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Research Note

Genetic evaluation of Cucumber [*Cucumis sativus*L.] genotypes for some yield and related traits

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Abstract

Thirty-eight advanced lines of cucumber (*Cucumis sativus* L.) were evaluated for variability, heritability and genetic advance for yield and contributing traits. Genotypic coefficient of variation and phenotypic coefficient of variation were highest for node at first female flower appearance followed by node at first male flower appearance, yield per plant, seed cavity breadth, average fruit weight and number of fruits per plant. High heritability and high estimated genetic advance over mean were observed for nodes per vine (83.43), node at first female flower appearance (82.17), days to first female flower opening (83.72), days to first male flower opening (92.63), days to first harvest (83.04), number of fruits per plant (85.78), fruit length (88.92), fruit breadth (86.91), seed cavity length (85.97), seed cavity breadth (85.09), number of seeds per fruit (95.17) and 100 seed weight (93.10) thus indicating that these characters had additive gene effect and therefore, they are more reliable for effective selection.

Keywords: Genetic improvement, selection, cucumber, yield attributes

Cucumber [*Cucumis sativus*L.] is the most important salad crop of the family Cucurbitaceae grown commercially throughout the country. The fruits are mainly consumed as salad, preparation of cosmetic item soap and cream and in many other ways (Dhiman and Chander Parkash, 2005). The crop is of Asian origin and the progenitor may be closely related to its wild relative *Cucumis sativus* var. *hardwickii*, first found in the Himalayan mountains (foothills of Nepal) and used by native peoples of Northern India as a laxative (Deakin *et a*l 1971). Cucumber cultivation goes back to at least 3000 years in India and 2000 years in china (Robinson and Decker-Walters, 1997). In India, it is cultivated in an area of 0.24 lakh hectares with an annual production of 1.52 lakh metric tonnes, whereas the world area is 1.972 million hectares with a production of 62.431 million metric tonnes (http://faostat3.fao.org/home/index.html2010).

India being the primary centre of origin, it has accumulated a wide range of variability providing good scope for improvement in yield and other character of cucumber through selection. For any effective selection programme, the information on the nature and the magnitude of variability present in genetic stocks, heritability and genetic advance are important. Crop improvement to a large extent depends on the existing genetic variability. Hence, the present investigation was undertaken with a view to assess the extent of genetic variation in some cucumber genotypes.

The present experiment was conducted in the Division of Vegetable Crops of Indian Institute of Horticultural Research (IIHR), Bangaluru during *Kharif* season of 2010. Thirty eight diverse genotypes, *viz.,* Swarna Ageti, Japanese Long Green, Sangeeta, Nandini, Barsati, Sweet Market More, Ajax, VR-101, VR-06-07, Local line, IIHR-405, Karur local, IIHR-407-1, IIHR0409-2, Punjab Naveen, IIHR-34, Himangi, Peb Kamal, VS-474, Poinsettia, 595920, IIHR-285, IIHR-304, IIHR-81, IIHR-82, IIHR-36, Gadag Local, IIHR-177, Phule Shubangi, Tender Green Burbless, VRC-06-08, IIHR-306, IIHR-34-S4, IIHR-337, Pilibhat Local, IIHR-384, *Cucumis sativus var. hardwickii* and IIHR-338 were grown in randomized block design with three replications at a spacing of 2.0 m x 0.6 m. Recommended cultural practices were adopted for proper growth and stand of the crop. The observations were recorded on seventeen economic traits from five randomly selected competitive plants from each of the genotypes and its

replications. The data were subjected to analysis of variance as per the procedure described by Panse and Sukhatme (1967). The coefficient of phenotypic and genotypic variations were calculated according to Burton and DeVane (1953). Heritability, genetic advance and genetic gain were calculated according to the formula of given by Johnson *et al.* (1955).

The mean sum of square was highly significant for all traits indicating the presence of wide range of variability in the genotypes . The range of variation was high for average fruit weight followed by days to first fruit harvest, days to first female flower opening, days to first male flower opening, fruit length and number of fruits per plant indicating the presence of sufficient variability among the genotypes used in the present study. This would help in selecting the best genotypes from existing collection. However, seed cavity length, 100-seed weight, node at first male flower appears and vine length recorded low value indicating minimum variation and less scope for selection from the present collection. High genotypic and phenotypic coefficients of variation were recorded for node at first female flower appears, node at 1st male flower appears, yield per plant, seed cavity breadth, flesh thickness, average fruit weight and number of fruits per plant.(Table 1) This reflects greater genetic variability among genotypes for these characters, to facilitate further improvement by selection. Reshmi (2006) and Arunkumar *et al*., (2011) also reported similar results. Phenotypic and genotypic coefficients of variation were quite low for days to 1st fruit harvest, days to 1st male and female flower opening, vine length and number of nodes per vine. Rest of the characters recorded moderate coefficient of variation. The information obtained showed that the estimates of phenotypic coefficient of variation (PCV) were higher than genotypic coefficient of variation (GCV). Although estimates of PCV were higher than that of GCV, they were close to one another implying that the influence of environment on the expression of these traits were negligible hence selection based on phenotypic values is feasible. Similar observations were reported earlier by Hanchinamani (2006) Solanki and Seth, 1980 and Joshi *et al* (1980) .The lowest GCV was noticed for days to first harvest.

The estimation of genetic coefficient of variation indicates the amount of genetic variation present for different desirable traits while the heritability gives an insight into the proportion of variation which is inherent. The heritability estimate gives an idea about the proportion of observed variability, which is attributed to genetic difference. Heritability in broad sense may play greater role about information of relative value of selection, but Johnson *et al*., (1955) had shown that heritability and genetic advance should be jointly considered for reliable conclusion.

Heritability estimates were high for characters like number of nodes per vine, node at first female flower appears, days to first female flower opening, days to first male flower opening, days to first harvest, number of fruits per plant, fruit length, fruit breadth, seed cavity length, seed cavity breadth, number of seeds per fruitand 100 seed weight. From the above heritability estimates, it is clear that these characters are less influenced by the environmental factors and are controlled by additive gene effect (Table 1). Similarly, high heritability for the above traits was reported by Dhiman and Chander Prakash (2005), Reshmi (2006) and Arunkumar *et al*., (2011). Average fruit weight, flesh thickness, yield per plant, yield per plot and yield per hectare recorded moderate heritability. Similar result was reported by Prasad and Singh (1994).

In the present study high genetic advance over mean coupled with high heritability was observed in characters like node at first female flower appearance and seed cavity breadth. However, the estimates were moderate for days to first male flower opening, number of fruits per plant, average fruit weight, fruit length, fruit breadth, flesh thickness, yield per plant, seed cavity length, number of seeds per fruit and 100 seed weight. Therefore, the present findings corroborated that the existing variability among the genotypes with respect to these traits is mainly due to additive type of genes (Panse 1957).

Higher heritability estimates were accompanied by lower genetic advance over the mean for days to first female flower opening and days to first fruit harvest. This suggests that selection may not be useful for the improvement of this trait because of the narrow range of phenotypic variation among the genotypes in respect to this character. Hanchinamani (2006) reported low genetic advance in cucumber.

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Table 1. Variability, heritability and genetic advance for growth and yield of 38 cucumber accessions

Character/Source	Mean	S. Em±	CD (5%)	CV (%)	Range	GV	PV	GCV (%)	PCV (%)	h^2 (%)	GAM (%)
Vine length	1.57	16.79	47.29	18.55	1.07-2.23	622.22	1467.46	15.91	24.43	42.40	21.34
Number of nodes per vine	33.23	1.17	3.29	6.08	24.71-43.27	21.16	25.25	13.84	15.12	83.82	26.11
Node at first female flower appears	5.51	0.65	1.84	20.5	2.00-11.00	5.88	7.17	44.01	48.55	82.17	82.18
Node at first male flower appears	3.51	0.63	1.77	31.11	1.67-6.20	1.62	2.82	36.39	47.88	57.78	56.99
Days to first female flower opening	39.15	1.39	3.92	6.16	27.21-56.40	29.94	35.77	13.97	15.27	83.72	26.34
Days to first male flower opening	36.47	1.29	3.64	6.14	25.23-54.60	63.08	68.10	21.77	22.62	92.63	43.17
Days to first harvest	50.26	1.48	4.17	5.11	36.33-68.00	32.26	38.85	11.30	12.40	83.04	21.21
Number of fruits per plant	6.35	0.37	1.05	10.15	3.90-10.25	2.50	2.92	24.93	26.92	85.78	47.57
Average fruit weight (g)	278.32	30.17	85	18.78	65.85-540.00	6747.65	9478.92	29.51	34.98	71.18	51.29
Fruit length (cm)	20.73	0.92	2.6	7.71	6.57-35.71	20.52	23.07	21.84	23.16	88.92	42.44
Fruit breadth (cm)	6.44	0.35	0.99	9.5	2.25-10.71	2.48	2.86	24.47	26.24	86.91	46.99
Flesh thickness (cm)	1.36	0.15	0.41	18.52	0.16-2.68	0.15	0.22	29.40	34.75	71.59	51.25
Yield per plant (Kg)	1.73	0.88	2.48	9.99	0.61-3.13	0.30	0.42	31.70	37.62	71.02	55.04
Yield per plot (Kg)	8.64	0.28	0.78	12.95	3.03-15.64	7.51	10.58	31.71	37.62	71.08	55.08
Estimated yield (t/ha)	16.07	8.66	24.4	5.35	5.63-29.08	25.96	36.54	31.71	37.62	71.07	55.08
Seed cavity length (cm)	15.24	0.11	0.3	6.73	3.97-25.58	14.19	16.51	24.72	26.66	85.97	47.22
Seed cavity breadth (cm)	3.72	0.2	0.57	20.25	1.93-6.13	1.32	1.56	30.94	33.54	85.09	58.80
Seed number per fruit	280.71	1.01	2.84	20.23	164.67-410.67	4438.21	4663.36	23.73	24.32	95.17	47.69
100 seed weight (gm)	2.74	1.88	5.29	20.23	0.82-3.93	0.45	0.49	24.73	25.63	93.10	49.17