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Genetic variability, Heritability and Genetic advances analysis for quantitative and qualitative traits in Cucumber (*Cucumis sativus* L.)

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Abstract
An experiment was conducted to study Genetic variability, heritability and genetic advance for some traits in Cucumber (*Cucumis sativus* L.). Twelve genotypes were used in this experiment. These genotypes were planted in Randomized Block Design with three replications during the rainy season of the year, 2014 at vegetable research farm, Department of Horticulture, Allahabad School of Agriculture, Sam Higginbottom Institute of Agriculture, Technology and Sciences, Allahabad (U.P.). Genetic Variability, heritability, genetic advance and genetic gain for different characters were studied in 12 genotypes of cucumber. The study indicated existence of considerable amount of genetic variability for all the traits in all the genotypes used in the experiment. The maximum phenotypic and genotypic coefficient (PCV and GCV) was observed for number of female flowers per vine (19.28 and 21.54), number of male flowers per vine (19.62 and 20.79), fruit yield per vine (19.86 and 19.88), number of branches per vine (13.79 and 16.29), number of fruits per vine (14.20 and 15.51), node number at which first appears of male flowers (10.11 and 15.22), node number at which first appears of female flowers (12.78 and 15.14) and fruit length (11.66 and 11.92). High genetic advance over mean coupled with high heritability was observed in characters like number of male flowers per vine, vine length and fruit weight (g). However, the estimates were moderate for number of female flower's per vine. Higher heritability estimates were accompanied by lower genetic advance over the mean for vitamin C, TSS, fruit yield per vine and days to first fruit harvest. The maximum genetic gain in per cent was recorded for fruit yield per vine (kg), number of male flowers per vine, number of female flowers per vine, number of fruit per vine, number of branches per vine, fruit length and node number at which first appears of female flower.

Keywords: Cucumber, genetic advance, heritability, genetic advance as % of mean

Introduction
India is world's largest producer of vegetables next to China with an annual production around 162.89 (Million tonnes) from 93.96 (Million hectare) of land. Among various Cucurbits, cucumber are grown in maximum area *i.e.* 43.28 ('000 ha) with 677.15 ('000 Metric tonnes) productivity (Indian Horticulture Database, 2013-2014).

Cucumber (*Cucumis sativus* L.) is a widely cultivated plant in the gourd family cucurbitaceous. It is a creeping vine that bears cylindrical fruits that are used as culinary vegetables. There are three main varieties of cucumber: slicing, pickling, and burpless. Within these varieties, several different cultivars have emerged. The cucumber is originally from Southern Asia, but now grows on most continents. Many different varieties are traded on the global market.

Planning and execution of a breeding programme for the improvement of quantitative attributes depends, to a great extent, upon the genetic magnitude of genetic variability. The genotypic and phenotypic coefficient variation are helpful in exploring the nature of variability in the breeding population whereas, the estimate of heritability provides index of transmissibility of characters. The estimate of direct selection parameters like coefficient of variation, heritability and genetic advance are useful in formulating suitable selection strategy for higher yield in cucumber. Estimates of heritability have to be considered with conjunction with genetic advance and change in mean value among successive generation, alone it do not provide idea about expected gain in next generation (Shukla *et al.*, 2006) [20]. For a successful planning of breeding improvement program, the analysis of variability among the traits and their association of a particular character in relation to yield and yield attributing traits it would be great importance (Mary and Gopalan, 2006) [15]. To start an efficient breeding improvement program it is necessary to evaluate the genetic parameter such as genetic coefficient of variation, heritability and genetic advance (Atta et al., 2008) [5]. The objectives of the present study were to evaluate genetic variability for heritable and non-heritable component in cucumber

genotypes based on different agro- and morphological parameters.

Material and Methods

The present investigation entitled "Varietal Evaluation Studies in Cucumber (*Cucumis sativus* L.) Genotypes under Allahabad agro-climate condition" was carried out during the rainy season of the year, 2014 at vegetable research farm, Department of Horticulture, Allahabad School of Agriculture, Sam Higginbottom Institute of Agriculture, Technology and Sciences, Allahabad (U.P.).

Experimental materials comprised of 12 genotypes. 6 genotypes from IIVR Varanasi and rest of 6 collected from local seed market Allahabad. All the genotypes were sown on 16th August, 2014 with spacing 0.5m and 1.0m, plant to plant and row to row, respectively. Adopting the recommended cultivation practices for raising a healthy crop and used the trellis system for vine climbing. The investigation consisted of 12 cucumber genotypes and laid out in randomized block design with three replications. Observation on 16 different characters namely Days to first appearance of male flower, Days to first appearance of female flower, Node number at which first male flower appear, Node number at which first female flower appear, Number of male flowers per vine, Number of female flowers per vine, Length of main vine (cm), Number of branches per vine, Number of fruits per vine, Fruit diameter (cm), Fruit length (cm), Fruit weight (g), Days to first fruit harvest, Fruit yield (kg/vine), Fruit yield (tones /hectare), Total soluble solid (°Brix), Vitamin 'C' mg/100g were recorded from five randomly selected plant of each genotype. Data was statically analyzed for the evaluation of genotypes.

Statistical analysis

Genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), broad sense heritability, genetic advance and genetic gain were computed as per standard formulas.

Estimation of variability parameters

Genetic variance

It is the variance contributed by genetic causes or the genetic occurrence of difference among the individuals due to their genetic makeup. It was calculated by using the formula given by Al-Jibouri, 1958.

$$Vg = \frac{MSV - V_3}{r} = \frac{b' - c'}{r}$$

Where,
Vg = Genotypic variance,
MSV= Mean square for varieties,
V_E = Error mean square and
r = Number of replication

Phenotypic variance

It is the sum of variance contributed by genetic causes and environmental factors and was computed as formula given by Al-Jibouri, 1958.

Vp = Vg + Ve = Vg + C'

Where,
Vp = Phenotypic variance,
Vg = Genotypic variance and
Ve = Error variance.

Genotypic coefficient of variation (GCV)

The magnitude of genetic variation existing in a character was estimated by the formula given by Burton (1952) [6].

$$GCV = \frac{\sqrt{Vg}}{\bar{x}} X100$$

Where,
Vg= Genotypic variance and
$\bar{x}$ = General mean of the character under study.

Phenotypic coefficient of variation (PCV)

The magnitude of phenotypic variation existing in a character was estimated by the formula given by Burton (1952)

$$PCV = \frac{\sqrt{V_p}}{\bar{x}} X100$$

Where,
V_p = Phenotypic variance and
x =General mean of the character under study.

Heritability

Heritability in the broad sense was calculated by the formula given by Burton and Lush (1949) [6].

$$h^2 = \frac{Vg}{Vp} \times 100$$

Where,
h^2 = Heritability (broad sense)
Vg = Genotypic variance and
V_p = Phenotypic variance

Expected genetic advance

It was measured by formula proposed by Lush (1949) [14].

$$GA = \frac{V_g}{V_p} = \sqrt{V_p} \times K = \frac{V_g}{\sqrt{V_p}} \times K$$

Where,
GA = Genetic advance
V_g = Genotypic variance
V_p = Phenotypic variance
K = Selection differential (constant) i.e. 2.06 at 5% selection intensity

Genetic gain

It was calculated by using the following formula suggested by Johnson *et al.* (1955) [10].

$$\text{Genetic gain} = \frac{GA}{\bar{x}} \times 100$$

Where,
GA = Genetic advance and
$\bar{x}$ = General mean of the character under study

Results and Discussion

The extent of variability present in twelve genotypes of cucumber was measured in terms of range, SEm±, phenotypic variance ($\sigma^2 p$), phenotypic coefficient of variation (PCV), genotypic ($\sigma^2 G$) variance, genotypic coefficient variation (GCV), heritability (broad sense) and genetic advance (GA) (Tables 2). The analysis of variance revealed that all the genotypes differed significantly with respect of different characters studied. Wide range of variation was observed for all characters. The widest range was recorded for vine length (cm) (186.06-249.13) followed by number of male flowers per vine (106.00-200.06), fruit weight (gm) (139.20 – 177.60), days to first fruit harvest (45.66–50.33), days to first appearance of female flower (35.33–39.86) and days to first appearance of male flower (30.86–36.46) indicating the

presence of sufficient variability among the genotypes used in the present study. This would help in selecting the best genotypes from existing collection. However, fruit yield per vine (kg), fruit diameter (cm), TSS (°Brix), node number at which first appears of male flower and node number at which first appears of female flower were recorded low value indicating minimum variation and less scope for selection from the present collection. Reshmi (2006) [18], Arunkumar *et al.* (2011) [4] and Veena *et al.* (2012) [24] also reported similar results in cucumber.

Environment play an important role in expression of various characters as the PCV was found to be higher than the corresponding GCV for all the characters. High values of PCV as well as GCV were recorded for number of female flowers per vine, number of male flowers per vine, fruit yield per vine, number of branches per vine, number of fruits per vine, node number at which first appears of male flowers, node number at which first appears of female flowers, and fruit length. The high magnitude of GCV further revealed that greater extent of variability presence in the characters, thereby suggesting good scope for improvement through selection of this crop. Similar findings have also been reported by Singh and Kumar (2002) [21] in bottle gourd, Kutty and Dharmatti (2004) [13] in bitter gourd and Afangideh and Uyoh (2007) [1] in cucumber. The estimation of genetic coefficient of variation indicates the amount of genetic variation present for different desirable traits while the heritability 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) [10] had shown that heritability and genetic advance should be jointly considered for reliable conclusion. In the present study, all the traits expressed high heritability which ranged from 71.22 per cent (node number at which first appears of female flower) to 99.75 per cent (fruit yield per vine) (Table 2). Heritability estimates were high for characters like fruit yield per vine (kg), fruit length (cm), TSS (Brix), days to first appears of male flower, days to first fruit harvest, number of male flowers per vine, number of fruit per vine, vine length (cm), number of female flowers per vine, fruit weight (g), vitamin C (mg/100g), number of branches per vine and node number at which first appears of female flowers suggesting the important role of genetic constitution in the expression of the character and such traits are considered to be dependent from breeding point of view. From the above heritability estimates, it is clear that these characters are less influenced by the environmental factors and are controlled by additive gene effect (Table 2). Similarly, high heritability for the above traits was reported by Dhiman and Prakash (2005) [8], Kumar *et al.* (2008) [11] in cucumber, Singh *et al.* (2012) in bitter gourd and Kumar *et al.* (2013) [12] in Sponge gourd. Days to first appearance of female flower and node number at which first appears of male flowers recorded moderate heritability. Similar result was reported by Mishra *et al.* (2007) [16] in cucumber and Sharma and Sengupta (2013) [19] in bottle gourd. Out of 12 characters studied, in the present study high genetic advance over mean coupled with high heritability was observed in characters like number of male flowers per vine, vine length and fruit weight (g). However, the estimates were moderate for number of female flowers per vine. Therefore, the present findings correlated that the existing variability among the genotypes with respect to these traits is mainly due to additive type of genes (Panse 1957) [17]. Therefore, they are more reliable for effective selection.

Higher heritability estimates were accompanied by lower genetic advance over the mean for vitamin C, TSS, fruit yield per vine and days to first fruit harvest. This suggests that selection may not be useful for the improvement of this trait because of the narrow range of phenotypic variation among the genotypes in respect to this character. Hanchinamani (2006) [9] reported low genetic advance in cucumber. The maximum genetic gain in per cent was recorded for fruit yield per vine (kg), number of male flowers per vine, number of female flowers per vine, number of fruit per vine, number of branches per vine, fruit length and node number at which first appears of female flower.

Table 1: List of genotypes used under study

Sr. No.	Name of genotypes
1	CUCUVAR-1
2	CUCUVAR-2
3	CUCUVAR-3
4	CUCUVAR-4
5	CUCUVAR-5
6	CUCUVAR-6
7	Super Green 40
8	AK-47
9	KARAN
10	HY-512
11	Prasad-100
12	Supriya-100

Table: 2. Components of variance, coefficient of variation, heritability, genetic advance and genetic advance as % of mean for different quantitative and qualitative traits.

Characters	Mean±SE	Range	Genotypic Variance (σ^2g)	Phenotypic Variance (σ^2p)	GCV	PCV	Heritability %	Genetic Advance	Genetic advance as % of mean
Days to first appearance of male flower	34.07±0.38	30.86-36.46	3.22	3.45	5.27	5.45	93.44	3.57	10.49
Days to first appearance of female flower	38.02±0.74	35.33-39.86	1.20	2.04	2.88	3.75	59.13	1.74	4.57
Node number at which first appears of male flower	4.44±0.41	3.76-5.46	0.20	0.45	10.11	15.22	44.11	0.61	13.83
Node number at which first appears of female flower	5.36±0.36	4.46-6.80	0.47	0.66	12.78	15.14	71.22	1.19	22.21
Number of male flowers per vine	147.91±8.31	106.00-200.06	842.33	945.82	19.62	20.79	89.04	56.41	38.14
female flowers per vine	21.28±1.66	14.00-28.53	16.84	21.02	19.28	21.54	80.14	7.56	35.56

Vine length (cm)	205.86±5.75	186.06-249.13	218.28	268.01	7.17	7.95	81.44	27.46	13.34
branches per vine	8.80±0.62	7.2-11.26	1.47	2.05	13.79	16.29	71.64	2.11	24.04
fruits per vine	10.04±0.51	8.13-13.06	2.03	2.42	14.20	15.51	83.83	2.69	26.79
Fruit diameter (cm)	3.62±0.26	3.17-4.19	0.04	0.14	5.57	10.60	27.59	0.21	6.03
Fruit length (cm)	16.22±0.32	12.38-19.33	3.57	3.74	11.66	11.92	95.67	3.81	23.50
Fruit weight (g)	157.21±5.03	139.20-177.60	147.47	185.46	7.72	8.66	79.51	22.30	14.18
Days to first fruit harvest	48.27±0.41	45.66-50.53	2.21	2.47	3.08	3.26	89.41	2.89	6.00
Fruit yield per vine (kg)	1.57±0.01	1.13-2.31	0.0982	0.0984	19.86	19.88	99.75	0.64	40.86
TSS (^{o}Brix)	4.68±0.09	3.98-5.38	0.1923	0.205	9.36	9.68	93.61	0.87	18.67
Vitamin 'C' (mg/100g)	6.78±0.09	6.44-7.10	0.037	0.051	2.86	3.33	73.43	0.34	5.04

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