

## Research Article

# Genetic variability, heritability and genetic advance in cucumber (*Cucumis sativus* L.)

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## ABSTRACT

Genetic variability in a crop population is important for successful plant breeding. Eight cucumber (*Cucumis sativus* L.) genotypes namely Green Long, Simran, Bhaktapur Local, Saihni-2, Ninja-179, Garima, Farmer's variety and wild genotype were evaluated at Lamahi Municipality, Dang district of Nepal to estimate the magnitude of their genetic variability and heritability. Analysis of variance revealed significant differences among genotypes for growth and yield traits. The estimates of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were highest for weight of fruit whereas traits namely fruit length, fruit diameter and days to maturity had medium value for both GCV and PCV. Broad sense heritability estimates ranged from 0.74 for fruit diameter to 0.98 for days to germination. Fruit yield showed high significant positive correlation with fruit diameter ( $r= 0.649$ ) and negative significant correlation ( $r= -0.538$ ) with days to flowering. Traits namely weight per fruit, days of germination, no. of flower and days to flowering can be used effectively in selection process of crop improvement program as they had high GCV, PCV and heritability along with high genetic advance as percentage of mean.

**Keywords:** Cucumber, variability, heritability, genetic advance, correlation coefficient

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## INTRODUCTION

Cucumber (*Cucumis sativus* L.), an important fruit with great nutritional, medicinal, and economic potential, belongs to the Cucurbitaceae family. It is believed to have originated in India, southern Asia (Papadopoulos, 1994) and thought to have been cultivated for at least 3000 years (Ullah et al., 2012). It is a highly cross-pollinated crop and usually monoecious in nature preferring warm weather and bright light for its better growth and development. In spite of the extensive cultivation and consumption, cucumbers have not much been taken up for systematic research work in order to understand the genetic architecture and endeavor in crop improvement programs in Nepal.

The success of any plant breeding program depends on the genetic variability and selection skill of plant breeder (Adhikari et al., 2018a). The understanding of magnitude of genetic variability present in a given crop species for the traits is imperative for the success of any plant breeding program (Handel *et al.*, 2018; Sankar *et al.*, 2006). The genotypic and phenotypic coefficients of variability are helpful in exploring the nature of variability in the breeding populations, whereas estimates of heritability provides index of transmissibility of characters. Heritability is the ratio of variation due to differences between genotypes to the total phenotypic variation for a trait in a population and shows the component of a character transmitted to future generations. Genetic advance shows the difference between the mean genotypic values of selected population and the original population from which these were selected. Heritability estimates along with genetic advance is more precise in predicting the genetic gain under selection. Variability, genetic diversity, expected genetic advances and heritability of the traits are key basis for genetic improvement of the trait (Adhikari *et al.*, 2018b).

The information on heritability alone may not help in identifying characters for enforcing selection and heritability estimates in conjunction with predicted genetic advance is more reliable (Johnson *et al.*, 1955). Heritability provides an idea to the extent of genetic control for expression of a particular trait and the reliability of phenotype in predicting its breeding value (Tazeen *et al.*, 2009). High heritability indicates less environmental influence in the observed variation (Mohanty, 2003). It also gives an estimate of genetic advance a breeder can expect from selection applied to a population and help in deciding on a crop breeding method to choose (Gatti *et al.*, 2005). Genetic advance which estimates the degree of gain in a trait obtained under a given selection pressure is another important parameter that guides the breeder in choosing a selection programme (Hamdi *et al.*, 2003). High heritability and high genetic advance for a given trait indicates that it is governed by additive gene action and, therefore, provides the most effective condition for selection (Tazeen *et al.*, 2009). The present study was carried out to estimate genetic variability and heritability.

## MATERIALS AND METHODS

### Experimental site

This experiment was carried out in the field of Lamahi Municipality, Dang district in the

Province number 5, inner Terai region of Nepal during the summer season, 2018. It was located at latitude of 28° 7' 0''N latitude, longitude of 82° 18' 0''E and 628 m altitude. The PH of the experimental site was slightly acidic and the texture of the soil was silt loam (Bartaula et al., 2019).

### **Plant materials**

Eight different genotypes of Cucumber viz. Green Long, Simran, Bhaktapur Local, Saihni-2, Ninja-179, Garima, Farmer's variety and wild genotype collected from the experimental locality.

### **Experimental design and crop management**

The experiment was conducted in Single Factorial Randomized Complete Block Design (RCBD) with three replication and eight genotypes. The nursery bed was raised to prepare the seedling of all genotypes used. 20 days old seedlings were transplanted on individual plots of size 12 m<sup>2</sup> at the spacing of 1 x 1 m<sup>2</sup>. All the crop management practices were followed as recommended by Nepal Agricultural Research Council (NARC).

### **Data observation and analysis**

Observations were taken on randomly selected 5 plants from each experimental plot for all the traits under consideration. Fruit yield was converted to ton per hectare from the data observed for yield per experimental plot. The data collected on all the characters were subjected to standard methods of analysis of variance (Panse and Sukhatme, 1985). Phenotypic and genotypic coefficient of variation was calculated as suggested by Falconer (1981) and Shrestha *et al.* (2019). Heritability (broad sense) (Johnson *et al.*, 1955; Shrestha *et al.*, 2019), genetic advance (Burton, 1952; Shrestha *et al.*, 2019) and genetic advance as a percent of mean (Johnson *et al.*, 1955) were also estimated.

### **Statistical analysis**

All agronomic data from trials were analyzed by ANOVA using a single factorial RCBD design. The experimental data were processed using Excel 2010 and analyzed by using R software. Least significant difference (LSD  $p \leq 0.05$ ) test was used for mean comparison to identify the significant components of the treatment means (Jan *et al.*, 2009; Sharma *et al.*, 2016; Gomez & Gomez, 1984; Shrestha, 2019; Kandel & Shrestha, 2019).

## **RESULTS AND DISCUSSION**

### **Genetic Variability**

The analysis of variance revealed the existence of significant differences among the genotypes for all the traits (Table 1), indicating the presence of considerable genetic variability among the experimental material under study. Thus, there is plenty of area and scope for improvement of different quantitative and qualitative traits through selection. The mean values, genotypic and phenotypic coefficient of variation, heritability, genetic advance and genetic advance as percent of mean (Table 2) of all eight genotypes were calculated for yield and yield attributes. The variation observed in the characters studied in the present investigation were classified as, low (less than 10%), moderate (10-20%) and high (more than 20 %) phenotypic and genotypic coefficients of variation.

The genotypic coefficient of variation (GCV) of different traits ranged from 10.84 for fruit diameter to 32.61 for weight per fruit. Similarly phenotypic coefficient of variation (PCV) ranged from 12.55 to 34.49 respectively for the same traits as GCV. Fruit length (19.08/18.75), days to fruit maturity (19.53/18.42) and fruit diameter (12.55/10.84) exhibited moderate phenotypic and genotypic coefficient variation. All other traits under observation days to germination. Flowering, fruiting, weight per fruit and total yield showed higher PCV and GCV.

Comparatively lower degree of variation in days to flowering and maturity, higher degree of variation in fruit weight and fruit yield was also observed by Ullah *et al.* (2012). Khan (2009) also found wide range of phenotypic variation along with high heritability in cucumber. The characters namely, fruit girth, fruit length, fruit weight, number of fruit per plant and fruit yield per plant showed moderate to high GCV. As reported by Gaikwad *et al.* (2011), all traits under study in our observation also showed higher value of PCV than GCV signifying the impact of environment on the expression of those traits. Ogbonna and Ubi (2005) also suggested that differences in the values between phenotypic and genotypic variation depicts environmental influence in the manifestation of the traits studied. Traits possessing higher degree of genotypic variation however, suggests 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 these traits (Pal *et al.*, 2016).

#### **Heritability and genetic advance**

Except fruit diameter (0.74), all other traits under consideration showed higher degree of heritability where days to germination (0.98), days to flowering (0.97), fruit length and weight per fruit (0.96) showed higher proportion of genetic variation in the traits than the environmental one. Traits days to germination, no. of flower and weight per fruit showed higher GCV coupled with higher heritability reveals that these characters are controlled by additive gene. So, these characters can be improved via direct selection. Similar result have been reported by Hossain *et al.* (2010).

Genetic advance as a per cent of mean is classified as low (less than 40%), moderate (40-50%) and high (more than 50%). Fruit diameter (19.29), days to fruit maturity (35.81) and fruit length (37.96) showed lower genetic advance as percent of mean and all other traits under study showed moderate to higher genetic advance as percent of mean. Weight per fruit (65), days to germination (64.24) and no. of flowers (63.52) reported higher values as compared to other traits under study. Among all the characters studied, days to maturity exhibited high heritability coupled with relatively moderate genetic advance as a per cent of mean suggesting expression of the trait is under the control of non-additive type of gene action, and its response to selection would be poor. In such case hybridization programme will be rewarding (Bartaula *et al.*, 2019).

The estimate of genetic advance is more useful as a selection tool when considered jointly with heritability estimates (Johnson *et al.*, 1955; Parnse, 1957). The attributes which had high to moderate heritability as well as genetic gain were fruit weight, flowers per plant and days to flowering, indicating that these are simply inherited traits. Similar results were reported by

Islam *et al.* (1993) for number of flowers per plant in cucumber. Similar results were reported by Kumar *et al.* (2008) for number of flowers/plant, fruit length and fruit diameter. Similar results for fruit length were reported by Joshi *et al.* (1981), Kumar *et al.* (2008) and Yogesh *et al.* (2009) and Kumar *et al.* (2013).

**Table 1:** Analysis of variance for different quantitative characters of eight Cucumber genotypes in Lamahi, Dang, Nepal (2018)

Parameters	Mean Sum of Squares		
	Replication (df=2)	Genotypes (df=8)	Error (df=14)
Days of Germination	0.0417	3.0417***	0.0417
Days to Flowering	0.87	45.52***	1.02
Days to Fruiting	0.54	56.57***	2.45
No. of Flower	50.54	53.12***	6.07
Fruit Length (cm)	5.803	12.014***	0.424
Fruit Diameter (cm)	0.846	3.205*	0.979
Weight per Fruit (g)	459	9476***	325
Days to Fruit Maturity	0.042	3.565***	0.423
Yield (t/ha)	0.476	11.619***	1.795

**Table 2.** Estimation of variability, heritability and genetic advance for yield and yield component characters of eight Cucumber genotypes in Lamahi, Dang, Nepal (2018)

Traits	$\sigma^2_g$	$\sigma^2_p$	Mean	GCV	PCV	H	GA	GAM
Days of Germination	3.03	3.07	5.54	31.39	31.61	0.98	3.56	64.24
Days to Flowering	45.18	46.2	26.88	25.01	25.29	0.97	13.69	50.94
Days to Fruiting	55.75	58.2	35.33	21.13	21.59	0.95	15.05	42.6
No. of Flower	51.09	57.17	21.91	32.61	34.49	0.89	13.92	63.52
Fruit Length (cm)	11.87	12.29	18.37	18.75	19.08	0.96	6.97	37.96
Fruit Diameter (cm)	2.88	3.85	15.65	10.84	12.55	0.74	3.01	19.29
Weight per Fruit (g)	9367.67	325	301.54	32.09	32.64	0.96	196.01	65.00
Days to Fruit Maturity	3.42	3.84	10.04	18.42	19.53	0.89	3.59	35.81
Yield (t/ha)	10.72	12.51	14.48	22.61	24.43	0.85	6.24	43.11

### Estimates of Phenotypic correlation coefficients

Estimates of phenotypic correlation of yield and other yield related traits are shown in Table 3.

**Table 3.** Simple correlation coefficient of different yield and yield attributes of eight Cucumber genotypes in Lamahi, Dang, Nepal (2018)

Traits	DOG	DTF	DTFR	No. of Flowers	FL	FD	wt/Fruit	DTFM	Yield
DOG	1	-0.063	0.089	0.236	0.136	0.28	0.008	0.209	
0.442*									
DTF		1	0.924**	-0.623**	-0.619**	-0.554**	0.052	0.434*	
0.538**									
DTFR			1	-0.533**	-0.645**	-0.483*	-0.085	0.594**	
0.436*									
No. of Flowers				1	0.620**	0.480*	-0.243	-0.007	
0.415*									
FL					1	0.602**	0.379	-0.454*	
0.450*									
FD						1	0.319	-0.37	
0.649**									
Wt./Fruit							1	-0.536**	0.277
DTFM								1	-0.156
Yield									1

\*\*Correlation is significant at the 0.01 level \*. Correlation is significant at the 0.05 level. DOG- Days of Germination, DTF- Days to flowering, DTFR- Days to fruiting, FL- Fruit length, FD- Fruit diameter, DTFM- Days to fruit maturity

Fruit diameter ( $r= 0.649$ ) showed positive and highly significant correlation with yield. Fruit

length ( $r= 0.450$ ), days of germination ( $r= 0.442$ ) and no. of flowers ( $r= 0.415$ ) showed moderately significant positive correlation with fruit yield.

Days to flowering ( $r= -0.538$ ) showed highly significant negative correlation, however, negative correlation of days to fruiting ( $r= -0.436$ ) was found to be moderately significant. Correlation of wt. of fruit ( $r= 0.277$ ) and days to fruit maturity ( $r= -0.156$ ) with fruit yield are found to be insignificant. Similar results for different traits were reported by Singh *et al.* (2017), Ullah *et al.* (2012), Cramer and Wehner (2000) and Islam *et al.* (1993).

## CONCLUSION

All the studied traits were significant, indicating that presence of genetic variability which can be exploited in crop improvement program. Traits namely weight per fruit, days of germination, no. of flower and days to flowering having high GCV, PCV and heritability along with high genetic advance as percentage of mean can be used effectively in selection process of crop improvement program. As fruit diameter was positively and highly correlated with fruit yield hence, selection for the trait might bring an improvement in grain yield. Highly significant negative correlation of days to flowering with fruit yield suggest selection of genotypes with less days to flowering may result in improved fruit yield.

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## Author contributions

A. Adhikari, U. Panthi, P. Karki and K. Timalsena helped in data recording. S. Bartaula conducted the trial and recorded data, analyzed and wrote the final manuscript.

## Conflict of interest

The authors declare no conflicts of interest regarding publication of this manuscript.

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