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Estimation of Various Genetic Parametres among Promising Genotypes of Cucumber (*Cucumis sativus* L.) for Yield and Yield Attributing Traits

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ABSTRACT

An investigation was carried out with nineteen genotypes of cucumber to study the nature and magnitude of genetic variability among them by considering twenty one traits at the Vegetable Research Farm of Department of Horticulture, Institute of Agricultural Sciences, Banaras Hindu University, Varanasi during Kharif 2016. High estimates of PCV and GCV were obtained for traits like number of node at which first pistillate flower appears, fruit yield (q/ha), fruit length while the moderate value was recorded for the traits like average fruit weight indicated a good deal of variability in those characters signifying the effectiveness of selection of desirable types for improvement of such characters will be rewarding. Heritability and genetic advance are important selection parameters and selection success is a reflectance of selection response. Heritability estimates along with genetic advance are normally more helpful in predicting the gain under selection than heritability estimates alone. High heritability coupled with high genetic advance as percentage of mean were observed for number of node at which first pistillate flower appears followed by fruit yield (q/ha), fruit length, average fruit weight, test weight, number of fruits per plant, number of nodes per vine, number of primary branches per vine, etc., indicating predominance of additive gene action for these characters. Hence, simple selection based on phenotypic performance of these characters would be more effective.

Key words: *Cucumis sativus L., Genetic variability, Heritability, Genetic advance, Yield traits*

INTRODUCTION

Cucumber (*Cucumis sativus* L.) constitutes an appreciable share of our daily diet. Although, the nutritive value of cucumber is low but this is the first choice for health conscious people and especially for those who desire to lose extra body weight. Cucumber is considered as a crop of good medicinal importance and one of the health ameliorating vegetables.

Cucumber is basically a summer season crop but they are now being cultivated almost round the year in one or other parts of India. It has, therefore, become pertinent to focus attention on developing season specific improved varieties with early maturity, high yield, quality, adaptability, and resistance against biotic and abiotic stresses.

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In order to achieve improvement in any crop species, the knowledge of genetic variability for characters of economic importance and their heritability and genetic advance is of utmost importance and very much essential for planning future breeding programmes. Keeping in view, then above facts an experiment was conducted to study the variability, heritability, and genetic advance on elite genotypes of cucumbers.

MATERIALS AND METHODS

The present experiment was conducted with 19 genotypes of cucumber during *Kharif* 2016 at the Vegetable Research Farm of Department of Horticulture, Institute of Agricultural Sciences, Banaras Hindu University, Varanasi. The experimental design followed was Randomized Complete Block Design (RCBD) and each line was replicated thrice with a spacing of 60 cm between plant to plant and 150 cm between row to row. Five plants from each replication were selected in a random manner and observations were recorded on twenty one characters viz., days to 50 per cent germination, vine length (cm), number of primary branches per plant, internodal length (cm), number of nodes per vine, number of node at which first staminate flower appears, number of node at which first pistillate flower appears, days to first staminate flowering, days to 50 per cent staminate flowering, days to first pistillate flowering, days to 50 per cent pistillate flowering, number of staminate flowers per plant, number of pistillate flowers per plant, sex ratio, days to first fruit picking, number of fruits per plant, fruit length (cm), fruit width (cm), average fruit weight (g), fruit yield (q/ha), and test weight (g). The mean over replication of each character was subjected to statistical analyses. Both phenotypic and genotypic coefficient of variation for all the characters were estimated using the formula of Burton[2]. The broad sense heritability (h^2b) was estimated for all the characters as the ratio of genotypic to the phenotypic variance as suggested by Lush[6] and Johnson *et al.*[4]. The expected genetic advance is defined as the difference between the mean of the progeny of selected individuals and the base population was computed with the help of the formula as suggested by Johnson *et al*[4].

RESULTS AND DISCUSSION

The analysis of variance revealed high significant variations among the genotypes for all the characters under study indicating sufficient variability existed in the materials selected for the present investigation and showing the scope for selection of suitable initial breeding parents for betterment of the crops. However the absolute variability in selected characters does not permit identification of the characters indicating the highest degree of variability. For any sound breeding programme, it is essential to have a large variation in available materials in the hand of breeder. The variability among the genotypes for the selected characters has been presented in the ANOVA (Table 1). Mean performances and range which showed a high variation among the genotypes for all the traits along with heritability, GCV, PCV, and genetic advance as per mean per cent are presented in the Figure 1 and Table 2. It had been recorded that PCV was found to be higher than GCV for all the recorded traits indicating that the apparent variation is not only due to genotypes but also due to influence of environment (Table 2). As the environmental variation is highly unpredictable as compared with genotypic and phenotypic, thus it is required to make selection on the basis of phenotypic variation. The high value of both genotypic and phenotypic coefficient of variations were noticed in case of traits viz., number of node at which first pistillate flower appears, yield (q/ha), fruit length (cm) while the moderate value was recorded for the traits like average fruit weight, number of primary branches per vine, test weight, number of nodes per vine, number of fruits per plant, internodal length, vine length, total number of pistillate flowers per plant, fruit width, and sex ratio whereas low level of GCV and PCV were recorded in the characters like days to first pistillate flowering, total number of staminate flowers per plant, days to 50 per cent pistillate flowering, days to first staminate flowering, days to 50 per cent staminate flowering, and days to first fruit picking. The maximum difference of GCV and PCV was seen in case of days to 50 per cent germination. It is also observed that PCV is more than GCV for all the recorded characters. These finding were found similar to the earlier findings of Shukla *et al.*[10], Choudhary *et al.*[3] and Muddarasu *et al.*[8]. The heritability estimates indicate the relative amount of heritable variation. Calculation of heritability facilitates plant breeders to limit the extent of selection pressure to be applied under a particular environment, which separates out the environmental influence from total variability. Therefore heritability in broad sense was estimated. Heritability estimates in cultivated plants could be placed in the following categories as suggested by Robinson *et al.*[9] i.e., Low: 0-30%, Moderate: 30-60%, High: > 60%. In the present investigation, most of the traits exhibited high heritability (> 60%) except days to 50 per cent germination and number of node at which first staminate flower appears with highest (99%) for average fruit weight (g), fruit yield (q/ha), and test weight (g). High heritability estimate indicates less influence of environment on respective traits. Hence, direct selection can be followed to improve early maturing genotypes. Results are resembled with the findings of Kumar *et al.*[5], Afreen *et al.*[1] and Mehta *et al.*[7]. Without high genetic advance there is no any significance of high heritability. Very often heritability in broad sense is not the true indicator of inheritance of traits, since only additive components of genetic variance is transferred from generation to generation. Therefore heritability in broad sense may mislead in judging the effectiveness of selection for the trait. Hence heritability along with genetic advance as per cent of mean (GAM) is reliable in predicting the resultant effect of selection. In the present investigation, high heritability (> 60%) coupled with high genetic advance was found in the traits like number of node at which first pistillate flower appears followed by fruit yield (q/ha), fruit length (cm), average fruit weight (g), test weight (g), number of fruits per plant, number of nodes per vine, number of primary branches per vine, internodal length (cm), vine length (cm), total number of pistillate flowers per plant, sex ratio, and fruit width (cm). This indicates that these characters were under strong influence of additive gene action and hence simple selection based on phenotypic performance of these traits would be more effective. Results are resembled with the findings of Singh *et al.*[11], Kumar *et al.*[5] and Mehta *et al*[7].

Table 1: Analysis of Variance (ANOVA) for yield and yield attributing characters in cucumber

Sources of variation	Degrees of freedom	Days to 50 per cent germination	Vine length (cm)	Number of primary branches per vine	Internodal length (cm)	Number of nodes per vine	Number of node at which first staminate flower appears	Number of node at which first pistillate flower appears	Days to first staminate flowering	Days to 50 per cent staminate flowering	Days to first pistillate flowering	Days to 50 per cent pistillate flowering	Number of staminate flowers per plant	Number of pistillate flowers per plant	Sex ratio	Days to first fruit picking	Number of fruits per plant	Fruit length (cm)	Fruit width (cm)	Average fruit weight (g)	Fruit yield (q/ha)	Test weight (g)
Replication	2	0.333	21.474	0.006	0.014	0.886	0.101	0.217	0.518	0.240	2.632	0.339	45.402	0.767	0.912	0.333	0.063	0.015	0.010	6.764	14.772	0.000
Genotypes	18	0.631	571.249*	1.253	4.153*	85.053	1.137	29.524*	14.234*	13.491*	57.771*	33.651*	1142.038*	9.732*	22.967*	22.625*	5.736*	37.271*	0.667	2412.322*	5774.883*	0.715
Error	36	0.277	10.373	0.102	0.335	2.476	0.229	0.407	0.763	0.933	1.878	1.909	14.601	0.430	1.249	0.222	0.074	0.337	0.039	4.527	10.824	0.001

*Significant at 5% level

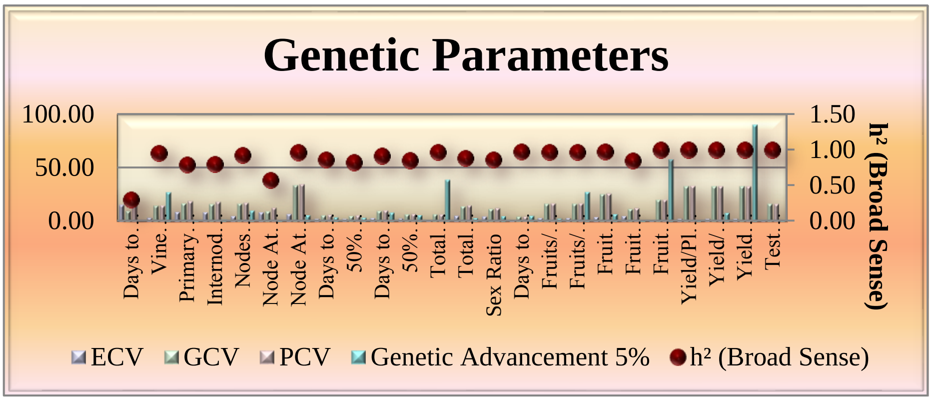

Fig 1: Genetic parameters of cucumber genotypes for various yield and yield attributing characters

Table 2: Estimates of variability and genetic parameters for yield and yield components in cucumber

Characters	Mean	Range		GCV	PCV	h^2b	GA	GA as per cent of mean
		Minimum	Maximum					
Days to 50 per cent germination	3.56	3.00	4.33	9.64	17.66	0.30	0.39	10.84
Vine length (cm)	94.63	70.83	113.73	14.45	14.84	0.95	27.42	28.97
Number of primary branches per vine	3.70	2.40	4.87	16.72	18.83	0.79	1.13	30.59
Internodal length (cm)	7.00	5.73	10.67	16.11	18.11	0.79	2.07	29.52
Number of nodes per vine	31.96	25.07	42.53	16.42	17.14	0.92	10.35	32.39
Number of node at which first staminate flower appears	5.75	5.07	7.07	9.57	12.69	0.57	0.85	14.86
Number of node at which first pistillate flower appears	9.38	5.47	18.40	33.21	33.90	0.96	6.29	67.01
Days to first staminate flowering	36.10	31.07	39.20	5.87	6.35	0.85	4.04	11.18
Days to 50 per cent staminate flowering	38.33	34.00	42.07	5.34	5.90	0.82	3.81	9.94
Days to first pistillate flowering	43.95	38.20	52.47	9.82	10.30	0.91	8.47	19.28
Days to 50 per cent pistillate flowering	49.13	41.20	55.67	6.62	7.19	0.85	6.17	12.55
Number of staminate flowers per plant	289.90	249.50	320.88	6.69	6.82	0.96	39.18	13.51
Number of pistillate flowers per plant	12.54	10.53	17.27	14.04	14.98	0.88	3.40	27.10
Sex ratio	23.47	17.03	28.40	11.46	12.41	0.85	5.12	21.81
Days to first fruit picking	59.97	57.00	66.33	4.56	4.62	0.97	5.55	9.25
Number of fruits per plant	8.42	5.48	10.67	16.32	16.63	0.96	2.78	32.96
Fruit length (cm)	13.95	10.73	26.93	25.16	25.50	0.97	7.13	51.13
Fruit width (cm)	3.99	3.09	4.63	11.47	12.50	0.84	0.87	21.68
Average fruit weight (g)	142.88	101.90	194.41	19.83	19.88	0.99	58.20	40.72
Fruit yield (q/ha)	135.99	61.99	230.36	32.23	32.32	0.99	90.04	66.21
Test weight (g)	2.97	2.16	3.90	16.42	16.47	0.99	1.00	33.70

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