10.	Fruit diameter (cm)	0.05	3.53**	0.32
11.	Average fruit weight (g)	160.65	2366.68**	273.00
12.	Shelf life (days)	1.34	0.48**	0.12
13.	Fruit yield per plant (kg)	0.01	0.31**	0.05

\* denotes significant at p = 0.05, \*\* denotes significance at p = 0.01

**Table.2** Mean, range and coefficient of variation for thirteen characters in cucumber

Sl. No.	Characters	Mean	Range		CV (%)
			Minimum	Maximum	
1.	Vine length at final harvest (cm)	212.74	163.83	303.06	12.81
2.	Number of primary branches per plant	8.95	7.13	11.00	9.31
3.	Inter nodal length (cm)	8.65	6.76	11.16	8.50
4.	Node number at which first female flower appeared	7.28	4.46	1186	6.98
5.	Appearance of first male flower (days)	31.51	27.33	34.60	6.07
6.	Appearance of first female flower (days)	40.70	36.43	44.26	5.50
7.	Days to first fruit harvesting	51.36	46.80	54.60	4.89
8.	Number of fruits per plant	9.20	7.80	10.93	7.97
9.	Fruit length (cm)	18.69	12.66	23.73	6.19
10.	Fruit diameter (cm)	4.95	2.83	6.36	11.56
11.	Average fruit weight (g)	211.77	156.5	254.20	7.80
12.	Shelf life (days)	4.54	3.66	5.03	7.68
13.	Fruit yield per plant (kg)	1.94	1.46	2.60	11.55

**Table.3** Genetic parameter of thirteen characters in cucumber

Sl. No.	Character	$\sigma^2_g$	$\sigma^2_p$	GCV (%)	PCV (%)	$h^2$ (b.s.) (%)	GA	5% GA as percent Mean
1.	Vine length at final harvest (cm)	1165.90	1909.49	16.64	20.53	0.61	54.96	25.83
2.	Number of primary branches per plant	1.14	1.84	11.97	15.17	0.62	1.74	19.47
3.	Inter nodal length (cm)	1.65	2.19	14.87	17.13	0.75	2.30	26.59
4.	Node number at which first female flower appeared	4.35	4.61	28.64	29.48	0.94	4.17	57.32
5.	Appearance of first male flower (days)	2.12	5.79	4.62	7.63	0.36	1.81	5.76
6.	Appearance of first female flower (days)	1.63	6.65	3.13	6.33	0.24	1.30	3.20
7.	Days to first fruit harvesting	1.92	8.24	2.70	5.59	0.23	1.38	2.69
8.	Number of fruits per plant	0.53	1.07	7.93	11.24	0.49	1.06	11.52
9.	Fruit length (cm)	8.05	9.39	15.18	16.39	0.85	5.41	28.96
10.	Fruit diameter (cm)	1.06	1.39	20.86	23.85	0.76	1.86	37.58
11.	Average fruit weight (g)	697.89	970.89	12.47	14.71	0.71	46.13	21.78
12.	Shelf life (days)	0.12	0.24	7.67	10.86	0.49	0.50	11.17
13.	Fruit yield per plant (kg)	0.08	0.13	15.28	19.16	0.63	0.48	25.12



**Table.4** Cluster mean for thirteen characters in cucumber

Characters Cluster	VL	INL	NNFF	NPB	FMF	FFF	DFH	SL	FL	FD	NF/P	AFW	FY/P
I	215.74	7.54	7.93	9.51	32.07	41.59	52.26	4.69	19.52	5.29	9.36	223.31	2.07
II	259.08	9.57	5.32	10.00	30.47	39.85	49.85	4.70	22.17	5.91	9.50	238.09	2.26
III	195.84	8.90	6.27	7.93	31.92	40.67	51.84	4.52	16.56	5.22	8.78	206.22	1.80
IV	179.93	7.43	4.68	8.86	28.68	37.53	47.85	3.95	13.28	3.28	8.90	189.68	1.68
V	198.74	9.96	10.69	8.25	32.46	41.61	52.45	4.46	19.12	3.90	9.27	183.21	1.67

**Table.5** Mean intra and inter cluster distance ( $D^2$ ) among five clusters in cucumber

Clusters	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V
Cluster I	42.79	89.82	73.03	55.92	153.19
Cluster II		47.27	99.46	178.74	292.66
Cluster III			63.81	88.02	200.54
Cluster IV				17.00	301.29
Cluster V					56.39

**Table.6** Contribution percentage of thirteen characters towards genetic divergence in cucumber

Sl. No.	Source	Times ranked 1 <sup>st</sup>	Contribution (%)
1.	Vine length at final harvest (cm)	3	1.3
2.	Number of primary branches per plant	4	1.73
3.	Inter nodal length (cm)	11	4.76
4.	Node number at which first female flower appeared	85	36.8
5.	Appearance of first male flower (days)	0	0
6.	Appearance of first female flower (days)	0	0
7.	Days to first fruit harvesting	0	0
8.	Number of fruits per plant	10	4.33
9.	Fruit length (cm)	36	15.58
10.	Fruit diameter (cm)	40	17.32
11.	Average fruit weight (g)	33	14.29
12.	Shelf life (days)	6	2.6
13.	Fruit yield per plant (kg)	3	1.3

The highest intra cluster distance was observed in cluster number III (63.81) followed by cluster number V (56.39), cluster number II (47.27), cluster number I (42.79) as well as cluster number IV (17.00) indicating difference in genotype within cluster.

Least intra cluster distance was reported in cluster number IV (17.00) indicating that close resemblance between the genotypes presented in this cluster.

The genotype in cluster number IV and cluster number V (301.29) exhibited maximum inter cluster distance between them, thus high degree of genetic diversity and thus may be utilized under inter varietal hybridization program (transgressive breeding) for getting high yielding recombinants. Similar inter varietal crosses attempted between genotypes in cluster number II and cluster number V, cluster number III and cluster number V, cluster number II and cluster number IV, cluster number II and cluster number III, cluster number I and cluster number II, cluster number I and cluster number III. These finding is validation with Hanchinamani and patil, 2011; Kunda *et al.*, 2012; Pal *et al.*, 2017; Reddy *et al.*, 2012; Shah *et al.*, 2018; Indrajia *et al.*, 2018.

The selection and choice of parents mainly depends upon contribution of characters toward divergence. The maximum contribution in the displaying of genetic divergence was recorded by node number at first female flower appearance (36.8%) followed by fruit diameter (17.32%), fruit length (15.58%), average fruit weight (14.29%), inter nodal length (4.76%), number of fruits per plant (4.33%), shelf life (2.6%) and number of primary branches (1.73%). Thus, the study suggested scope for improvement in the characters were

rewarding. These finding is confirmation with Ahirwar *et al.*, (2017), Punit *et al.*, (2012), Yadav *et al.*, (2005), Mahohar and Murthy (2011).

The analysis of variance exhibited significant variation amongst the twenty-two genotypes for the thirteen quantifiable traits signifying a wide range of variability. The phenotypic coefficient of variation was somewhat higher than the equivalent genotypic coefficient of variation which representative the role of genotypes in the manifestation of studied thirteen traits.

The high heritability attached with high genetic advance as percent of mean were detected for node number at which first female flower appeared, fruit length, fruit diameter, inter nodal length, average fruit weight, fruit yield per plant, number of primary branches per plant and vine length at final harvest. Selection on these studied traits in an early generation will be effective in crop improvement program.

The twenty-two genotypes were grouped into five various clusters which does not have any geographical similarity. The genotypes in cluster number IV and cluster number V, due to maximum inter cluster distance between them, exhibited high degree of genetic diversity and thus may be utilized under inter varietal hybridization programme for getting high yielding recombinants.

The maximum contribution in the manifestation of genetic divergence was exhibited by node number at which first female flower appeared, fruit diameter, fruit length, average fruit weight, inter nodal length, number of fruits per plant, shelf life and number of primary branches. This indicated that selection of genotypes for these traits may be effective for future utilization in breeding programme for yield improvement.



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