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To study the extent of variability, heritability and genetic advance for fruit yield and its components in cucumber (*Cucumis sativus* L.)

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Abstract
Twenty five cucumber genotypes were evaluated during *Summer* season of 2016at the Horticultural Research Farm, Department of Horticulture, Institute of Agricultural Sciences, Banaras Hindu University, Varanasi. The objective was to study the extent of variability, heritability and genetic advance for fruit yield and its components in cucumber (*Cucumis sativus* L.). The magnitude of PCV was found to be higher than the GCV for most of the traits and the difference was much wider for node at which first male flower appear (18.52 and 9.38) indicating that this character is highly influenced by environment effect. High level of genotypic coefficient of variation was observed for average fruit weight (24.75), node at which first female flower appear (21.81). Further high heritability coupled with high genetic gain was noted for these traits. These results show the presence of sufficient variability in the germplasm, predominance of additive gene action and high transmissibility of the characters. Therefore, direct selection will be rewarding depending upon the traits. High heritability and moderate genetic advance as percent of mean values observed for the traits like days to 50% germination, days to first male flower appearance, node at which first male flower appear and days at 50% male flower. This indicates the influence of non-additive gene action and considerable influence of environment on the expression of these traits. These traits could be exploited through manifestation of dominance and epistatic components through heterosis.

Introduction

Cucumber is an important vegetable crop of India cultivated throughout the country. It is distinct from other Cucumis species (Deakin *et al*., 1971) [5] as it has seven pairs of chromosomes (2n=2x=14), whereas most of the other *Cucumis* species have 12 pairs of chromosomes or multiple of 12 (i.e., 2n=2x=24, 2n=4x=48, etc.) (Deakin *et al*., 1971) [5]. Globally, cucumber (*Cucumis sativus* L.) is regarded as second most widely cultivated cucurbit after watermelon and is also regarded as fourth most important vegetable after tomato, cabbage and onion (Tatlioglu, 1993). The cucumber is commonly a monoecious, annual, trailing or climbing vine with angled, hirsute or rough stem (Bailey, 1969) [2]. It is an annual plant species and is found to be day neutral. Cucumber is believed to be native to India or Southern Asia and has been apparently cultivated for the last 3000 years (De Candolle, 1886).It has been well documented that effectiveness of the selection in a crop under plant improvement program is mainly dependent on the variability present in the population and the extent to which it is heritable. Diversity in plant genetic resources provides an opportunity for plant breeders to develop new and improved cultivars with desirable characteristics, which include both farmer preferred traits (yield potential and large seed, etc.) and breeders preferred traits (pest and disease resistance and photosensitivity, etc.) (Govindaraj *et al*. 2015) [7]. The greater genetic variability in population, more the genetic potentiality and thereby wider scope for the improvement of crop. Further, estimatesof heritability have to be considered in conjugation with genetic advance to find the expected genetic gain in next generation (Shukla *et al.,* 2006) [17]. Depending on genetic variability present in base population *viz*., character association, cause and effect relationship, heritability and genetic advance breeders can make an effective selection in a breeding program. To explore the purpose of improvement by selection it is essential to study first the extent of genetic variability and heritability along

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with genetic advance. Therefore, an attempt was made with an objective to know the nature and magnitude of existing genetic variability, heritability in broad sense and genetic gain for different horticultural and yield traits in the available cucumber germplasm.

Materials and Methods
Experimental site and climatic conditions
The present study was carried out at the Horticultural Research Farm, Department of Horticulture, Institute of Agricultural Sciences, Banaras Hindu University, Varanasi, during the summer season of 2016.The average annual rainfall is about 1110 mm. The major part of the rain occurs from July to September. The mean relative humidity is about 68 percent which rises up 81percent during July to September and falls down to 39 percent during the end of April to early June.

Experimental material, layout and observations
The experiment was laid out in Randomized Block Design with three replications and the experiment material comprised of twenty five genotypes. Seeds were sown on 12th april, 2016 in hills spaced 120 cm x 60 cm. standard cultural practices were followed for a healthy crop stand. Five plants were selected randomly from each plot and tagged for recording the observations like days to 50% germination, node at which first male flower appear, node at which first female flower appear, days to first male flower appearance, days at 50% male flower appearance, days to first female flower appearance, days at 50% female flower appearance, vine length (cm), primary branches per vine, fruit length (cm), fruit diameter (cm), fruits per plant, average fruit weight (kg), fruit yield per plant (kg), fruit yield per plot and fruit yield (q/ha).

Statistical analysis
The data was subjected to analysis of variance as per procedure described by Cochran and Cox (1957) [4]. The phenotypic and genotypic coefficients of variation were calculated by using the formulae given by Cochran and Cox (1957) [4].

$$\text{Genotypic variance } \sigma^2 g = \frac{\text{MSS due to genotypes -MSS due to error}}{R}$$

Phenotypic coefficient of variability (PCV)

$$\text{Phenotypic coefficient of variability (PCV \%)} = \frac{\sqrt{\text{Phenotypic variance}}}{\text{Grand Mean}} \times 100$$

Genotypic coefficient of variability (GCV)

$$\text{Genotypic coefficient of variability (GCV \%)} = \frac{\sqrt{\text{Genotypic variance}}}{\text{Grand Mean}} \times 100$$

PCV and GCV were classified into three following categories as suggested by Sivasubramanian and Madhamenon (1973). Low: Less than 10%; Moderate: 10-20%; High: More than 20%

Heritability in broad sense (h^2)
The broad sense heritability (h^2_{bs}) was estimated for all characters as the ratio of genotypic variance to the total of phenotypic variance as suggested by Lush (1949) [16] and Hanson et al. (1956).

$$h^2 = \frac{Genotypic\ variance}{Phenotypic\ variance} \times 100$$

Heritability estimates in cultivated plants could be placed in the following categories as suggested by Robinson et al. (1966) [9]. Low: 0-30%; Moderate: 30-60%; High: > 60%

Genetic advance (GA)
The expected genetic gain or advance for each character was estimated by using the following method suggested by Johnson et al. (1955) [9].

$$GA = h^2bs \times \sigma_p \times K \times \sigma_p$$

Where
h^2bs =   Heritability estimate in broad sense
σ_p =   Phenotypic standard deviation of the trait
K =   Standard selection differential which is 2.06 at 5 per cent selection intensity.

Genetic advance was classified as high (>20%), moderate (10-20%) and low (<10%).
Further, the Genetic advance as per cent of mean was computed by using the following formula

$$\text{GA as per cent of mean} = \frac{GA}{\text{Grand mean}} \times 100$$

Genetic advance as per cent mean was categorized into following groups as suggested by Johnson et al. (1955) [9]. Low-Less than 10%; Moderate-10-20%; High-More than 20%.

Results and Discussion
Analysis of variance (ANOVA) of twenty five diverse genotypes of cucumber for sixteen characters is presented in Table 2 revealed that the treatments differed significantly for all the characters showing that the material under study had sufficient genetic variability. The comparison of variability among all the characters would be possible only after working out their coefficient of variability. The high value of genotypic and phenotypic coefficient of variations was observed in case of average fruit weight, node at which first female flower appear, fruit yield per plant, fruit yield per plot, fruit yield and primary branches per plant. PCV is higher than the GCV for more of its traits but its difference is much wider for node at which first male flower appear (18.52 and 9.38) which indicated that this character was highly influenced by environment effect. These finding are similar to the finding of Kumar et al. (2008) [10].

Table 1: The cultivars/germplasm included in the trial

Symbol used	Name of germplasm	Source
T$_1$	South Kheera Long	KAU, Thrissur
T$_2$	Cucumber Moti	Market, Varanasi
T$_3$	Local Selection-1	Market, Varanasi

T$_4$	K-90	YSPUHF, Solan
T$_5$	Kheera Parshad-100	IIVR, Varanasi
T$_6$	Rajan	Market, Varanasi
T$_7$	Imperial Green	Market, Varanasi
T$_8$	Rajendra-1	RPCAU, Bihar
T$_9$	Lovely	Market, Haryana
T$_{10}$	PusaUday	IIVR, Varanasi
T$_{11}$	100 Number	Market, Varanasi
T$_{12}$	Local Selection-2	Market, Varanasi
T$_{13}$	SS-45	KAU, Thrissur
T$_{14}$	Subera	KAU, Thrissur
T$_{15}$	SwarnaAgete	IIVR, Varanasi
T$_{16}$	Super Long Green	Market,Varanasi
T$_{17}$	Green Wonder	Market, Kanpur
T$_{18}$	Priya	Market, Kanpur
T$_{19}$	Mudiki Local	KAU, Thrissur
T$_{20}$	Kamini-017	IIVR, Varanasi
T$_{21}$	Super Green	Market, Kanpur
T$_{22}$	Local Selection-3	Market, Varanasi
T$_{23}$	K-75	YSPUHF, Himachal Pardesh
T$_{24}$	Local Selection-4	Market, Varanasi
T$_{25}$	SwarnaSheetal	IIVR, Varanasi

Table 2: Analysis of variance (ANOVA) of twenty five genotypes for sixteen characters in cucumber

S. No.	Characters	Replication (df=2)	Treatments (df=24)	Error (df=48)
1.	Days to 50% germination	0.001	0.230**	0.035
2.	Node at which first male flower appear	0.210	0.314**	0.154
3.	Node at which first female flower appear	0.610	6.564**	0.606
4.	Days to first male flower appearance	2.440	11.888**	1.370
5.	Days at 50% male flower	3.640	22.020**	1.390
6.	Days to first female flower appearance	4.093	87.055**	1.648
7.	Days at 50% female flower	0.413	24.918**	2.052
8.	Vine length (cm)	6.743	804.800**	25.247
9.	Number of primary branches per plant	0.023	1.181**	0.238
10.	Number of fruitsper plant	1.033	6.640**	1.192
11.	Fruit length (cm)	1.346	6.189**	0.431
12.	Fruit diameter (cm)	0.134	1.631**	0.130
13.	Avg. fruit weight (kg)	0.000	0.005**	0.000
14.	Fruit yield/plant (kg)	0.040	0.372**	0.073
15.	Fruit yield/plot (kg)	4.009	37.248**	7.300
16.	Fruit yield (q/ha)	260.738	2422.523**	474.750

Table 3: Estimation of range, mean, phenotypic and genotypic coefficient of variation, heritability and genetic advance, genetic advance as percent of mean of 16 characters of 25 genotypes of cucumbers

S. No.	Characters	Range		Grand mean	P.C.V. (%)	G.C.V. (%)	Heritability broad sense (%) (h^{2}bs)	Genetic advance	Genetic advance in percent of mean (gs %)
		Lowest	Highest						
1.	Days to 50% germination	4.00	5.00	4.08	7.77	6.23	73.85	0.53	13.21
2.	Node at which first male flower appear	2.00	3.16	2.46	18.52	9.38	68.48	0.30	12.55
3.	Node at which first female flower appear	2.00	9.66	6.46	24.92	21.81	75.45	3.25	50.40
4.	Days to first male flower appearance	30.00	36.66	32.40	6.81	5.77	74.84	4.19	12.93
5.	Days at 50% male flower	50.00	59.66	54.40	5.28	4.81	76.31	6.31	11.59
6.	Days to first female flower appearance	32.33	47.66	41.66	13.17	12.80	77.76	13.69	32.86
7.	Days at 50% female flower	60.66	71.33	65.18	4.77	4.23	75.74	6.46	9.92
8.	Vine length (cm)	66.66	125.00	99.43	16.98	16.21	77.33	40.62	40.86
9.	Number of primary branches per plant	2.00	4.33	3.09	24.03	18.11	72.83	1.11	36.06
10.	Number of fruits per plant	7.33	12.40	9.90	17.51	13.61	73.30	2.76	27.92
11.	Fruit length (cm)	10.00	15.45	13.43	11.41	10.31	76.11	3.30	24.60
12.	Fruit diameter (cm)	3.18	5.53	4.67	16.98	15.12	75.81	1.66	35.57
13.	Avg. fruit weight (kg)	0.10	0.25	0.17	25.47	24.75	77.74	0.11	63.49
14.	Fruit Yield per plant (kg)	0.88	2.06	1.72	24.14	18.34	72.95	0.63	36.81
15.	Fruit Yield per plot (kg)	8.82	20.69	17.22	24.14	18.34	72.95	6.33	36.81
16.	Fruit Yield (q/ha)	71.13	166.86	138.87	24.14	18.34	72.95	51.12	36.81

Parameters of Variability

Variability of yield contributing characters: Information on genetic variability of yield components is of paramount importance in a crop improvement programme. The extent of genotypic variability indicates the amenability of given character for its improvement, it is essential to have a large variation in available material in the hand of breeder. The comparison of variability among all the characters would be

possible only after working out their coefficient of variability. Wide range of genotypic coefficient variation was observed among all the traits. High level of genotypic coefficient of variation was observed in case of average fruit weight (24.75), node at which first female flower appear (21.81).While moderate level of genotypic coefficient of variation was seen in case of fruit yield (18.34), fruit yield per plot (18.34), fruit yield per plant (18.34), primary branches per plant (18.12), vine length (16.21), fruit diameter (15.12), fruits per plant (13.61), days to female flower appearance (12.80), whereas low level of genotypic coefficient of variation was seen in case of fruit length (10.31), node at which first male flower appear (9.38), days to 50% germination (6.23), days to male flower appearance (5.78), days to 50% male flower appearance (4.81) and days to 50% male flower (4.23). In case of phenotypic coefficient of variation average fruit weight (25.47), node at which first female flower appear (24.92), fruit yield per plant (24.14), fruit yield per plot (24.14), fruit yield (24.14), primary branches per plant(24.03), whereas moderate level of phenotypic coefficient of variation was seen in case of node at which first male flower appear (18.52), fruit per plant (17.52), fruit diameter(16.98), vine length (16.98), days to female flower appearance(13.17), whereas low level of phenotypic coefficient of variation was seen in case of fruit length (11.41), days to 50% germination (7.77), days to male flower appearance (6.81), days to 50% male flower (5.28) and days to 50% female flower (4.23). These finding are similar to the finding of Kumar *et al*. (2008) [10], Hossain *et al*. (2010) [8] and Hasan *et al*. (2012) and Kumar *et al*. (2013) [14]. The high value of genotypic and phenotypic coefficient of variations was observed in case which indicated that this character was highly influenced by environment effect.

Estimation of heritability and genetic advance: The heritability in combination with genetic advance increases the intensity of selection in a breeding programme. Thus, genetic advance measures the difference between the mean genotypic values of the original population from which these are selected. Johnson *et al*. (1955) [9] pointed out that without genetic advance the estimates of heritability would not be of practical importance in selection based on phenotypic appearance. It is seen that if a character is governed by non-additive gene action, it may have high heritability but low genetic advance, whereas, if it is governed additive gene action heritability and genetic advance would be high. The estimate of genetic advance is more useful as a selection tool when considered jointly with heritability estimates (Johnson *et al*., 1995; Panse, 1957). Although, genotypic coefficient of variation alone does not give an idea about the amount of heritable variations. The heritable variations can be obtained with the help of heritability estimates and genetic gain. In the present in investigation, heritability was estimated only based on broad sense. High heritability estimates were observed for days to first female flower appearance (77.76), average fruit weight (77.74), vine length (77.33), fruit length (76.11), fruit diameter (75.81), days to 50% female flower (75.74), node at which first male flower appear (75.45), days to first male flower appear (74.84), days to 50% germination (73.85), number of fruits per plant(73.30), fruit yield (72.95), fruit yield per plot (72.95), fruit yield (72.95), number of primary branches per plant (72.83) and node at which first male flower appear was (68.48).As mention earlier there is no meaning of high heritability without a high genetic advance value. Therefore, comparing these two, high heritability coupled

with high genetic advance as percent of mean value was found in average fruit weight, node at which first female flower appear, vine length, fruit yield per plant, fruit yield per plot, fruit yield, primary branches per plant, fruit diameter, days to first female flower appearance, fruits per plant and fruit length, this indicates that this character 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 Islam *et al*. (1993), Afangideh and Uyoh (2007) [1], Munshi *et al*. (2007), Kumar *et al*. (2008) [10] and Choudhary *et al*. (2015) [3]. Selection for economic traits is made on phenotypic basis and the phenotype is due to the action of both genotypic and environment. The genetic advance as percent of mean indicates the relative magnitude of genetic improvement that can be realized in traits. Genetic advance is the improvement in the mean genotype value of the selected families over the base population after one complete cycle of selection. In this present investigation, the highest genetic advance was recorded for fruit yield (q/ha) (51.12) followed vine length (40.62), while moderate genetic advance was recorded in days to first female flower appearance (13.70) and lowest genetic advance was recorded in average fruit weight (0.113). Other genetic advance values were recorded as days to 50% female flower (6.46), fruit yield per plot (6.34), days to 50% male flower (6.31), days to first female flower appearance (4.19), fruit length (3.30), node at which first male flower appear (3.25), fruits per plant (2.76), fruit diameter (1.66), primary branches per plant (1.11), fruit yield per plant (0.63), days to 50% germination (.053) and node at which first male flower appear (0.30) which were also considered as low. The genetic advance as percent of mean as in Table 3 shows that genetic advance percent mean was observed in average fruit weight (63.50),vine length (40.86), fruit yield per plot (36.81), fruit yield (36.81), fruit yield per plant((36.81), primary branches per plant(36.08), fruit diameter (35.57), days to first female flower appearance (32.86), fruits per plant (27.92), fruit length (24.60), days to 50% germination(13.21), days to first male flower appearance (12.93), node at which first male flower appear (12.55), days to 50% male flower (11.59), days to 50% female flower (9.92) and node at which first male flower appear (0.40). High heritability and moderate genetic advance as percent of mean values observed for the traits like days to 50% germination, days to first male flower appearance, node at which first male flower appear and days at 50% male flower. Results are resembled with the findings Kumar *et al*. (2008) [10]. This indicates the influence of non-additive gene action and considerable influence of environment on the expression of these traits. These traits could be exploited through manifestation of dominance and epistatic components through heterosis.

Conclusion
From the above results obtained under the present investigation it can be concluded that the genotype had high amount of genetic variability that indicated good scope for further selection. High heritability coupled with high genetic gain was noted for average fruit weight, node at which first female flower appear. These results show the presence of sufficient variability in the germplasm, predominance of additive gene action and high transmissibility of the characters. Therefore, direct selection will be rewarding depending upon the traits. High heritability and moderate genetic advance as percent of mean values observed for the

traits like days to 50% germination, days to first male flower appearance, node at which first male flower appear and days at 50% male flower. These traits could be exploited through manifestation of dominance and epistatic components through heterosis.

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