

Genetic Variability, Heritability, Genetic Advance, and Association of Characters in Small Pod Hot pepper (*Capsicum annuum* L.) Landraces in West Hararghe, Eastern Ethiopia

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Abstract

Hot pepper is the dominant vegetable crop grown in different parts of Ethiopia with long history of cultivation and considerable genetic diversity for most important morphological traits. The study was undertaken to genetic variability and association among yield and yield related traits in the hot pepper. Analysis of variance revealed that there were a significant ($P < 0.05$) differences in genetic variation among genotypes for all morphological and fruit characters. The genotypic coefficient of variation ranged from 16.4% to 63.3% and phenotypic coefficients of variation ranged from 17.3% to 86.8%. All traits except fruit diameter showed highest genotypic coefficient of variation and phenotypic coefficients of variation. This indicates the presence of slight environmental influence to some degree in the phenotypic expression of the characters and it implies that the existence of substantial variability for such characters and selection may be effective based on these characters. The broad sense heritability values ranged from 53.3% to 99.4% whereas genetic advance as percent of mean was estimated in the ranged from 31.7% to 93.0%. Accordingly, both broad sense heritability and genetic advance were high for plant height, fruit number per plant, fruit diameter, fruit length, fruit diameter, and marketable yield. Hot pepper yield had positive and significant genotypic and phenotypic correlations with fruit weight, fruit length, fruit number per plants, unmarketable and marketable yield. Plant height, fruit diameter, fruit weight, fruit length, marketable yield, and unmarketable yield had positive direct effect in hot pepper yields at both genotypic and phenotypic levels.

Key words: Associations, Genetic Advance, Genetic Variability, Heritability

1. Introduction

Hot pepper is belonging to member of the Solanaceae family and family Solanaceae comprises five domesticated species and 30 wild species and this specie is diploid ($2n=2x=24$) (Rohami *et al.* 2010). Peppers are an important cash crop for smallholder farmers in developing countries, hot pepper dominates world spice trade has become a popular vegetable and cash crop in the tropics for smallholders (Lin *et al.*, 2013). Hot pepper has grown widely in tropical agro climate conditions of Ethiopia (Berhanu *et al.*, 2011). In Ethiopia, it is a high value crop due to its high pungency which serve as in the preparation of local flour called “Berberie” and it used as food for consumption and source of cash earning for smallholder farmers/or producers in both green and dry form [1]. Currently, it is produced in many parts of the country, because food is tasteless without hot pepper for most Ethiopians.

The productivity of the crop is low due to many limiting factors such as shortage of adapted high yielding varieties, using unknown

seed sources and poor-quality seeds, poor irrigation system, lack of information on soil fertility, the prevalence of fungal, and bacterial as well as viral diseases. Diversity studies are an essential step and pre-requisite in plant breeding and could produce valuable knowledge for crop improvement programmers [2]. The presence of genetic variability in crops is essential for its further improvement by providing options for the breeders to develop new varieties and hybrids [3]. Hence, generating information on the degree and pattern of genetic diversity of the hot pepper genotypes were less evaluated scientifically using either molecular or morphological studies in Ethiopia. The evaluation and the documentation of existing diversity are essential to maintain an active basis for the exploration of the genetic variability in pepper breeding programs [4]. Analysis of genetic diversity using quantitative or predictive methods has been used in the analysis of composition of populations. However, the magnitude of this diversity has not yet evaluated. Therefore, the objectives of this study were, to estimate phenotypic and genotypic variations, Genetic variability,

heritability, expected genetic advance, correlation coefficient of yield, yield related traits in the hot pepper, make the necessary information available for future breeding, and crop improvement programs in genotypes.

2. Materials and Methods

2.1. Description of the Study Area

The study was conducted at Mechara Agricultural Research Center (McARC) experimental field, in the West Hararghe zone of Oromia National region, Eastern Ethiopia during 2021 cropping season under rain fide condition. It is located at about 434 km away from Addis Ababa. McARC site is located between 8o.34' N latitude and 40.20' E longitude m.a.s.l. The altitude of the area is about 1760 m.a.s.l. It has a warm climate with annual mean maximum

and minimum temperature is 31.8oc and 14oc, respectively. The mean annual rainfall is 1100mm. Daro labu district is characterized mostly by flat and undulating land features and the rainfall is erratic; onset is unpredictable, its distribution and amount are also quite irregular. The soil of the experimental site is well-drained slightly acidic Nit sol.

2.2. Experimental Materials

Thirty-four Landraces genotypes along with two-released variety as checks (Dinsire and Dame) were used in this study. The landraces were collected from different agro-ecologies of varying altitude, rainfall, temperature, and soil type of West Hararghe, Eastern Ethiopian.

Code	Accession name	Collection Woreda	Code	Accession name	Collection Woreda
1	OBGL-50	Oda Bultum	19	DLML6	Daro labu
2	OBSS-146	Oda Bultum	20	BKAR205	Boke
3	BKRRK-158	Boke	21	OBGB100	Oda Bultum
4	BKRRK-164	Boke	22	OBGB92	Oda Bultum
5	BKAR-200	Boke	23	BKAR220	Boke
6	OBSS-131	Oda Bultum	24	OBGB68	Oda Bultum
7	OBSS120	Oda Bultum	25	BKDL243	Boke
8	BKRRK189	Boke	26	OBGB112	Oda Bultum
9	BKAR214	Boke	27	BKRRK160	Boke
10	OBSS156	Oda Bultum	28	BKRRK180	Boke
11	OBSS130	Oda Bultum	29	BKRRK190	Boke
12	DLML4	Daro labu	30	OBGB74	Oda Bultum
13	OBGB72	Oda Bultum	31	OBSS135	Oda Bultum
14	OBSS144	Oda Bultum	32	OBSS151	Oda Bultum
15	BKRRK172	Boke	33	OBSS141	Oda Bultum
16	ODBR14	Oda Bultum	34	OBGB-67	Oda Bultum
17	ODBR1	Oda Bultum	35	Dame	
18	ODBR34	Oda Bultum	36	Dinsirey	

Table 1: Description of Experimental Materials

2.3. Experimental Design and Trial Management

The experiment was laid out in 6 × 6 simple lattice design. Seeds of each genotypes were sown in the main field in a plot size of 8.4m² (2.8 m × 3 m) directly by drilling. Each plot consisted of four rows with inter and intra-row spacing of 0.7 and 0.3 m, respectively. DAP as a source of Phosphorus was applied at the rate of 200 kg ha⁻¹ during planting and nitrogen fertilizer was applied in the form of Urea at the rate of 150 kg ha⁻¹ in splits, half during sowing and the rest as side dressing at 45 days after sowing. Weeding, hoeing, and other field management activities were done uniformly for all genotypes as per the recommendation for hot pepper.

2.4. Data Collected

Data collected: quantitative characters on recorded on five randomly selected plants from the two middle rows of each plot by

adopting descriptors list for hot pepper [5].

Plant height (cm): was measured from the soil surface to the top most growth points of above ground plant part at the last harvesting time.

Canopy diameter: was determined by measuring the diameter of the plant from north to south and east to west at maturity.

Pod length (cm): of ten randomly selected pods from each plot at each harvest was measured using a caliper.

Pod diameter (cm): the pod center body width at the center of each fruit was measured from marketable pods of a sample from each plot using a caliper

Pod dry weight (g): of ten individual pods from each plot was taken.

The number of pods per plant: the number of physiologically matured pods was counted from randomly taken plants at each

successive harvest.

Marketable yield (qu ha⁻¹): After drying, the dried marketable fruits were separated, the weight of the respective categories are recorded and converted to qu ha⁻¹.

Unmarketable yield (qu ha⁻¹): Unwanted pods by consumers from marketable dried pods were recorded at each harvest and converted to qu ha⁻¹.

Total dry pod yield (qu ha⁻¹): total yield (marketable and unmarketable) summed up to estimate yield per hectare.

2.5 Data Analysis

The analysis of variance (ANOVA) was done by using **R-software** and the least significant difference (LSD) test at 5% level of significance was used for genotypes mean comparisons, whenever genotype differences were significant.

2.6 Estimation of Variance Components

Different genetic parameters including genotypic variance ($\sigma^2 g$), phenotypic variance ($\sigma^2 p$), phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were estimated by using the formula, adopted from Burton and De vane (1953) and Johnson *et al.*, 1955a and 1955b. Genotypic variance ($\sigma^2 g$) = (MSg σ MSe) / r Where: $\sigma^2 g$ = genotypic variance, MSg = mean square due to genotypes, MSe = environmental variance (error mean square), r = number of replication. Phenotypic variance ($\sigma^2 p$) = $\sigma^2 g + \sigma^2 e$ Where, $\sigma^2 g$ is genotypic variance, $\sigma^2 e$ = Environmental variance. Genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) was calculated as suggested by Burton and De vane (1953).

$$PCV(\%) = \frac{\sqrt{Vp}}{Mean} \times 100 \quad GCV(\%) = \frac{\sqrt{Vg}}{Mean} \times 100$$

Both phenotypic and genotypic coefficients of variations were categorized depending up on cut points suggested by Deshmukh *et al.* (1986) as low (<10%), moderate (10-20%) and high (>20%).

2.7 Estimation of Broad Sense Heritability and Genetic Advance

Broad sense heritability (H²b): Heritability in broad sense (H²b) was estimated according to the formula suggested by Johnson *et al.*, 1955 and Hanson *et al.*, 1956. $H^2 b = (\sigma^2 g / \sigma^2 p) * 100$. Where, H²b=Heritability in broad sense, $\sigma^2 g$ =Genotypic variance, $\sigma^2 p$ =Phenotypic variance. The heritability was categorized as low (0-30%), moderate (30- 60%) and high (60% and above) as given by Robinson *et al.*, 1949[6].

Genetic Advance Under Selection (GA) is expected genetic advance for different characters under Selection was estimated using the formula suggested by Lush and Johnson *et al.*, (1955). $GA (\%) = K.H^2 b \times \sigma p$. Where, H²b=Heritability in broad sense, σp =Phenotypic standard deviation, GA=Expected genetic advance and k=the standardize selection differential at 5% selection intensity (K=2.063). **Genetic advance as percent of mean** was calculated using the formula given by Robinson and Comstock (1949). Genetic advance per population mean = (GA / grand mean) * 100. Genetic advance as percent mean was categorized as low (0-10%), moderate (10-20% and $\geq 20\%$) as given by Johnson *et al.*, 1955 and Falconer and Mackay (1996).

3. Results and Discussions

3.1. Analysis of Variances

The analysis of variance showed that the genotypes differed significantly ($p < 0.05$) for fruit diameter, fruit length, fruit weight and unmarketable yields and highly significant ($p < 0.001$) for plant height ,fruits number per plant, marketable yield and total yield (Table 2). This indicates the existence of substantial amount of variability among the genotypes tested which confirms the possibility to select best genotypes and exploit them for variety development. The significant genetic variation among genotypes might be because genotypes were genetically diverse and it could be a good opportunity for breeders to select genotypes for trait of interest for different crop improvement program. Several researchers reported significant differences among hot pepper genotypes studied [3,7,8].

The mean total yield per hectare ranged from 11.33 to 39.73 quintal per hectare. Among the studied genotypes, 27.78% of genotypes gave above the grand mean. Number of fruit per plant ranged from 14 to 78 with a mean value of 38.88 numbers. The range observed for marketable yield per hectare was 10.26 to 35.25 with overall mean of 17.8 quintals per hectare. The maximum and minimum values of plant height were 23 and 77.8 respectively, with a mean value of 51.48. This high range and mean value for each trait of interest suggests that great opportunity to improve the various desirable traits through selection as short-term strategy and through hybridization as long-term strategy. Hence, there is an opportunity to find genotypes having disease resistance and high yielding potential among the tested entries that perform better than the existing varieties to utilize for the future hot pepper improvement breeding programs.

Traits	Max	Min	Mean	Mean sum square of		CV %	LSD at 5%	R-Square
				Genotypes	Error			
Plant height	77.8	23	51.5	269.2**	16.4	7.9	7.9	0.45
Fruits number per plant	78	14	38.9	620.2**	1.74	3.4	3.4	0.98
Fruit diameter	2.1	0.9	1.4	0.12*	0.01	5.7	5.7	0.98
Fruit weight	1.98	0.24	0.8	0.23*	0.01	8.8	8.8	0.94
Fruit length	10.2	2.62	4.1	3.8*	0.07	6.3	6.3	0.99
Marketable yield	35.3	10.3	17.8	63.3**	8.78	16.6	16.6	0.88
Unmarketable yield	12.3	1.0	2.4	6.68*	2.04	59.3	59.3	0.77
Total yields	39.7	11.3	20.2	80.8**	20.8	23.1	23.1	0.87

Table 2: The ANOV and range for eight Traits of 36 genotypes

3.2. Estimation of Variance Components

The estimates of phenotypic and genotypic variances, genotypic coefficient of variation (GCV) and phenotypic coefficients of variation (PCV), broad-sense heritability (H²), genetic advance (GA) and genetic advance expressed as percent of the mean (GAM) are presented in Table 3. The phenotypic and genotypic variances have slightly difference for fruit number per plants, fruit length, fruit weight and fruit diameters and this indicating less influence of the environment on the phenotypic expression of these traits. In addition, variation among genotypes for these traits due to genetic diversity rather than environmental factors and this imply that selection of genotypes based on these traits effective. Phenotypic variance was higher than the genotypic variances for all the characters indicating the influence of the environmental factors on these traits.

The genotypic coefficient of variation ranged from 16.4% (fruit diameter) to 63.3% (unmarketable yield) and phenotypic coefficients of variation ranged from 17.3% to 86.8% for same traits, respectively. All traits except fruit diameter showed highest genotypic coefficient of variation and phenotypic coefficients of variation. High values of PVC and GCV indicate the existence of substantial variability for such characters and selection may be effective based on these characters [9]. In the present study, phenotypic coefficients of variation were slightly higher than the genotypic coefficients of variation for all the traits studied. This indicates the presence of slight environmental influence to some degree in the phenotypic expression of the characters. Similar finding was reported by Berhanu et al. (2011) indicating that high GCV and PCV values for fruit weight, number fruits per plant. In addition, similar findings were also reported by [4,10].

3.3. Broad Sense Heritability (H²b) and Genetic Advance as percent of mean (GAM)

The effectiveness of selection for any trait depends not only on the

extent of genetic variability but also on the extent of transferring genes from one generation to the other [9]. Accordingly, the estimates of heritability of all traits in the current study were moderate to very high. The broad sense heritability (H²) values ranged from 53.3% for unmarketable yield to 99.4% for fruit number per plant. Whereas genetic advance as percent of mean (GAM) was estimated in the ranged from 31.7% to 93.0% for fruit diameter and fruit number per plant, respectively. Accordingly, both broad sense heritability and genetic advance as percent of mean values were high for plant height, fruit number per plant, fruit diameter, fruit length, fruit diameter, and marketable yield (Table 4). The characters having very high heritability and genetic advance as percent of mean indicated relative small contribution of the environment factors to the phenotype and selection for such characters could be easy due to high additive effect. This indicated that these traits are highly heritable and selection of high performing collections is possible for the improvement of the traits.

Traits with broad sense heritability and genetic advance as percent of mean could easily be passed from one generation to the next then enhancing the efficiency of selection in hot pepper improvement program. This indicated that the traits are under genetic control and the environmental factors did not greatly affect their phenotypic variation. Similar findings were reported by earlier workers for some characters with moderate to high heritability and GAM estimates, for fruit yield per plant, fruit diameter, fruit length, average fruit weight and number of fruits per plant [2,11,12]. Since, the efficiency of selection would depend upon the magnitude of variability that is heritable and caused by genetic factors the higher values, therefore, heritability accompanied by high genetic advance for the characters studied should be quite valuable [13].

Traits	GV	PV	GCV	PCV	Hb%	GA	GAM (%)
Plant height	126.4	142.8	21.8	23.1	88.5	21.8	42.4
Fruits number per plant	309.2	311.0	45.2	45.4	99.4	36.2	93.0
Fruit diameter	0.06	0.1	16.4	17.2	89.0	0.5	31.7
Fruit weight	0.1	0.12	39.9	41.7	91.7	0.7	78.9
Fruit length	1.9	1.95	33.8	34.0	96.5	2.8	63.1
Marketable yield	27.2	36.0	30.3	34.9	75.6	9.4	54.4
Unmarketable yield	2.3	4.4	63.3	86.8	53.3	2.2	91.4
Total yields	30.0	50.8	27.1	35.3	59.1	8.7	43.0

Table 3: Genetic Variability Components for Quantitative Traits of 36 Hot Pepper Genotypes.

3.4. Estimation of association among Traits and Yields

The results of genotypic and phenotypic correlation coefficients of yield with morph agronomic traits are presented in Table 4. Hot pepper yield had positive and significant genotypic and phenotypic correlations with fruit weight, fruit length, fruit number per plants, unmarketable and marketable yield. In addition, yield showed positive and significant genotypic correlations with plant height. This indicated that the chance of simultaneous improvement of the Hot pepper yield with the traits that showed positive and significant association. This suggested that, selection and improvement of genotypes based on those characters would result in a substantial increment on fruit yield of hot pepper. These results agreed with the findings of earlier researchers (Razzaq *et al.*, 2016; Shimalies *et al.*, 2016; Fasikaw *et al.*, 2019) indicating genotypic and phenotypic correlations between plant height, fruit length, fruit diameter, average fruit weight, number of fruit per

plant and marketable yield.

Marketable yield per hectare and fruit number per plant have positive phenotypic and genotypic correlations with all tested traits except fruit diameter and these two traits have positive and significant association with total yield. This indicate that complementary gene actions for the traits that could be selected simultaneously and the most important traits for improving the genotypes for higher fruit yield and may be applied for selection in hot pepper improvement. This suggested that, selection and improvement of genotypes based on those characters would result in a substantial increment on fruit yield of hot pepper. These results are in agreement with Abraham *et al.* (2017) who advocated that importance should be given to number of fruits per plant, fruit weight, fruit length, fruit diameter and plant height during selection process because these characters contribute directly towards the yield.

	PH	FW	FL	FD	FNPP	MY	UY	TY
PH		0.03NS	0.14NS	-0.25 ^{NS}	0.2 ^{NS}	0.32 ^{NS}	0.09 ^{NS}	0.33*
FW	0.09 ^{NS}		0.66**	-0.13 ^{NS}	0.54**	0.64**	0.42**	0.7**
FL	0.13 ^{NS}	0.64**		-0.32 ^{NS}	0.36*	0.51**	0.14 ^{NS}	0.6**
FD	-0.17 ^{NS}	-0.1 ^{NS}	-0.27*		-0.2 ^{NS}	-0.2 ^{NS}	0.09 ^{NS}	-0.09 ^{NS}
FNPP	0.18 ^{NS}	0.53**	0.35**	-0.18 ^{NS}		0.3 ^{NS}	0.3 ^{NS}	0.33*
MY	0.21 ^{NS}	0.53**	0.43**	-0.16 ^{NS}	0.26*		0.24 ^{NS}	0.96**
UY	0.1 ^{NS}	0.35**	0.07NS	0.02 ^{NS}	0.24*	0.2 ^{NS}		0.37*
TY	0.21 ^{NS}	0.53**	0.41**	-0.08 ^{NS}	0.27*	0.87**	0.53**	

Note: PH=Plant height, FNPP=Fruits number per plant, FD=Fruit diameter, FW=Fruit weight, FL=-Fruit length, MY=Marketable yield, UNY=Unmarketable yield and TY=Total yields.

Table 4: Genotypic (above diagonal) and phenotypic (below diagonal) correlation of quantitative traits with yield

3.5. Path Coefficient Analysis

Plant height, fruit diameter, fruit weight, fruit length, and unmarketable yield had low magnitude and positive direct effect in hot pepper yields at both genotypic and phenotypic levels while, marketable yield had high magnitude and positive direct effect on hot pepper yield (Table 5). The positive direct effect of Plant height, fruit diameter, fruit weight, fruit length, and unmarketable yield on yield had path coefficient values lower than their correlation values, indicating higher indirect influence of these traits via other component traits. The results suggested that improvement of these

traits also directly improved the hot pepper yield. Hence, the large magnitude correlation coefficient was largely due to the positive indirect effects of these traits via others traits. Fruits number per plant exhibited negative direct effect on hot pepper yield and positive correlation coefficients at genotypic level. Hence, the positive correlation coefficient was largely due to the positive indirect effects of these traits via others traits.

Fruit diameter had the positive direct effect and exhibited, negative correlation with yield at both genotypic and phenotypic levels.

The negative correlation they showed with yield was mainly due to negative indirect effects through other traits. This indicated that restricted simultaneous selection should be followed; as restrictions are to be imposed to nullify the undesirable indirect effects in order to make use of the direct effect of these traits. The highest and positive indirect genotypic effects on hot pepper yield exhibited by plant height, fruit weight, fruit length and fruit number per plant via marketable yield per hectare. The present finding is in agreement with the finding of Kumari (2017), [3,8,10] they reported that direct and indirect effect of different morph agronomic traits of hot pepper on its yield.

In this study, the estimated residual effect (0.03) indicated the characters studied in path analysis contributed about 97% of the variability in yield at genotypic level. However, at phenotypic level the estimated residual effect (0.106) indicated the traits studied in path analysis contributed about 89.4% of the variability. This implied that traits, which were included in this path coefficient analysis were, good enough to explain or in confirming the results of and collections and exploration in the hot pepper. This 10.6% magnitude of residual effect towards yield in this study might be mainly due to the other traits or factors, which were not included in the study.

Causal factor	Effect via						
	PH	FW	FL	FD	FNPP	MY	UY
Plant height	0.038	0.000	0.014	-0.020	-0.004	0.291	0.011
Fruit weight	0.001	0.008	0.066	-0.010	-0.010	0.588	0.057
Fruit length	0.005	0.005	0.100	-0.026	-0.006	0.470	0.019
Fruit diameter	-0.009	-0.001	-0.032	0.081	0.003	-0.144	0.011
Fruit No per plant	0.008	0.004	0.036	-0.016	-0.018	0.272	0.040
Marketable yield	0.012	0.005	0.051	-0.013	-0.005	0.918	0.032
Unmarketable yield	0.003	0.003	0.014	0.007	-0.005	0.218	0.133
Residual: 0.03							

Table 5: Estimates of Direct (bold diagonal) and Indirect Effects (off diagonal) of Morph-Agronomic Traits on Hot Pepper Yield at Genotypic Level.

Causal factor	Effect via						
	PH	FW	FL	FD	FNPP	MY	UY
Plant height	0.007	-0.007	0.016	-0.011	-0.003	0.165	0.039
Fruit weight	0.001	-0.085	0.076	-0.006	-0.010	0.422	0.136
Fruit length	0.001	-0.054	0.119	-0.017	-0.007	0.345	0.027
Fruit diameter	-0.001	0.008	-0.032	0.061	0.003	-0.129	0.007
Fruit No per plant	0.001	-0.045	0.042	-0.011	-0.019	0.208	0.095
Marketable yield	0.001	-0.045	0.052	-0.010	-0.005	0.796	0.080
Unmarketable yield	0.001	-0.029	0.008	0.001	-0.005	0.162	0.393
Residual: 0.106							

Table 6: Estimates of direct (bold diagonal) and indirect effects (off diagonal) of morph-agronomic traits on hot pepper yield at phenotypic level.

4. Conclusion

The analysis of variance showed that the genotypes differed significantly for all morph agronomic and yield traits. The phenotypic and genotypic variances have slightly difference for fruit number per plants, fruit length, fruit weight and fruit diameters and this indicating less influence of the environment on the phenotypic expression of these traits. The genotypic coefficient of variation ranged from 16.4% to 63.3% and phenotypic coefficients of variation ranged from 17.3% to 86.8%. All traits except fruit diameter showed highest genotypic coefficient of variation and phenotypic coefficients of variation. This indicates the presence of slight environmental influence to some degree in the phenotypic

expression of the characters. The broad sense heritability values ranged from 53.3% to 99.4% whereas genetic advance as percent of mean was estimated in the ranged from 31.7% to 93.0%. Accordingly, both broad sense heritability and genetic advance were high for plant height, fruit number per plant, fruit diameter, fruit length, fruit diameter, and marketable yield. These estimates suggested that selection based on these traits is helpful for breeding program since these traits are under additive gene action.

Hot pepper yield had positive and significant genotypic and phenotypic correlations with fruit weight, fruit length, fruit number per plants, unmarketable and marketable yield. This

suggested that, selection and improvement of genotypes based on those characters would result in a substantial increment on fruit yield of hot pepper. Plant height, fruit diameter, fruit weight, fruit length, and unmarketable yield had low magnitude and positive direct effect in hot pepper yields at both genotypic and phenotypic levels while, marketable yield had high magnitude and positive direct effect on hot pepper yield and it suggested selection of genotypes for high performance of these traits also improve yield. Generally, the present study showed existence of significant genetic variability among tested genotypes indicating the presence of a huge opportunity for further improvement through selection and other breeding approaches. Hence, there is an opportunity to exploit these genotypes to develop varieties that perform better for the future hot pepper improvement.

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