



STUDIES ON GENETIC VARIABILITY, HERITABILITY AND GENETIC ADVANCE IN CUCUMBER (*Cucumis sativus* L.)

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ABSTRACT: A field experiment was conducted with 20 diverse genotypes (BSC-1, BSC-2, CH-122, 126, 128, CHC-1, Swarna Ageta, VRC-11-2, CC-3, CC-8, DR/NKV/02, VRC-19, CC-2, 4, 5, 6, 7, 9, 1 and Ranchi-1) in randomized block design with three replications. Analyzed data revealed that among all the genotypes CC-5, BSC-2, BSC-1, CH-128, CHC-2 and CC-2 gave promising results.

Keywords : *Cucumber, heritability, genetic advance, correlation coefficient, path analysis.*

Cucumber is one of the most important cucurbits in India and grown during summer season as well as rainy season. Cucumber is second most widely cultivated cucurbits after watermelon. Its tender fruits are consumed as *salad* and for pickling. It contains protein carbohydrate, iron, phosphorus, vitamin-C and calcium. The fruit and seed possess cooling properties. Fruits are good for people suffering from constipation, jaundice and indigestion (Thambhuraraj and Singh, 6). It is cross-pollinated crop and has a wide genetic diversity. Parameters of genotypic and phenotypic coefficient of variation (GCV & PCV) are useful in detecting the amount of variability present in the available genotypes. Heritability and genetic advance help in determining the influence of environment in expression of the characters and the extent to which improvement is possible after selection. The present investigation was, therefore, under taken to ascertain magnitude and extent of genetic variability, heritability and genetic advance, in cucumber.

MATERIALS AND METHODS

The experimental material included 20 diverse entries (BSC-1, BSC-2, CH-122, CH-126, CH-128, CHC-1, Swarna Ageta, VRC-11-2, CC-3, CC-8, DR/NKV/02, VRC-19, CC-2, CC-4, 2 CC-5, CC-6, CC-7, CC-9, CC-1 and Ranchi-1) and were sown in during *rainy* season in the year of 2005-06 in randomized block design with three replications at

Vegetable Research Farm, Banaras Hindu University, Varanasi. Row-to-row and plant-to-plant spacings were maintained at 1.5 and 50 cm, respectively. All the agronomic package of practices were adopted to grow a healthy crop in each replication. Randomly 5 plants in each genotype were marked for observation. Observations were recorded on sixteen characters *viz.*, days to 50% germination, days to first male flower anthesis, days to first female flower anthesis, node no. bearing first male flower, node no. bearing first female flower, vine length (m), no. of branches/ vine, nodes no. bearing female flower/ vine, no. of fruits/vine, fruit diameter at edible stage(cm), fruit length at edible stage (cm), fruit weight at edible stage(g), 100- seed weight (g), cavity of fruit at edible stage (cm), days to first harvest and fruit yield / vine. The recorded data were analyzed as suggested by Panse and Sukhatme (5) for analysis of variance. The genotypic and phenotypic coefficient of variance was calculated as per the formula suggested by Burton and De Vane (1) and Johnson *et al.* (2) for heritability and genetic advance.

RESULTS AND DISCUSSION

The mean sum of square was highly significant for all traits, indicating the presence of wide variability in the genotypes (Table 1). Fruit weight at edible stage showed a wide range (97.75-230.43), the minimum and maximum fruit weight at edible stage was recorded in genotypes

DR/NKV/02 and CC-7, respectively. Days to 50% germination ranged from 3.96 (CH-126) to 5.73 (CC-5), with a mean of 4.84. Days to first fruit harvest and days to first female flower anthesis also registered considerable variability, which ranged from 43.24 (CC-7) to 58.27 (CC-9) and 35.45 (CC-7) to 49.55 (CC-9), respectively. Maximum vine length was recorded in VRC-19 and minimum in CHC-1 while maximum and minimum no. of branches/ vine were recorded in CC-5 and CC-3, respectively. The present set of genotypes possessed an average of 3.95 node numbers bearing first male flower, which ranged from 2.91 (Swarna Ageta) to 4.94 (DR/NKV/02), while in case of nodes no. bearing first female flower 4.51 (Swarna Ageta) to 7.60 (CC-6) and its mean value was 6.03. The genotype CC-7 exhibited maximum length of edible fruit (24.94 cm) while it was minimum in CC-1 (13.80 cm). Average no. of fruits/vine showed wide range (7.84-13.80). The minimum and maximum 100 seed weight was recorded in CH-122 and CC-5, respectively. Maximum cavity of fruits at edible stage was recorded in CC-1 whereas, minimum in CC-9, respectively. The maximum and minimum fruit diameter was recorded in BSC-1 and VRC-11-2. Node numbers bearing female flower/vine showed a wide range (9.49-16.25), with maximum and minimum in CC-1 and CHC-1, respectively. Days to first male flower anthesis was recorded maximum in CC-9 and minimum in CC-7, respectively. The minimum and maximum fruit yield/vine was recorded in CC-6 and CC-5, respectively. Results are in accordance with findings of Joshi *et al.* (3) and Mariappan and Pappiah (4).

In general, the phenotypic variance and phenotypic coefficients of variation were higher than the respective genotypic variance and genotypic coefficients of variation for all the traits (Table 2) indicating a considerable influence of environment on their expression. In the present investigation, genotypes were found to possess a high to moderate phenotypic variation for various characters as revealed by PCV. Phenotypic

coefficient of variation varied from 6.55% (days to first fruit harvest) to 670.54 (days to first female flower anthesis). The PCV expressed in form of percentage were comparatively high for days to first female flower anthesis followed by node numbers bearing female flower/vine, no. of branches/vine, vine length, fruit yield/vine, days to 50% germination, cavity of fruit at edible stage, node numbers bearing first male flower, numbers of fruits/vine and nodes numbers bearing first female flower. As the estimates of phenotypic variability can not differentiate between the effects of genetic and environmental effects, so the study of genetic variability is effective in partitioning out the real genetical differences. Higher the GCV, more the chances of improvement in that characters.

In the present investigation, GCV were comparatively high for days to first female flower anthesis followed by node numbers bearing female flower/vine, cavity of fruit at edible stage, no. of branches/vine, fruit yield/vine, numbers of fruits/vine, fruit length, 100-seed weight, node numbers bearing first male flower and vine length. The GCV was less than the corresponding PCV, indicating the role in the expression of the traits under observation. The difference between GCV and PCV were more in case of days to first female flower anthesis and node numbers bearing female flower/vine. The large difference between GCV and PCV indicated that environmental affects to a large extent the traits. The character having high GCV possessed better potential for further gain and improvement (Burton and DeVane, 1).

Burton and De Vane (1) suggested that GCV together with heritability estimate would give the best option expected for selection. Heritability estimated were high > 90% for days to first male flower anthesis, nodes no. bearing first female flower, vine length, numbers of branches/ vine, no. of fruits/vine, fruit diameter at edible stage, fruit length, fruit weight at edible stage, 100 seed weight, days to first fruit harvest and fruit yield /vine.

High heritability for the characters controlled

Table 1: Range, mean and analysis of variance for different quantitative characters in cucumber.

Characters	Range		Mean	Standard MSS value error		CD (P =0.05)
	Minimum	Maximum				
Days to 50% germination	3.96 (CH-126)	3.73 (CC-5)	484	0.75	1.31**	1.51
Days to first male flower anthesis	33.32 (CC-7)	46.81 (CC-9)	40.06	0.74	2.32**	1.53
Days to first female flower anthesis	35.45 (CC-7)	49.55 (CC-9)	42.50	0.42	503.15* *	0.863
Nodes no. bearing first male flower anthesis	2.91 (Swarna Ageta)	4.97 (DR/NKV/02)	3.95	0.39	00.230	0.80
Nodes no. bearing first female flower anthesis	4.51 (Swarna Ageta)	7.60 (CC-6)	6.03	0.49	0.761**	1.05
Vine length (m)	1.45 (CHC-1)	2.68 (VRC-19)	2.06	0.29	0.157	0.59
No.of branches/vine	1.43 (CC-3)	3.20 (CC-5)	2.32	0.11	0.118	0.21
Nodes no. bearing female flower/vine	9.49 (CHC-1)	16.25 (CC-1)	12.87	0.15	72.42**	0.30
No.of fruits/vine	7.84 (Swarna Ageta)	13.80 (CC-5)	10.82	0.32	0.104	0.65
Fruit diameter at edible stage (cm)	2.80 (VRV-11-2)	4.25 (BSC-1)	3.52	0.55	0.161	0.11
Fruit length at edible stage (cm)	13.80 (CC-1)	24.94 (CC-7)	19.37	0.56	1.32**	0.12
Fruit weight at edible stage (g)	97.75 (DR/NKV/02)	230.43 (CC-7)	164.0 9	0.21	9.58**	0.43
100 seed weight (g)	2.01 (CH-122)	2.98 (CC-5)	2.49	0.14	0.184	0.28
Cavity of fruit at edible stage (cm)	0.20 (CC-9)	0.38 (CC-1)	0.29	0.09	0.464*	0.16
Days to first fruit harvest	43.24 (CC-7)	58.27 (CC-9)	50.97	0.12	2.78**	0.25
Fruit yield /vine	1.41 (CC-6)	2.59 (CC-5)	2.00	0.13	6.71**	0.26

by polygene might be to plant breeder for making effective selection. Moderate heritability (70-80%) are found for node numbers bearing female flower/vine and cavity of fruit at edible stage suggested that the environmental effects constitute a major portion of the total phenotypic variation and hence direct selection for these traits will be less effective. Johnson *et al.* (2) reported that the heritability estimates along with genetic advance is more useful than the resultant effect for selecting the best genotype(s) as it suggest the presence of additive gene effect. High estimate of genetic advance was recorded for days to first female

flower anthesis followed by fruit weight at edible stage.

The information on heritability alone may be misleading when used in combination with genetic advance, the utility of heritability estimates increases. In the present study, high genetic advance coupled with high heritability was observed for no. of branches/vine followed by cavity of fruit at edible stage, fruit yield/vine, no. of fruits/vine, fruit length and 100 seed weight. It indicated that additive gene effects were more important for these traits. Therefore, improvement

Table 2: Components of variance, coefficient of variation, heritability, genetic advance as percentage of mean for different quantitative traits.

Characters	Variance		Coefficient of variation		Heritability	Genetic advance	Genetic advance as % of mean
	P	G	P	G			
Days to 50% germination	1.87	1.03	20.36	8.43	55.17	0.31	6.72
Days to first male flower anthesis	2.41	2.28	8.75	8.10	94.57	6.48	16.72
Days to first female flower anthesis	1205.91	151.77	670.54	214.53	12.58	1148.78	141.39
Node nos. bearing first male flower anthesis	2.23	2.21	17.52	13.50	99.95	0.94	22.49
Node nos. bearing first female flower anthesis	0.10	0.59	16.21	12.71	56.22	1.23	20.58
Vine length (m)	1.26	1.15	21.97	12.81	99.60	0.33	15.51
No. of branches / vine	1.17	1.16	24.99	18.57	99.57	1.11	48.69
Node nos. bearing female flower / vine	84.41	66.43	497.05	24.32	78.69	0.54	1.46
No. of fruits / vine	7.24	7.14	16.44	16.12	98.66	3.45	32.98
Fruit diameter at edible stage (cm)	0.16	0.16	11.51	11.34	99.98	0.84	22.96
Fruit length at edible stage (cm)	1.32	1.32	15.12	15.02	100.00	5.72	30.93
Fruit weight at edible stage (g)	9.59	9.58	11.26	11.16	99.91	38.84	23.20
100 seed weight (g)	1.81	1.80	15.40	13.77	99.39	0.63	25.14
Cavity of fruit at edible stage (cm)	0.55	0.42	19.26	18.96	76.36	0.11	28.46
Days to first fruit harvest	2.70	2.77	6.55	6.54	99.74	6.60	13.47
Fruit yield /vine	6.73	6.70	21.52	18.53	99.58	0.65	36.60

in these traits would be more efficiently done through selection in the present materials.

Depending upon the variability, heritability and genetic advance estimates, it could be predicted that improvement by direct selection was possible in cucumber for traits like nodes bearing female flowers/vine, no. of branches /vine, node numbers bearing first female flower, node numbers bearing first male flower, 100 seed weight and fruit yield /vine.

REFERENCES

- Burton, G.W. and Devane (1952). Quantitative inheritance in grass. Pro. 6th 11411. *Grassland Congress J.I.*: 277-283.
- Johnson, H.W., Robinson, H. F. and Comstock, R.E. (1955). Estimates of genetic and environmental variability in Soybean. *Agron. J.*, **47**: 314-318.
- Joshi, S., Singh, M.C., Singh, B. and Visnoi, A.K. (1981). Genotypic and phenotypic variability in cucumber (*Cucumis sativus* L.). *Veg. Sci.*, **8** (2): 114-119.
- Mariappan, S. and Pappiah, C.M. (1990). Genetical studies in cucumber (*Cucumis sativus* L.). *South Indian Hort.*, **38** (2): 70-74.
- Panse, V.G. and Sukhatme, P.V. (1967). *Statistical Methods for Agricultural Workers*, I C A.R., New Delhi.
- Thamburaj and Singh, (2004). *Vegetables and tuber crops and spice*. Published by Directorate of information and publication of Agriculture (ICAR), New Delhi PP-254.