Original Research Article

Evaluation of Genetic Variability, Heritability and Genetic Advance in Cucumber (*Cucumis sativus* L.) for Various Quantitative, Qualitative and Seed Characters

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A B S T R A C T

Keywords Variability, heritability, genetic advance, GCV, PCV and additive gene	Genetic variability, heritability and genetic advance were studied in 13 genotypes of cucumber. The phenotypic coefficient of variations (PCV) was higher than the genotypic coefficients of variations (GCV) for all traits studied, indicating that the apparent variation is not only genetic but also influenced by the growing environment in the expression of the characters. The genotypic coefficients of variation and phenotypic coefficients of variation were moderate to low for all the characters except number of nodes bearing first male flower (33.02%, 33.66%) showed high GCV and PCV. High heritability coupled with high genetic advance was estimated for most of the traits viz., fruit length (100%, 58.40%), fruit weight (99%, 39.92%), vine length (98%, 36.12%), number of seeds per fruit (98%, 50.16%), number of nodes per vine (97%, 53.57%), number of fruits per vine (97%, 44.33%), number of nodes bearing first male flower (96%, 66.74%), total soluble solids (96%, 44.25%), calcium content (95%, 21.75%), number of nodes bearing first female flower (94%, 58.36%), duration of harvesting (93%, 36.04%), total fruit yield per vine (92%, 35.93%) and diameter of fruit (92%, 35.80%) thus indicating that these traits had additive gene effect so that, they are more reliable for effective selection.

Introduction

Cucumber (*Cucumis sativus* L.) is the most important crop of the family Cucurbitaceae grown commercially throughout the country. The fruits are used for preparation of cosmetic items like soap and cream and in many other ways (Dhiman and 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 al.,* 1971). It is an ideal summer vegetable crop chiefly grown for its edible tender fruits, preferred as a salad ingredient, pickles, and as a cooked vegetable (Shah *et al.,* 2016). It may further be mentioned that cucumber juice is commonly used for treating diseases of teeth and gums. Its juice is still useful for rheumatic conditions and healthy growing hair (Khulakpam *et al.,* 2015).

India being the primary centre of origin, it has accumulated a ample range of variability providing good extent for improvement in

yield and other character of cucumber through selection. The role of genetic variability in a crop is of paramount importance in selecting the best genotypes for making rapid improvement in yield and related characters as well as to select most potential parents for making the hybridization programme successful (Naseeruddin *et al.,* 2011 and Singh *et al.,* 2014). Any crop improvement programme primarily depends on the amount of genetic variability available and the extent to which the economic traits are heritable. The coefficient of variation of phenotypic and genotypic is helpful in detecting the amount of variation present in the available strains. Heritability is the ratio of genotypic variance to the phenotypic variance. It is a good index of the transmission of characters from parents to offspring (Falconer, 1981). Heritability indicates the accuracy with which a genotype can be identified by its phenotypic performance. Indeed, heritability in broad sense contains both additive and non-additive effects (Hanson *et al.,* 1956). The knowledge of heritability and genetic advance helps the plant breeder in predicting the behaviour of the succeeding generation and making desirable selections for the improvements. Hence, the present investigation was undertaken with a view to assess the extent of genetic variation in some cucumber genotypes.

Materials and Methods

The present experiment was conducted at the Horticultural Research Centre and Department of Horticulture, H.N.B. Garhwal University, Srinagar (Garhwal), Uttarakhand (India), during summer season of 2015. Thirteen strains *viz.*, GP-1, HP-1, HP-2, K-90, Mandal, New Manipur-1, New Manipur-2, PB- Naveen, RAJ-1, RAJ-2, Seven Star, SPP-63 and Swarna Purna collected from different region of India were grown in

randomized block design with three replications at a spacing of 1.50 x 0.50 m. Recommended cultural practices were adopted for proper growth and stand of the crop. The observations were recorded for 27 different traits *viz.,* length of vine (cm), number of primary branches per vine, number of nodes per vine, days taken to opening of first male flower, number of nodes bearing first male flower, days taken to opening of first female flower, number of nodes bearing first female flower, percent of fruit setting, days to first fruit harvest, number of fruits per vine, total fruit yield per vine (kg), length of fruit (cm), weight of fruit (g), diameter of fruit (cm), duration of harvesting, (%), carbohydrate content (g/100g), protein content (g/100g), vitamin C (mg/100g), total soluble solids (°Brix), calcium content (mg/100g), phosphorus content (mg/100g), number of seeds per fruit, length of seed (mm), diameter of seed (mm), test weight (g), seed viability (%) and germination percentage (%). Five competitive plants were selected randomly from each of the plots and its replications for recording the data. The quality analysis was estimated by the procedure given by Ranganna (2004) and Mazumdar & Majumder (2003). The obtained data were subjected to analysis of variance as per the procedure described by Panse and Sukhatme (1961). Genetic variability for different parameters was estimated as suggested by Burton & De Vane (1953). Heritability and expected genetic advance was calculated according to Burton (1952) and Johnson *et al.,* (1955).

Results and Discussion

In the present investigation, the analysis of variance (Table 1) revealed significant differences at 1% level of significance for almost all the character except carbohydrate content, which showed a wide range of

variability among the 13 genotypes for all the characters. The range of variation was high for length of vine, number of primary branches per vine, number of nodes per vine, days taken to opening of first male flower, number of nodes bearing first male flower, days taken to opening of first female flower, number of nodes bearing first female flower, number of fruits per vine, length of fruit (cm), weight of fruit (g), diameter of fruit (cm), phosphorus content (mg/100g), number of seeds per fruit, seed viability (%) and germination percentage signifying the presence of enough variability among the genotypes used in the present study.

From the present experiment (Table 2), the phenotypic coefficient of variation was higher than genotypic coefficient of variation for all the characters, but the differences were narrow indicating low environmental influence in the expression for almost all the traits, thus the selection based on phenotypic performance would be reliable. Similar results have also been reported earlier by Singh & Lal (2005) in musk melon, Kumar *et al.,* (2008) in cucumber, Jat *et al.,* (2014) in kakri and Singh *et al.,* (2014) in bitter gourd. Traits which showed less variation between PCV and GCV can be directly selected for further breeding programmes. The genotypic coefficient of variation and phenotypic coefficient of variation were moderate to low for almost all the characters under this experiment. Similar findings are also reported by Arunkumar *et al.,* (2011) in cucumber and Jat *et al.,* 2014 in kakri. Number of primary branches per vine, carbohydrate content, protein content and diameter of seed were reported high differences between PCV and GCV which indicate greater environmental influence, while these characters need more improvement for direct selection. Similar results were also noted by Arunkumar *et al.,*

(2011) and Hanchinamani *et al.,* (2011) in cucumber. The highest phenotypic coefficient of variation and genotypic coefficient of variation was observed in number of nodes bearing first male flower.

An estimate of heritability in the broad sense includes both additive and non-additive gene effects and in the narrow sense includes only additive effects (Hanchinamani, 2006). In the present research work, high heritability was observed for most of the characters. Similar results are also reported by Hanchinamani *et al.,* (2011) in cucumber, Arunkumar *et al.,* (2011) in cucumber, Rabbani *et al.,* (2012) in ridge gourd, Dubey *et al.,* (2013) in ridge gourd, Kumar *et al.,* (2013) in cucumber and Jat *et al.,* (2014) in kakri. The traits like, carbohydrate content and diameter of seed showed low heritability, whereas other characters like, number of primary branches per vine, percent of fruit setting, days to first fruit harvest, and protein content registered moderate heritability. Similar estimate of heritability for different traits have also reported by Rabbani *et al.,* (2012) in ridge gourd, Jat *et al.,* (2014) in kakri and Arunkumar *et al.,* (2011) in cucumber.

The heritability estimates alter in interaction with the environment as well as genetic condition; in general, it should be studied along with the genetic gain for characters in concern for effective and a pin point for selection (Rajput *et al.,* 1996). In present research work, high heritability with high genetic advance over mean were recorded for length of vine, number of nodes per vine, number of nodes bearing first male flower, number of nodes bearing first female flower, number of fruits per vine, total fruit yield per vine, length of fruit, weight of fruit, diameter of fruit, duration of harvesting, TSS, calcium content, phosphorus content and number of seeds per fruit.

Table.1 Analysis of variance of cucumber (*Cucumis sativus* L.) strains for growth, yield, quality and seed parameters

Source of variance	Mean sum of square		
	Replication	**Treatment**	**Error**
Degree of freedom	**2**	**12**	**24**
Length of vine (cm)	11.105	3739.14**	23.39
Number of primary branches per vine	0.287	2.749**	0.280
Number of nodes per vine	0.062	114.27**	1.028
Days taken to opening of first male flower	0.036	26.45**	0.342
Number of nodes bearing first male flower	0.064	5.669**	0.072
Days taken to opening of first female flower	0.809	33.72**	0.311
Number of nodes bearing first female flower	0.064	8.25**	0.157
Percent of fruit setting	4.563	36.80**	2.773
Days to first fruit harvest	0.435	9.00**	1.342
Number of fruits per vine	0.830	30.72**	0.297
Total fruit yield per vine (kg)	0.001	0.530**	0.014
Length of fruit (cm)	0.166	95.83**	0.150
Weight of fruit (g)	25.303	2935.09**	9.163
Diameter of fruit (cm)	0.046	1.44**	0.038
Duration of harvesting	1.267	8.34**	1.156
Carbohydrate content (g/100g)	0.008	0.035*	0.0137
Protein content (g/100g)	0.008	0.008**	0.0009
Vitamin C (mg/100g)	0.102	0.532**	0.0381
Total Soluble Solids (° Brix)	0.086	3.238**	0.0455
Calcium content (mg/100g)	0.155	3.479**	0.0611
Phosphorus content (mg/100g)	0.580	15.790**	0.8195
Number of seeds per fruit	15.10	6830.66**	40.1859
Length of seed (mm)	0.002	0.022**	0.0010
Diameter of seed (mm)	0.057	0.140**	0.0416
Test weight (g)	0.242	7.016**	0.2089
Seed viability (%)	1.673	57.41**	3.4541
Germination %	1.702	105.22**	1.7275

* Significant at 5% level ** Significant at 1% level

Table.2 Estimation of component of variance, coefficients of variance, heritability, genetic advance and genetic advance over mean for growth, yield, quality and seed characters in cucumber strains

Characters	Range	Variance		Coefficients of variance (%)		Heritability h^2 (%)	Genetic advance (GA)	Genetic advance over mean GAM (%)
		GV	PV	GGV	PCV			
Length of vine (cm)	143.33-255.33	1238.58	1261.98	17.70	17.87	98	71.82	36.12
Number of primary branches per vine	4.84-8.00	0.82	1.10	13.07	15.14	75	1.61	23.25
Number of nodes per vine	16.14-38.84	37.75	38.78	26.36	26.71	97	12.49	53.57
Days taken to opening of first male flower	31.81-40.73	8.70	9.05	8.35	8.52	96	5.96	16.88
Number of nodes bearing first male flower	2.53-6.84	1.87	1.94	33.02	33.66	96	2.76	66.74
Days taken to opening of first female flower	32.29-43.37	11.14	11.45	8.91	9.03	97	6.78	18.10
Number of nodes bearing first female flower	3.58-8.87	2.70	2.86	29.15	29.98	94	3.29	58.36
Percent of fruit setting	83.13-94.13	11.34	14.12	3.72	4.15	80	6.22	6.86
Days to first fruit harvest	50.21-55.31	2.46	3.90	3.05	3.77	66	2.67	5.09
Number of fruits per vine	11.28-20.97	10.14	10.44	21.83	22.15	97	6.47	44.33
Total fruit yield per vine (kg)	1.73-3.01	0.17	0.19	18.16	18.92	92	0.82	35.93
Length of fruit (cm)	11.94-33.75	31.89	32.04	28.42	28.48	100	11.61	58.40

Characters	Range	Variance		Coefficients of variance (%)		Heritability h^2 (%)	Genetic advance (GA)	Genetic advance over mean GAM (%)
		GV	PV	GGV	PCV			
Weight of fruit (g)	111.76-225.76	975.31	984.47	19.47	19.56	99	64.03	39.92
Diameter of fruit (cm)	2.70-5.08	0.47	0.51	18.09	18.82	92	1.36	35.80
Duration of harvesting (days)	60.30-65.45	30.50	32.89	18.17	18.87	93	10.95	36.04
Carbohydrate content (g/100g)	2.18-2.53	0.01	0.02	3.53	6.04	34	0.10	4.24
Protein content (g/100g)	0.26-0.42	0.00	0.00	14.88	17.38	73	0.09	26.26
Vitamin C (mg/100g)	6.12-7.34	0.16	0.20	5.94	6.59	81	0.75	11.02
Total Soluble Solids (° Brix)	2.79-5.85	1.06	1.11	21.94	22.40	96	2.08	44.25
Calcium content (mg/100g)	7.94-11.34	1.14	1.20	10.84	11.12	95	2.14	21.75
Phosphorus content (mg/100g)	18.94-27.16	4.97	5.86	9.84	10.69	85	4.23	18.67
Number of seeds per fruit	143.33-315.00	2263.49	2303.68	24.57	24.78	98	97.15	50.16
Length of seed (mm)	0.93-1.24	0.01	0.01	7.81	8.34	88	0.16	15.08
Diameter of seed (mm)	3.05-3.69	0.03	0.07	5.46	8.21	44	0.25	7.49
Test weight (g)	27.24-32.14	2.27	2.48	5.17	5.40	92	2.97	10.19
Seed viability (%)	78.38-91.94	17.99	21.44	4.98	5.44	84	8.00	9.40
Germination %	70.59-89.42	34.50	36.23	7.37	7.55	95	11.81	14.81

High heritability with high genetic advance shows genotypic variance for these characters due to high additive gene effect (Panse, 1957). Hence, there is an ample scope for selection of traits under present study. The selection based on phenotypic performance of above mentioned characters would be useful for achieving desired results. The above results are also corroborated with the findings of Sanwal *et al.,* (2007) in sweet gourd, Kumar *et al.,* (2008) in cucumber, Singh *et al.,* (2008) in ridge gourd, Hanchinamani *et al.,* (2011) in cucumber, Samadia (2011) in ridge gourd for, Veena *et al.,* (2012) in cucumber, Kumar *et al.,* (2013) in cucumber, Jat *et al.,* (2014) in kakri, Singh *et al.,* (2014) in bitter gourd.

The days taken to opening of first male and female flower, vitamin C, phosphorus content, seed length, test weight and germination % had high heritability value coupled with a moderate genetic gain. This suggested that expression of these traits is due to the predominance role of both additive and non-additive gene action. Hence, these traits can be improved by mass selection. The results of present investigation are in line with the findings of Arunkumar *et al.,* (2011) & Hanchinamani *et al.,* (2011) in cucumber and Jat *et al.,* (2014) in kakri. High heritability with low genetic gain was observed for seed viability which suggested that predominance of non-additive gene action could be exploited through heterosis breeding. The number of primary branches per vine and protein content were moderate heritability along with high genetic gain which revealed the additive gene effects coupled with high environmental impact. The characters like percent of fruit setting and days to first fruit harvest had moderate heritability with low genetic gain which is highly influence by environmental factors. Similar result was

also reported by Arunkumar *et al.,* (2011) in cucumber. Carbohydrate content and seed diameter revealed low heritability with low genetic gain which indicates that these traits were also highly interfered by environment and selection would be ineffective.

From the present study, it is obvious that genotypes studied may provide good source of material for advance breeding program. Therefore, information on the genetic parameters such as genetic correlation coefficient, coefficient of variation, heritability and genetic advance can help the breeder to develop suitable cultivars within a short time. On the basis of results as summarized above, it is concluded that traits like length of vine, number of nodes per vine, number of nodes bearing first male flower, number of nodes bearing first female flower, number of fruits per vine, total fruit yield per vine, length of fruit, weight of fruit, diameter of fruit, duration of harvesting, TSS, calcium content, phosphorus content and number of seeds per fruit can be considered as suitable selection criteria for the improvement of high yielding cucumber varieties.

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