

## Variability, Heritability and Genetic Advance in Hot Pepper (*Capsicum annuum* L.) Genotypes in West Shoa, Ethiopia

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**Abstract:** Twenty *Capsicum* genotypes were evaluated to estimate the nature and magnitude of variability among green fruit yield per plant and related characteristics at Bako Agricultural Research Center, Ethiopia, during 2007/2008 cropping season. Significant genotypic variability among the tested genotypes was observed for all the traits studied. In general phenotypic coefficient of variation (PCV) was higher than that of genotypic coefficient of variation (GCV). The highest PCV of 183.03% and GCV of 182.35% were recorded for unmarketable fruit yield followed by PCV of 72.69% and GCV of 71.09% for single fruit weight. Broad sense heritability estimates ranged from 33.63% for stem diameter to 97.77% pungency index. Genetic advance that could be expected from selecting the superior 5% of the genotypes as percent of mean varied from 6.24% for days to maturity to 143.22% for fruit weight. The study had demonstrated the existence of adequate genetic variability, high degree of genetic determination and genetic advance among *Capsicum* genotypes for the majority of the traits.

**Key words:** *Capsicum annuum* L. • Genetic advance • Genotypic coefficient of variation • Heritability • Phenotypic coefficient of variation

### INTRODUCTION

*Capsicum* species belong to the *Solanaceae* family and genus *Capsicum* is the second most important vegetable crop of the *Solanaceae* family after tomato [1, 2]. The crop varies in certain characteristics depending on the type of species [3].

*Capsicum* species can be divided into various groups based on fruit characteristics like pungency (hotness), color, shape, intended use and genetics [1]. The fruits are consumed as fresh, dried or processed products as vegetables and as spices or condiments [4].

Fruits of *Capsicum* plants are among the most heavily consumed spices throughout the world, due to their unique flavor and pungency [5, 6]. It is also the leading spice crop in Ethiopia and the pungent *Capsicum* type (hot pepper) is locally consumed in various food preparations particularly for flavoring and adding color to local stew. In addition to dietary benefits, *Capsicums* are also high value crops and can often provide excellent

income-generating opportunities to small farmers. Further, the crop is the main industrial raw material for processing of *Capsaicin* and color oleoresins [7].

Since many years before, several hot pepper (*Capsicum annuum* L. var. *annuum*) genotypes have been widely grown in tropics and typical tropical climate within Ethiopia (between 3° and 18° North latitude; 48° east of longitude) over centuries. In Ethiopia, about 64,774 hectare land was covered by hot pepper and 116,739 tones was harvested in 2004 only [8]. However, the productivity of pepper is low even when compared to that of other developing countries [9]. At farmers' level, the yield of pepper is about 0.4 tones per hectare [7] while in Turkey the average yield exceeds 14 tones per hectare [10]. Moreover, the varieties of peppers at the hands of growers are very old; they were released in the early 1980s. This calls for urgent breeding work in order to develop cultivars with better yielding potential. For efficient and effective breeding work, investigation and better understanding of the variability existing in the

existing genotypes and determination of heritability for the most important traits and the genetic advance that could be obtained is indispensable.

Revealing the relationship between yield and other agronomic traits in crops has also been considered as a good source of information for the breeder in order to focus on key traits with strong correlation with the target trait. Thus, several works have been done so far in different crops and reports are available in rice [11], field pea [12], oat seeds [13], soybean [14] and Khorasan wheat [15].

Genetic variability in pepper estimated by morphological data and AFLP markers was done with the aim of grouping pepper genotypes into clusters according to their distances as estimated by morphological traits and the markers and to assess the relationships between the two [16]. Similar work has been done elsewhere in order to identify and characterize accessions of the *Capsicum* spp. collection and estimate the genetic divergence among accessions [17]. However information is not available on the existing variability and the genetic advance expected among the genotypes which are found in the area originating from around the world. Therefore the objective of this study was to investigate the variability, determine the heritability and genetic advance of the capsicum genotypes under Bako, Ethiopia condition.

## MATERIALS AND METHODS

Twenty *Capsicum* genotypes including one local cultivar from Bako Agricultural Research Center were used for this experiment. The present study was conducted under irrigation condition in 2007 /2008 cropping season at Bako Agricultural Research Center. Bako is located between 9°07'N latitude and 37°05'E longitude at an altitude of 1650 m.a.s.l [18] on the distance of 258 km west of Addis Ababa. The mean daily maximum and minimum temperature are 30.3°C and 15.1°C, respectively and receives an average of 1200 mm rain per year [19]. The soil type of the area belongs to the Nitosol series, which is reddish-brown in color and has a clay to sandy clay-loam texture with pH ranging from 5.3-6.0 [18].

The experiment was performed in a Randomized Complete Block Design with three replications. In each plot, an intra-row spacing of 0.3 m and inter-row spacing 0.7 m were maintained to accommodate seven plants per row and 35 plants per plot.

In this study, 16 traits were recorded from sample plants in each plot and the results were expressed as mean values. All the data were represented per plant observation except for marketable fruit yield and unmarketable fruit yield which were computed from the plot observation.

Table 1: Source, description and origin of the test *Capsicum* genotypes

Genotype	Pedigree	Origin/Source
PBC 223	Jo Saeng Jin	Korea/The World Vegetable Center-AVRDC
PBC 600	LC-Serdang	Malaysia/The World Vegetable Center-AVRDC
Mareko-Fana	N/A	BARC/Ethiopia
Bako-Local	Bako-Local	BARC/Ethiopia
PBC 579	N/A	Sri Lanka/The World Vegetable Center-AVRDC
Oda-Haro	N/A	BARC/Ethiopia
Oda-Haro	N/A	MARC/Ethiopia
Malka-Zala	PBC579	Malaysia /The World Vegetable Center-AVRDC
Malka Eshet	N/A	MARC/Ethiopia
Local Check	Local Check	BARC/Ethiopia
PBC 830	Bangchang	Thailand/The World Vegetable Center-AVRDC
ICPN 9 #1	PBC 76/PBC 517	France/The World Vegetable Center-AVRDC
ICPN 9 #2	PBC 1363/PBC 504	Bulgaria/France/The World Vegetable Center-AVRDC
ICPN9 #11	PBC 495/PBC 3802	France/Indonesia/The World Vegetable Center-AVRDC
ICPN9 #12	PBC 284/PBC 1574	France /Thailand/The World Vegetable Center-AVRDC
ICPN9 #15	Pant C-1	India/The World Vegetable Center-AVRDC
ICPN9 #18	PBC 506/PBC3851	Franc/Malaysia /The World Vegetable Center-AVRDC
ICPN9 #20	PBC 385/PBC 504	Malaysia/France/The World Vegetable Center-AVRDC
ICPN10 #7	N/A	France/Indonesia/The World Vegetable Center-AVRDC
ICPN12 #1	N/A	India/The World Vegetable Center-AVRDC

GenRes Statistical Software Package [20] was employed for analysis of variance and estimation of correlation among the traits.

To estimate the extent of variability, genotypic and phenotypic coefficients of variability were estimated based on the following formula. [21]:

$$\text{Genotypic coefficient of variation} = [(\sigma^2_g)^{1/2}/\text{mean}] \times 100;$$

$$\text{Phenotypic coefficient of variation} = [(\sigma^2_p)^{1/2}/\text{mean}] \times 100$$

Where  $\sigma^2_g$  = Genotypic variance = [(Mean square of genotypes) - (Error mean square)]/replications,

$\sigma^2_p$  = Phenotypic variance =  $\sigma^2_g + \sigma^2_e$  and  $\sigma^2_e$  = Error mean square from the analysis of variance

Broad sense heritability ( $h^2$ ) of the traits was determined according to the formula suggested by [23] as follows:

$$h^2 = (\sigma^2_g) / (\sigma^2_p) * 100$$

Where,

$h^2$  = Heritability in broad sense

$\sigma^2_g$  = genotypic variance and

$\sigma^2_p$  = Phenotypic variance

The genetic advance (in broad sense) expected under selection, assuming the selection intensity of 5 percent was calculated by the formula suggested by [21]

$$\text{Genetic advance} = K (\sigma_p) h^2$$

$$\text{Genetic advance as\% of mean} = (\text{GA}/\text{Grand mean}) * 100$$

Where,

( $\sigma_p$ ) = The phenotypic standard deviation of the character,  $h^2$ = heritability estimate and

K = The selection differential (K=2.06 at 5 per cent selection intensity)

## RESULT AND DISCUSSION

The analysis of variance indicated significant genotypic variability among the tested genotypes with respect to all the recorded traits (Table 2).

The present investigation revealed considerable amount of variability among the tested genotypes with respect to all the traits studied. Overall mean values ranged 89 to 104 days regarding the duration needed to attain green fruit maturity and 0.054 to 0.421 gram green fruit yield per plant suggesting possibility of selection for earliness and high green fruit yield in the studied genotypes. Scope of wide variability for improvement of the crop population for such traits was also reported by [23]. In general PCV was larger than the corresponding genotypic GCV for each trait (Table 3).

The highest PCV of 183.03% and GCV of 182.35% were recorded for unmarketable fruit yield followed by PCV of 72.69% and GCV of 71.09% for single fruit weight. This result is in agreement with earlier report of [23]. High PCV and GCV could be an advantage as they can offer opportunity for selection of superior genotypes with

Table 2: Analysis of variance for 16 traits in 20 *Capsicum* genotypes

Traits	Mean squares		
	Replication (2)	Genotypes (19)	Error (38)
B/P	0.425	11.660**	1.420
PH	227.184	118.448**	20.624
SD	0.046	0.0186**	0.0074
DFL	46.667	60.056**	0.825
F/P	86.150	578.031**	15.589
DM	35.806	33.012**	2.098
UMFY	0.000004	0.004**	0.000009
MFY	0.568	5.581**	0.232
FL	3.211	11.285**	0.719
FD	0.056	0.527**	0.0145
SI	0.843	34.017**	3.511
FW	1.634	67.854**	1.017
CD	113.164	100.392**	9.925
PcT	0.0011	0.0279**	0.0012
PI	0.0035	1.988**	0.0147
FY/P	0.0026	0.0253**	0.001

\*\* = Significant differences at 1% percent probability level

B/P=Number of primary branch per plant, PH=Plant height, SD= Stem diameter, Dfl = Days to flower, F/P=Fruit per plant, DM=Days to maturity, UMFY= Unmarketable fruit yield, MFY= Marketable fruit yield, FL= Fruit length, FD= Fruit diameter, SI= Shape Index, FW=Fruit weight, CD= Canopy diameter, PcT= Pericarp thickness PI= Pungency index = FY/P= Fruit yield per plant

Table 3: Estimates of mean, range, phenotypic (PCV) and genotypic (GCV) coefficients of variation, phenotypic ( $\sigma^2_p$ ), genotypic ( $\sigma^2_g$ ) and environmental ( $\sigma^2_e$ ) variances, for different traits of *Capsicum* genotypes

Traits	Range of means	Overall Mean± SE	Local (mean)	PCV (%)	GCV (%)	( $\sigma^2_p$ )	( $\sigma^2_g$ )	( $\sigma^2_e$ )
B/P	4.90-13.20	8.79±0.79	11.57	25.01	21.02	4.833	3.413	1.420
PH	34.50-68.10	49.65±3.03	52.27	14.69	11.50	53.232	32.608	20.624
SD	0.72-1.24	0.999±0.06	1.05	10.50	6.089	0.011	0.0037	0.0074
DFI	60-75.00	66.07±0.61	64.00	6.86	6.73	20.569	19.744	0.825
F/P	8-70.00	28.25±2.63	13.00	50.44	48.47	203.07	187.48	15.589
DM	89-104.00	96.58±0.97	93.67	3.65	3.32	12.403	10.305	2.098
UMFY	0.025-0.133	0.02±0.002	0.00	183.03	182.35	0.00134	0.00133	0.000009
MFY	0.65-6.25	2.44±0.321	4.52	58.18	54.73	2.015	1.783	0.232
FL	6.77-16.15	9.53±0.57	12.07	21.61	19.69	4.241	3.522	0.719
FD	0.48-2.06	1.09±0.08	0.99	39.46	37.94	0.186	0.171	0.0145
SI	4.87-22.23	9.90±1.25	15.52	37.36	32.21	13.68	10.169	3.511
FW	1.86-20.15	6.64±0.67	7.59	72.69	71.09	23.296	22.279	1.017
CD	23.94-50.15	36.30±2.10	39.17	17.44	15.13	40.08	30.156	9.925
PcT	0.13-0.56	0.31±0.02	0.397	32.42	30.43	0.0101	0.0089	0.0012
PT	0.0-2.90	1.82±0.08	1.97	45.08	44.57	0.673	0.658	0.0147
FY/P	0.054-0.421	0.16±0.02	0.30	59.29	55.90	0.009	0.008	0.001

B/P= Number of primary branch per Plant, PH= Plant height, SD= Stem diameter, DFI=Days to flower, F/P=Fruit per plant DM= Days to maturity, UMFY= Unmarketable fruit yield, MFY= Marketable fruit yield, FL= Fruit length, FD= Fruit diameter, SI= Shape Index, FW= Fruit weight, CD= Canopy diameter, PcT=Pericarp thickness, PI= Pungency index, FY/P=Fruit yield per plant

Table 4: Estimates of heritability in broad sense ( $h^2$ ), genetic advance (GA) and genetic advance as percent of mean (GAM), phenotypic and genotypic variance for studied traits of *Capsicum* genotypes

Traits	( $\sigma^2_p$ )	( $\sigma^2_g$ )	$h^2$ (%)	GA	GAM
B/P	4.833	3.413	70.62	3.20	36.38
PH	53.232	32.608	61.26	9.21	18.55
SD	0.011	0.0037	33.63	0.07	7.00
DFI	20.569	19.744	95.99	8.97	13.58
F/P	203.07	187.48	92.32	27.10	95.93
DM	12.403	10.305	83.08	6.03	6.24
FL	4.241	3.522	83.05	3.52	36.94
FD	0.186	0.171	92.43	0.82	75.23
SI	13.68	10.169	74.33	5.66	57.17
FW	23.296	22.279	95.63	9.51	143.22
CD	40.08	30.156	75.24	9.81	27.02
PcT	0.0101	0.0089	88.12	0.18	58.06
PI	0.673	0.658	97.77	1.65	90.66
FY/P	0.009	0.008	88.89.	0.17	106.25

B/P= Number of primary branch per Plant, PH= Plant height, SD= Stem diameter, DFI=Days to flower, F/P=Fruit per plant DM= Days to maturity, FL= Fruit length, FD= Fruit diameter, SI= Shape Index, FW= Fruit weight, CD= Canopy diameter, PcT= Pericarp thickness, PI= Pungency index, FY/P=Fruit yield per plant

respect to character of interest [24]. The recorded PCV and GCV for days to maturity were lowest. Similar results were reported by [23] in variability study in green chilli. However, GCV was near to PCV for the traits like days to flower (6.86%) and (6.73%), days to maturity (3.65%) and (3.32%), unmarketable fruit yield (183.03%) and (182.35%), pungency index (45.08%) and indicating high contribution of genotypic effects for phenotypic expression of such traits. In other traits, there are wider gaps between estimate of PCV and GCV suggesting visible contribution of environmental factors in addition to genotypic effect for expression of the traits.

Such results of present study are in agreement with similar reports of [25].

The heritability values estimated in broad sense, for the studied traits are shown in Table 3 All the traits considered in the study exhibited high heritability estimates with the exception of stem diameter indicating genetic variances with lesser influence of the environment. Selection for such traits should fairly be easy due to closer correspondence between genotype and phenotype arising from relatively smaller contribution of environment to the phenotype.

The estimated values of broad sense heritability ( $h^2$ ) for traits studied were ranged from 33.63% (stem diameter) to 97.77% (pungency index).

The expected genetic advance values (Table 3) suggested the progress that could be expected from selecting the top 5 percent of the genotypes and varied from 0.07 (stem diameter) to 27.1 (fruit per plant). Similarly, values of the expected genetic advance as percent of mean showed variation that ranged from 6.24% (days to maturity) to 143.22% (fruit weight). Other higher values of expected genetic advance as percent of mean were recorded in respect of fruit weight (143.22%), fruit yield per plant (106.25%), fruit per plant (95.93%), pungency index (90.66%) and fruit diameter (75.23%). The results suggested the potentiality for improvement of these traits using different selection procedures.

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