

P-ISSN: 2349–8528 E-ISSN: 2321–4902 IJCS 2018; 6(5): 236-238 © 2018 IJCS Received: 05-07-2018 Accepted: 10-08-2018

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Genetic variability and correlation studies for productivity traits in cucumber (Cucumis sativus L.)

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Abstract

Thirty cucumber cultivars were evaluated for growth and yield traits at College of Horticulture, Sirsi Karnataka. Results revealed that significant genetic variability present among genotypes for various traits, a high range of variation; high GCV and high heritability coupled with high genetic advance was recorded for node at first female flower, number of male flower, number of female flower, fruit weight, flesh thickness, fruit length and fruit width. It reveals that broad genetic base, less environmental influence and these traits are under control of additive genes. Further correlation analysis showed that number of female flower, fruit diameter and fruit number / vine had highly significant association with fruit yield. These traits can be used for parental selection in the improvement of local cultivars.

Keywords: genetic variability, correlation, heritability, genetic advance and cucumber

Introduction

Cucumber (*Cucumis sativus* L.) is one of the most widely cultivated vegetables, ranked fourth after tomato, onion and cabbage. It is native to India. Cucumber is nutritionally very rich in vitamins and minerals. Cucumber cultivation goes back to at least 3000 years in India and 2000 years in China. In India, it is cultivated in an area of 0.26 lakh hectares with an annual production of 1.65 lakh metric tonnes, whereas the world area is 2.44 million hectares with a production of 80.61 million metric tonnes (http://www.fao.org/faostat/en/#data/QC).

In Karnataka cucumber is growing in almost all corners. But available variability for cucumber crop improvement is limited. Uttara Kannada district is a land of indigenous vegetables. It is located between 13°55' to 15°32' N latitude and 74°05' to 75° 05' E longitude. It has geographical area of 10,291 km². Topographically, this district may be divided into three distinct zones or regions; the narrow coastal line, the abruptly rising hills of the Western Ghats, and the flatter, elevated eastern portion that merges with the Deccan Plateau. Uttara Kannada District has unique types of cucumber cultivars (Mull southe) which is used as major ingredient for preparation of various dishes. Owing to the high cross pollination in cucumber hardly any purity can be found or maintained. It shows a wide range of variability in existing germplasm also there is no uniformity in important traits such as fruit size, shape, colour, quality and yield. For attaining the uniformity in these traits a good understanding of genetic stock of cucumber and selection of superior genotypes is very important in hybridization programme. In general, variability is the basic material for any crop improvement programme. Therefore, knowledge about the existence of genetic variability is the useful adjunct to carry out effective selection for improving yield.

An estimate of phenotypic and genotypic variation quantifies the amount of variability present within a set of breeding material with regard to its essential characteristics. Heritability and predicted genetic advance indicate the quantum of improvement attainable through selection. Further yield is a complex trait and depended on other associated traits. Correlation studies helps for deciding which trait contribute towards yield positively or negatively. With this background present investigation is taken to evaluate available cucumber genotypes for assessing genetic variability and correlation present in various growth and yield related traits.

Material and Methods

The experimental material for the study consisted of 25 diverse cucumber germplasm lines obtained from Indian Vegetable Research Institute, Varanasi and five local cucumber lines

were collected from different regions of Karnataka. These diverse lines were evaluated for different growth and yield parameters at College of Horticulture Sirsi Karnataka following the recommended package of practice. The experiment was laid out in complete randomized design with three replications and all the entries were allotted randomly using random number table. Genotypes were first raised portrays by using coco peat as a media and seedlings were transplanted into the main field after 21 days. The spacing 1m between plant to plant and 2 m between row to row was followed and each row contains eight seedlings. Recommended cultural operations and plant protection measures were taken up to ensure uniform and healthy crop stand as per package of practices. The observations were recorded for five plants in each replications on ten yield traits and mean values were used for analysis. The analysis of variance for different characters was carried out using mean data in order to assess the genetic variability among genotypes as given by Cochran and Cox (1957) [5]. The phenotypic and genotypic coefficients of variability were computed as per the methods of Burton and De Vane (1953) ^[4]. The method of (Johnson *et al.*, 1955) ^[8] was followed for estimation of broad sense heritability and genetic advance for all the traits recorded. The correlation co-efficient among all possible character combinations were estimated employing formula (Al-Jibouri et al. 1958)^[2].

Results and Discussion

The analysis of variance for yield and its related traits in the present set of cucumber accessions revealed significant differences for all the traits (Table 1). This suggested that there is an inherent genetic difference among the genotypes. The results of Phenotypic Coefficient of Variability (PCV), Genotypic Coefficient of Variability (GCV), heritability and genetic advance were presented in Table 2. For all the characters PCV were generally higher than GCV which indicated that substantial influence of environment in the expression of these characters. The characters like node at first female flower appears, number of female flowers, Fruit yield/vine, flesh thickness, number of branches at 60 DAS, fruit length, fruit diameter and fruit number per vine showed high phenotypic and genotypic coefficient of variation. This reflects greater genetic variability among genotypes for these characters, to facilitate further improvement by selection. Since the narrow difference between PCV and GCV values for all the characters may be expected that the influence of environment on the expression of these traits were negligible simple selection would be highly effective for further improvement. Veena et al., (2012)^[10] also reported similar results for traits like node at first female flower appears, yield per plant, flesh thickness, average fruit weight and number of fruits per vine.

The co-efficient of variation at genotypic and phenotypic levels explain only the extent of variability in different traits, but this variation fails to explain the amount of heritable portion. In this situation, heritability in broad sense has an important role in the determining the heritable portion of variation.

Knowledge of heritability of a trait is an essential measure to breeder in choosing suitable genotypes to employ in improving the trait under specified situation and it 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) [8] had shown that heritability and genetic advance should be jointly considered for reliable conclusion. The results in the experiment revealed higher heritability estimate for all the characters. High heritability indicates less influence of environment and is governed by additive gene effects. Similar results was also reported by Dhiman and Chander Prakash (2005)^[6] and Arunkumar et al., (2011)^[3] and Veena et al. (2012)^[10].

Genetic advance under selection depends mainly on the extent of genetic variability in the base population, intensity of the selection, magnitude of the masking effect of environment and interaction components of variability.

In the present study all the characters studied showed high heritability coupled with high genetic advance which indicated additive gene action in the control of making these characters to respond better for selection. The characters with high genotypic variance and high heritability coupled with high genetic gain would be effective for selection in improvement of the crop. Veena *et al.* (2012)^[10] noticed high heritability coupled with high genetic advance in traits *viz.*, nodes at first female flower appears, fruit yield per vine, fruit length, fruit width and flesh thickness. 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)^[9]. Thus the traits with high heritability coupled with high genetic advance can be consider improvement of cucumber cultivars.

Yield being a complex quantitative character, direct selection for yield may not result in successful improvement. Correlation coefficient analysis measures the mutual relationship between various plant characters and determines the component characters on which selection can be based for improvement of an associated complex quantitative character like yield. The correlation study revealed that number of female flower, fruit diameter and number of fruits per vine had positive highly significant correlation with fruit yield per plant. However, vine length @ 60DAS had negative highly significant correlation with fruit yield per plant. The fruit number per vine had positive highly significant correlation with number of female flower whereas flesh thickness had negative highly significant correlation with fruit number per vine (Table 3). These findings are in agreement with the earlier reports of Afangideh and Uyoh, (2007)^[1] and Hossain et al. (2010)^[7]. In conclusion selection based on number of female flower, fruit length, fruit diameter and average fruit weight traits will enhance the productivity of cucumber and these trait can be consider for selection of parents for the improvement of local cultivars.

Table 1: Analysis of variance (mean square values) of cucumber genotypes for 10 different growth and yield characters

Source of variation	df	Node at first female flower	Number of female flower	Vine length @60DAS (cm)	Number of branches @60DAS	Fruit length (cm)	Fruit Width (cm)	Flesh thickness (cm)	Fruit diameter (cm)	Fruit number / vine	Fruit yield / vine (g)
Genotype	29	22.893**	4.083**	3146.67**	2.169**	36.49**	4.23**	0.706**	43.35**	0.525**	20841.56**
Replication	2	0.833	0.033	104.533	0.033	1.194	0.070	0.008	0.374	0.075	64.974
Error	58	1.144	0.395	144.012	0.275	2.124	0.1	0.018	1.143	0.023	1298.491

Table 2: Estimates of mean range a	nd genetic parameter	s for growth and vie	eld traits in the cucumb	er genotypes.

Characters	Moon	Range		PCV	GCV	Heritability in broad sense	GA as%
Characters	Mean±SE	Lowest	Highest	(%)	(%)	(%)	Mean
Node at first female flower appears	5.30±0.50	1.00	10.50	54.66	50.8	86.37	97.26
Number of female flower	2.37±0.21	1.00	6.00	53.84	46.84	75.68	83.95
Vine length @60DAS (cm)	80.53±5.91	31.75	143.00	42.02	39.28	87.42	75.66
Number of branches @60DAS	1.97±0.16	1.00	4.00	48.4	40.39	69.65	69.45
Fruit length (cm)	12.19±0.64	5.50	20.95	30.23	27.76	84.36	52.53
Fruit Width (cm)	5.97±0.26	3.00	8.30	20.36	19.66	93.23	39.11
Fruit diameter(cm)	17.85±0.69	10.80	27.30	21.85	21.06	92.49	41.63
Flesh thickness(cm)	1.30±0.15	0.50	3.00	38.25	36.84	92.72	73.07
Fruit number / vine	1.15±0.076	1.00	3.00	37.93	35.57	87.92	68.71
Fruit yield / vine (g)	172.47±15.22	40.00	405.00	51.25	46.8	83.38	88.03

Table 3: Phenotypic correlation coefficients among fruit yield and its components in cucumber

Characters	X1	X2	X3	X4	X5	X6	X7	X8	X9	X10
X1	1.000	-0.257	0.135	-0.063	-0.073	-0.023	0.050	0.156	-0.280	-0.078
X2		1.000	0.026	0.297	0.044	0.051	0.155	-0.232	0.843**	0.629**
X3			1.000	0.003	-0.106	-0.070	0.232	0.041	0.068	-0.424**
X4				1.000	0.425	0.152	0.100	-0.074	0.256*	0.155
X5					1.000	0.210	0.018	0.033	-0.023	0.076
X6						1.000	0.256	0.058	-0.051	0.152
X7							1.000	0.138	0.171	0.498**
X8								1.000	-0.350**	-0.106
X9									1.000	0.658**
X10										1.000

Note: *, ** indicates P=0.05 & P=0.01 significant level respectively

X1- Node at first female flower appears, X2- Number of female flower, X3- Vine length @60DAS (cm), X4- Number of branches @60DAS, X5- Fruit length (cm), X6- Fruit Width (cm), X7- Fruit diameter(cm), X8- Flesh thickness(cm), X9- Fruit number / vine, X10- Fruit yield / vine (g)

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