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Assessment of genetic variability in cucumber (*Cucumis sativus* L.)

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Abstract

Information on genetic variability of yield and quality components is of vital importance in crop improvement programme. Plant breeding is mainly the exploitation of genetic variation and in view of the possible decline of variation breeders should always examine means of conserving variability and creating new germplasm. The extent of genotypic variability indicates the amenability of given character for its improvement. The present investigation was carried out during summer season of 2018 in *Tarai* region of Uttarakhand. The experimental material comprised of 36 genotypes including 8 parents and 28 F_1 hybrids. Assessment of genetic variability parameters revealed that there is lot of variation present among the genotypes studied. In general, the value of phenotypic coefficient of variation (PCV) was higher than the genotypic coefficient of variation (GCV) for all the characters studied in the present findings, indicating the considerable influence of environmental factors on the performance of genotypes for different characters. Phenotypic coefficient of variation (PCV) was higher than the genotypic coefficient of variation (GCV) for all the characters studied in the present findings, indicating the considerable influence of environmental factors on the performance of genotypes for different characters. Moderate to high GCV together with moderate to high heritability and genetic advance as per cent of mean was reported for majority of the characters. Thus these traits have ample scope for the improvement of concerned traits through selection.

Keywords: Genetic variability, heritability and genetic advance

Introduction

Cucumber (*Cucumis sativus* L.) is one of the important Asiatic species and member of the Cucurbitaceae family having chromosome number $2n=2x=14$ which has 120 genera and more than 800 species (Jeffrey, 1980). Out of these, 34 genera and 108 species occur in India, including 38 endemic species and another 38 non-endemic species. Cucumber is originated in India (Sebastian, 2010) ^[14] from its wild progenitor *Cucumis sativus* var. *hardwickii* R., which is still found in southern foothills of Himalayas. Its spread eastwards to China and westwards to Asia Minor, North Africa and Southern Europe (Seshadri and Parthasarathy, 2002) ^[15]. One hundred gram of edible cucumber fruits contain 96g water, 0.6g protein, 0.1g fat, 2.2g carbohydrate, 45IU Vitamin A, 0.03mg Vitamin B1, 0.02mg Vitamin B2, 0.3mg Niacin, 12mg Vitamin C, 12mg Calcium, 0.3mg Iron, 15mg Magnesium and 24mg phosphorus (Alcazar and Gulick, 1983) ^[1]. It is well known for its economic importance as food plant, primarily cultivated for tender fruits, which are used as salad, pickles, and also used with curd for preparation of "Rayata". Mature fruits are also used as vegetable in India. The fruits and seed have cooling effect. Fruits are good for people suffering from constipation, Jaundice and indigestion. Fruits are demulcent and diuretic. Fruits contain photolytic enzyme, ascorbic acid oxidase, succinic and malic dehydrogenase. Fruits are also used as an astringent and antipyretic and the seed oil of cucumber is highly valuable for development of brain, therefore it is also used in Ayurvedic medicines (Robinson and Decker-Walters, 1999) ^[12]. In any crop improvement programme, it is necessary to assess the nature and magnitude of genetic variability, heritability and genetic advance in the initial parental material. The efficiency of selection largely depends upon the magnitude of variability present in the breeding population. Hence, knowledge of variability present in the gene pool of a crop species is essential to start a judicious breeding programme.

Material and Methods

The experimental material comprised of 36 genotypes (8 parents and 28 crosses) parents were selected based on their diversity for different characters. From these 8 parents, 28 F₁ crosses were developed in a half diallel mating design during February, 2018 to June, 2018 in open field condition. F₁ hybrid along with their parents were evaluated in RBD design at Vegetable Research Centre, Pantnagar during February, 2019 to June, 2019 with three replications. Fourteen quantitative characters *viz.* days to first male flower, node number to first male flower, days to first female flower, node number to first female flower, days to first harvest, days to last harvest, internodal length (cm), plant height (m), fruit length (cm), average fruit diameter (cm), number of fruits per plant, average fruit weight (g), fruit yield per plant (kg) and fruit yield (q/ha) were scored on each genotype in this experiment. Five plants were randomly selected from each genotype in each replication for recording of observations for all the plant traits. The analysis of variance for design of experiment was done for partitioning the variance into treatments and replications according to procedure given by Panse and Sukhatme (1967) [10]. Genotypic and phenotypic coefficients of variance were estimated according to Burton and Devane (1953) [2] based on estimate of genotypic and phenotypic variance. The broad sense heritability (h²_{bs}) was estimated by following the procedure suggested by Weber and Moorthy (1952) [16] and the software used for analysis was STPR-3 in the following manner.

Result and Discussion

Variability

Phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) are the best criteria to measure available variability. Genotypic coefficient of variation values for different characters are presented in Table 1. GCV was found highest for node number to first male flower (41.11%) followed by node number to first female flower (34.02%), fruit yield per hectare (31.37%), fruit yield per plant (31.36%) and number of fruits per plant (24.63%). Whereas, moderate GCV was observed for plant height (14.97%), average fruit weight (13.40%) and Fruit length (10.41%). Low GCV observed for average fruit diameter (9.70%), days to first male flower (6.13%), inter nodal length (6.98%), days to last harvest (4.51%), days to first female flower (4.51%) and days to first harvest (2.98%).

Phenotypic coefficient of variation values for different characters are presented in Table 1. PCV was found highest for node number to first male flower (45.22%) followed by node number to first female flower (38.99%), fruit yield per hectare (31.66%), fruit yield per plant (31.65%), number of fruits per plant (25.51%), plant height (15.86%), fruit length (13.39%), and average fruit weight (13.71%) whereas, moderate PCV was observed for inter nodal length (12.63%) and average fruit diameter (12.67%). Low PCV was observed for days to first male flower (7.13%), days to first female flower (7.02%), days to last harvest (5.39%), and days to first harvest (5.10%).

Phenotypic coefficient of variation (PCV) was higher than the genotypic coefficient of variation (GCV) for all the characters studied in the present findings, indicating the considerable influence of environmental factors on the performance of genotypes for different characters. Rastogi and Arya (1990) [11], Karupiah *et al.* (2002) [4], Kumar *et al.* (2008) [6], Mehdi and Khan (2009) [9], Kumar *et al.* (2013) [7, 8] and Krishna Reddy, (2014) [5] reported that the coefficients of genotypic and phenotypic variability were moderate to high for different characters in cucumber.

Heritability and Genetic advance as per cent of Mean

The broad sense heritability estimate provides information on relative magnitude of genetic and environmental variation in germplasm pool. Estimates on broad sense heritability ranged from 30.60 per cent (Inter nodal length) to 98.2 per cent (Fruit yield per hectare) (Table 1). Fruit yield per plant (kg) and fruit yield q/ha exhibited maximum heritability (98.2%) followed by average fruit weight (95.5%), number of fruits per plant (93.3%), plant height (89.2%), node number to first male flower (82.60%) and node number to first female flower (76.2%). The moderate heritability recorded for days to first male flower (73.9%) followed by days to last harvest (69.9%), fruit length (60.50%), average fruit diameter (58.70%). Low heritability recorded for days to first female flower (41.2%), days to first harvest (34.1%) and inter nodal length (30.60%). The heritability estimates for these traits implies that these characters are least influence by the environment. Saikia *et al.* (1995) [13] recorded high heritability for fruit yield per vine and node to first female flower. Kumar *et al.* (2008) [6] observed high heritability for days to first female flower, number of fruit per plant, fruit length, fruit weight and fruit yield per hectare. Further, Kumar *et al.* (2013) [7, 8] reported high heritability for yield per plot.

Low to high estimates of broad sense heritability indicates that these characters are greatly influenced by environmental effects. Due to the masking effect of the environment on genotypes, genetic improvement through selection in these traits is difficult.

High value of genetic advance was observed for node number to first male flower (98.65) followed by fruit yield (82.06), fruit yield per plant (82.04), node number to first female flower (78.40) and number of fruits per plant (62.82) plant height (37.33), average fruit weight (34.57) and fruit length (21.38). Moderate value of genetic advance was observed for average fruit diameter (19.63), days to first male flower (13.92) and Inter nodal length (10.20). Low value of genetic advance was observed for days to last harvest (9.96), days to first female flower (7.64) and days to first harvest (4.59).

High heritability along with high genetic advance indicate that mostly the heritability is due to additive gene effects and selection may be effective. Similarly, High estimate of heritability along with genetic advance for all traits studied revealed that these characters are controlled by additive gene action (Kumar *et al.*, 2008) [6], Mehdi and Khan (2009) [9]. In contrast, Yadav *et al.* (2009) [17] observed high heritability and genetic advance for some of the traits.

Table 1: Fruit yield per plant (kg) and fruit yield q/ha exhibited maximum heritability

S. N.	Characters	Range	General Mean	GCV (%)	PCV (%)	ECV (%)	Heritability (%)	GA as % of mean 5%	GA as % of mean 1%
1.	Days to first male flower	37.67-48.33	41.68	6.137	7.139	3.648	73.9	10.867	13.926
2.	Node number to first male flower	2.00-10.00	5.40	41.11	45.226	18.852	82.6	76.978	98.651
3.	Days to first female flower	45.00-58.00	49.82	4.511	7.024	5.384	41.2	5.968	7.648
4.	Node number to first female flower	3.00-11.33	6.11	34.032	38.996	19.041	76.2	61.181	78.407

5.	Days to first harvest	57.20-68.67	61.69	2.982	5.109	4.148	34.1	3.586	4.596
6.	Days to last harvest	94.13-115.47	106.87	4.514	5.397	2.959	69.9	7.777	9.966
7.	Inter nodal length (cm)	8.61-12.09	10.45	6.98	12.637	10.528	30.6	7.963	10.205
8.	Plant height (m)	1.85-3.33	2.8151	14.976	15.86	5.223	89.2	29.129	37.331
9.	Fruit length (cm)	14.12-22.71	17.9464	10.41	13.398	8.426	60.5	16.686	21.383
10.	Average fruit diameter (cm)	3.9-5.51	4.6981	9.70	12.674	8.146	58.7	15.322	19.636
11.	Number of fruits per plant	4.13-12.13	7.8526	24.639	25.512	6.616	93.3	49.02	62.821
12.	Average fruit weight (g)	167.11-280.91	215.96	13.404	13.719	2.924	95.5	26.977	34.573
13.	Fruit yield per plant (kg)	0.78-2.59	1.7091	31.365	31.656	4.285	98.2	64.017	82.041
14.	Fruit yield (q/ha)	104.6-346.46	227.852	31.374	31.666	4.292	98.2	64.034	82.063

Conclusion

Moderate to wide range of mean values among the genotypes for different characters were observed. The value of PCV estimates was higher than the corresponding GCV estimates for all the characters, indicating the considerable influence of environmental factors on the performance of genotypes for different characters. Moderate to high GCV together with moderate to high heritability and genetic advance as per cent of mean was reported for majority of the characters under study indicating predominant additive gene action thus these traits has ample scope for the improvement of concerned traits through selection.

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