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Sudhir Kumar Mishra

Research Student, Department of Horticulture, Sam Higginbottom University of Agriculture, Technology & Sciences, Naini, Allahabad, Uttar Pradesh, India

Sapna Roy

Research Student, Department of Horticulture, Sam Higginbottom University of Agriculture, Technology & Sciences, Naini, Allahabad, Uttar Pradesh, India

Naveen Kumar

Assistant Professor, Department of Entomology National Post Graduate College Barhalganj Gorakhpur, Uttar Pradesh, India

VM Prasad

Professor and Head, Department of Horticulture, Sam Higginbottom University of Agriculture, Technology & Sciences, Naini, Allahabad, Uttar Pradesh, India

Corresponding Author:**Sudhir Kumar Mishra**

Research Student, Department of Horticulture, Sam Higginbottom University of Agriculture, Technology & Sciences, Naini, Allahabad, Uttar Pradesh, India

Genetic evaluation of cucumber (*Cucumis sativus* L.) genotypes for yield and yield contributing traits

Sudhir Kumar Mishra, Sapna Roy, Naveen Kumar and VM Prasad

Abstract

A field experiment was conducted at research field, Department of Horticulture, Sam Higginbottom University of Agriculture, Technology & Sciences, Naini, Prayagraj for genetic evaluation of twelve genotypes of cucumber for yield and related traits. Analysis of variance indicates that twelve diverse genotype of cucumber including one commercial cultivar (Pusa Barkha) differed significantly for the seventeen traits. The higher magnitude of coefficient of variation at phenotypic as well as genotypic levels was recorded among the genotypes. High heritability in broad sense were observed for average fruit yield followed by number of fruits per vine, vine length, fruit length, nodal position to first male flower and nodal position to first female flower where as in case of high genetic advance was observed for fruit yield followed by primary branches/vine, number of fruits per vine. The characters mentioned above have high heritability coupled with high genetic advance showing additive gene effect and selection for these traits is reliable for developing high yielding cultivar of cucumber.

Keywords: cucumber, GCV, PCV, heritability and genetic advance

Introduction

Cucumber (*Cucumis sativus* L.) is one of the most important cucurbitaceous vegetable crops grown extensively in tropical and sub-tropical parts of the country. It is thought to have been originated in India ^[1] because of the fact that *Cucumis sativus* var. *hardwickii*, progenitor of cultivated cucumber is found in the Himalayan foot hills of India. From India, it spreaded Eastwards to China and Westward to Asia Minor, North Africa and Southern Europe long before written history ^[2].

Cucumber is monoecious and cross-pollinated crop and having appreciable number of seeds per fruit; in which a large amount of variation has been observed for most of the economically important traits in the land races cultivars for qualitative and quantitative traits. With the increasing zeal for its cultivation, the farmers are aptly looking towards improved varieties to meet out the higher standards of quality and quantity. Although a huge number of high yielding hybrids of cucumber varying widely in respect to their yield potential, adaptability and response to inputs have been released for cultivation in open fields but only few are promising, this intact draws the attention of plant breeder for its improvement ^[3].

Selection of indeterminate type, high yielding varieties/hybrids with desirable shape, colour and quality attributes is very essential to meet the increasing demand of the consumers, improvement programme and identifying the promising hybrids and genotypes for commercial cultivation. Genetic variability, heritability and genetic advance plays an important role in crop breeding for selecting the elite genotypes for making rapid improvement in yield and other desirable characters. The main objective of any breeding programme is to search out high yielding varieties/hybrids along with disease resistance, abiotic stress tolerance, earliness, uniformity in size and increase in fruiting period.

Materials and Methods

Materials for the study comprised of twelve accessions of cucumber including one check variety ie. Pusa Barkha. The experiment was laid out in a Randomized Block Design with three replications at Department of Horticulture, Sam Higginbottom University of Agriculture, Technology & Sciences, Naini, Prayagraj during June-sep. 2017. The experiment site had sandy loam soil, low in organic carbon and slightly alkaline having pH=7.4. Twelve plants were raised separately for each accession at spacing of 150cm×50cm under three replications. The observations on seventeen characters were recorded from the selected five plants separately for each genotype.

The estimates of variability, heritability and genetic advance were computed by adopting the standard statistical methods [4, 5].

Result and Discussion

Analysis of variance in the experiment indicated that the genotypes evaluated differed significantly for all the seventeen traits. The suggested existence of wide range variability in the genotypes studied (Table 1).

The variability present in the genotypes provided the raw material for plant breeding programme on which selection acts to evolve superior genotypes. In general magnitude of PCV for all the traits were higher than the magnitude of GCV (Table 2) which indicated that environment influenced considerably in expression of these traits. The variances of various characters were compared on the basis of coefficient of variation. The estimates of phenotypic as well as genotypic coefficient of variability were observed higher for average fruit yield (48.95, 48.70%), followed by number of primary branches per vine (33.34, 32.95%), number of fruits per vine (33.02, 32.66%) and nodal position to first male flower (21.87, 21.47%), while Moderate level of phenotypic as well as genotypic coefficient of variance was seen in case of inter nodal length between 10th and 11th node (16.62, 15.76%) followed by ascorbic acid (13.88, 13.87%), fruit girth (14.22, 13.32%), average fruit weight (10.87, 12.90%) and Fruit length (12.48, 12.27%). Low level of phenotypic as well as genotypic coefficient of variability was seen in case of TSS

(9.84, 8.30%) followed by crop duration (8.13, 6.33%). These findings are similar to earlier reports of [6, 7].

The estimates of heritability in broad sense (h^2_{bs}) ranged from 24 (Days to first male flower appearance) to 99 per cent (average fruit yield). Highest estimates of heritability (> 71.00%) were observed for all the character except crop duration (61%) and days to first fruit harvest (53%), which indicated moderate heritability, while Days to first male flower appearance (24%) indicated low heritability. These findings are similar to earlier reports of [8, 9].

Highest estimates of genetic advance in per cent of mean was recorded for average fruit yield (99.81) followed by No. of primary branches per vine (67.09), number of fruits per vine (66.53%), node number to first male flower (43.42) and node number to first female flower (37.28). The Moderate genetic advance in percent of mean for other characters were Inter nodal length (30.67), vine length (27.79), ascorbic acid (27.18), fruit girth (25.71) and fruit length (24.87). The lowest value of genetic advance in percent of mean was found for first female flower appearance (4.98) and Days to first male flower appearance (2.99). The presence of high heritability coupled with high genetic advance in per cent of mean were observed for average fruit yield, number of fruits per vine, fruit length, nodal position to first male flower and nodal position to first female flower and indicating additive gene effect for those particular traits. These findings are similar to earlier reports of [10, 11].

Table 1: Analysis of variance (mean squares) for seventeen characters in cucumber.

S. No.	Characters d.f.	Source of variation		
		Replications	Treatments	Error
		2	11	22
1.	Days to 1st Male Flower Appearance	2.62	9.38**	4.88
2.	Node Number to First Male Flower	0.031	1.90**	0.023
3.	First Female Flower Appearance (days)	2.77	15.18**	4.73
4.	Node Number to First Female Flower	0.003	3.99**	0.07
5.	Days Taken to First Fruit harvest	1.61	42.99**	9.67
6.	Fruit Length (cm)	0.22	12.41**	0.14
7.	Fruit Girth (cm)	0.20	10.56**	0.47
8.	Yield Per Vine kg	0.002	1.05**	0.003
9.	Fruits Per Vine	0.095	21.12**	0.16
10.	Fruit Weight (g)	49.04	1165.43**	62.87
11.	Crop Duration days	4.94	92.35**	16.47
12.	Inter-nodal Length (cm)	0.18	7.51**	0.27
13.	Vine Length (cm)	0.30	1109.36**	10.59
14.	Primary Branches/ Vine	0.02	8.76**	0.07
15.	Flesh Thickness (cm)	0.001	0.036**	0.002
16.	TSS (°Brix)	0.012	0.33**	0.04
17.	Ascorbic Acid (mg/100 G)	0.005	0.88**	0.03

* - Significant at 5 per cent probability level

** - Significant at 1 per cent probability level

Table 2: Estimates of range, grand mean, phenotypic, genotypic, environmental, coefficients of variation, heritability in broad (h^2_{bs}) sense and genetic advance in per cent of mean (\bar{GA}) for seventeen characters in cucumber genotypes.

	Characters	Mean Value Range		Grand mean	P.C.V. (%)	G.C.V. (%)	Heritability Broad Sense (%) (h^2_{bs})	Genetic Advancement 5%	Genetic Advance in per cent of mean
		Lowest	Highest						
1.	Days to 1st Male Flower Appearance	38.33	44.67	40.94	6.17	2.99	24	1.22	2.99
2.	Node Number to First Male Flower	2.33	5.00	3.69	21.87	21.47	96	1.60	43.42
3.	First Female Flower Appearance (days)	45.33	52.67	50.22	5.71	3.72	42	2.50	4.98
4.	Node Number to First Female Flower	4.33	8.00	6.16	19.04	18.56	95	2.30	37.28
5.	Days Taken to First Fruit harvest	53.83	66.67	58.51	7.79	5.70	53	5.02	8.58
6.	Fruit Length (cm)	13.33	21.00	16.48	12.48	12.27	97	4.10	24.87
7.	Fruit Girth (cm)	10.46	15.83	13.77	14.22	13.32	88	3.54	25.71
8.	Yield Per Vine (kg)	0.40	2.26	1.21	48.95	48.70	99	1.21	99.81

9.	Fruits Per Vine	3.44	11.89	8.09	33.02	32.66	98	5.39	66.53
10.	Fruit Weight (g)	127.33	184.33	148.56	13.97	12.90	85	36.49	24.57
11.	Crop Duration days	71.33	89.33	79.50	8.13	6.33	61	8.06	10.14
12.	Inter-nodal Length (cm)	7.33	12.00	9.86	16.62	15.76	90	3.03	30.76
13.	Vine Length (cm)	100.67	168.33	139.83	13.88	13.69	97	38.87	27.79
14.	Primary Branches/ Vine	2.67	8.33	5.17	33.34	32.95	98	3.47	67.09
15.	Flesh Thickness (cm)	0.86	1.20	1.05	11.15	10.02	81	0.20	18.56
16.	TSS (°Brix)	3.12	4.20	3.73	9.84	8.30	71	0.54	14.41
17.	Ascorbic Acid (mg/100 G)	3.03	4.62	3.84	14.58	13.87	90	1.04	27.18

Conclusion

On the basis of results shown in the present investigation it is concluded that the characters fruit yield per vine (kg), number of primary branches per vine, number of fruits per vine, node number to first male flower and node number to first female flower indicated good response to selection owing to their high heritability, variability and genetic advance showing additive gene effect. These characters also keep an important role in improvement of economic yield and component traits by selection in cucumber.

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