Indian Journal of Advanced Botany (IJAB)
ISSN: 2582-9475 (Online), Volume-5 Issue-1, April 2025

Genetic Variability Analysis of Hot Pepper (Capsicum Annuum.L) Landraces at Haramaya University, Eastern Ethiopia

Abdurazak Sufiyan

***Abstract:** Hot pepper is a globally important spice utilized for food flavoring, enhancement, and coloring, with a growing demand over time. In the 2023/2024 cropping season, this study aimed to assess the genetic variability among 19 landrace genotypes and one improved hot pepper genotype under semi-irrigation conditions. Twelve quantitative parameters were evaluated using a randomized complete block design with three replications. Analysis of variance revealed highly significant differences ($P \leq 0.01$) for all traits except days to harvest and fruit weight, which were non-significant. Coefficients of variation ranged from 2.92 for days to fifty percent flowering to 31.47 for number of fruits per plant, indicating substantial variability among accessions. Fruit length varied from 4.5cm (accession 229694) to 11.17cm (accession 229699), while fruit width ranged from 8.33cm to 31.4cm, and fruit weight from 11.25g to 24.88g. Accession 229697 exhibited the highest fruit number per plant (42.67), while M/fana showed the lowest (12.67), with a mean value of 23.64. Fruit yield per plot ranged from 0.26kg/plot (accession 229696) to 0.91kg/plot (accession 28337), with approximately 40% of genotypes surpassing the population mean (0.5935kg/plot). High phenotypic and genotypic coefficients of variation, along with high genetic advance and heritability, were observed for yield per plot, number of fruits per plant, and fruit width, suggesting potential for improvement through selection. Based on the study results, accession 28337 for yield per plot, accession 229697 for fruit number per plant, and accession 229695 for fruit width are recommended for future selection.*

***Keywords:** Genetic Variability Study, Phenotypic and Genotypic Coefficients, Heritability, Genetic Advance, Hot Pepper, Ethiopia*

Abbreviations:
RCBD: Randomized Complete Block Design
PH: Plant Height
DFL: Days to 50% Flowering
DF: Days to 50% Fruiting
NFLA: Number of Flowers Per Axil
DH: Days to First Harvest
NFP: Number of Fruits Per Plant
FL: Fruit Length
FW: Fruit Width
FWT: Fruit Weight
NSF: Number of Seeds Per Fruit
TSW: 1000-Seed Weight [g]
FYPP: Yield per plot [Kg]
GA: Genetic Advance
PMC: Populations Mean Character
CV: Coefficient of Variation
SD: Standard Deviation
SE: Standard Error
PH: Plant Height
DFL: Days to 50% Flowering
PCV: Phenotypic Coefficient of Variation
GCV: Genotypic Coefficient of Variation
ANOVA: Analysis of Variance
GAM: Genetic Advances Mean
H%: Heritability
GA: Genetic Advance
DAP: Diammonium Phosphate
GCV: Genotypic Coefficient of Variation

Manuscript received on 10 February 2025 | First Revised Manuscript received on 18 February 2025 | Second Revised Manuscript received on 17 March 2025 | Manuscript Accepted on 15 April 2025 | Manuscript published on 30 April 2025.

*Correspondence Author(s)

Abdurazak Sufiyan*, Researcher, Department of Genetics, Ethiopia Biodiversity Institute, Harar Biodiversity Center, Harar (Harari), Ethiopia. Email ID: zakoahmado@gmail.com, ORCID ID: 0000-0002-6097-0004

I. INTRODUCTION

Hot pepper, as cited in [33], holds the distinction of being the second most important vegetable globally, following tomatoes. It reigns as the predominant spice used extensively for flavoring, enhancing taste, and adding color to food, all while supplying essential vitamins and minerals. It is a common and widely distributed spice crop throughout the tropics [31]. Over 100 species have been named under the genus Capsicum, but most workers recognize only two species, Capsicum annuum L. and Capsicum frutescens L [32]. The genus Capsicum, which is commonly known as red chile, hot red pepper, chili pepper, tabasco, paprika, cayenne, etc., belongs to the nightshade family Solanaceae.

Hot Pepper can be difficult to separate from the cultivated C. chinense (the hottest pepper) and C. frutescens (tabasco pepper), and their morphological features can overlap. These three species have the same ancestral gene pool and are sometimes very confusing, with pepper, chili, chile, chili, aji, paprika, and capsicum all used interchangeably to describe the plant [45].

Hot pepper has many importance. Nutritionally, hot pepper is rich in vitamins A and C. A large part of the vitamin intake for Ethiopians comes from hot pepper. The daily consumption of hot pepper peppers is about 15 grams per person. In Ethiopia, hot pepper is grown on approximately 246,000 ha. The crop is mainly cultivated on small patches of farmland. The average national yield is 400 kg ha-1 of dry fruit [14].

Despite its importance, hot pepper production has stayed low with a national average yield of 7.6 t/ha for the green pod and 1.6 t/ha for the dry pod [1] and [15]. The decline of hot pepper production is attributed to poor varieties, poor cultural practices, and the prevalence of fungal (blights) and bacterial as well as viral diseases [18]. According to

[11], the increased commercial interest in chili pepper fruit for fresh consumption or industrial and ornamental purposes has brought together a high demand for new chili pepper varieties combining high yield, food industry profitability, as well as aesthetic attractiveness. Improving the productivity of chili through developing high-yielding varieties with desirable qualities could reverse the existing trend of low productivity of this crop.

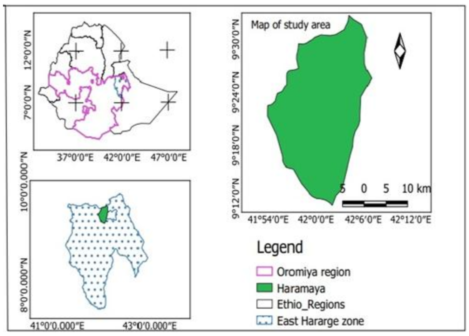
It is well known that the extent of genetic variation present in the crop is the basis for the improvement of that crop, and the degree of improvement depends on the magnitude of available beneficial genetic variability [9] and [8]. In Ethiopia, regarding genetic diversity studies of hot pepper using morphological markers or traits, several studies have been conducted for their theses and research purposes [38] and [5]. In addition [7], and [25].

Similar research was conducted by [3] at Dire Dawa University Tony Farm Site. However, present accessions considered for the study were not characterized previously as well and there is no genetic variability study of hot peppers conducted at the present environment condition (highland) which is different from the environment condition of Dire Dawa (lowland). Therefore, the aim of this study was to morphologically characterize hot pepper accessions.

II. METHODOLOGY

A. Description of Study Area

The study area of these field experiments was found in Haramaya Woreda as shown in the map below Haramaya (Fig 1). Haramaya University is located in the Haro Maya district, East Hararghe Zone of the Oromia Regional State in Ethiopia. Haramaya University is situated approximately 510 kilometers (320 mi) east of Addis Ababa, the capital city of Ethiopia.



[Fig.1: Map of Study Area]

Table-I: Passport of Experimental Material Used for this Study was Obtained from EBI

Accession No.	Region	Zone	Woreda	Latitude	Longitude	Altitude
20206	Oromia	Misrak Wellega	Sasiga	09-12-47-N	36-25-52-E	1667
20207	Oromia	Misrak Wellega	Wama hagelo	08-48-31-N	36-55-12-E	1597
20212	Oromia	Illubabor	Metu	08-20-07-N	35-35-08-E	1678
20213	Oromia	Illubabor	Ale	08-11-36-N	35-32-27-E	1758
20214	Oromia	Illubabor	Chora	08-21-53-N	36-03-13-E	1652
27845	South Ethiopia	Bench Maji	Gurra Farda	06-46-37-N	35-11-50-E	1408
27846	South Ethiopia	Bench Maji	Gurra Farda	06-90-46-N	35-18-32-E	1121
28334	Oromia	Illubabor	Harrumu	08-21-36-N	35-43-39-E	1657
28336	Oromia	Illubabor	Durame	08-26-45-N	35-52-54-E	1868
28337	Oromia	Illubabor	Durame	08-25-43-N	35-52-48-E	1877
28338	Oromia	Illubabor	Algae	08-84-43-N	35-45-60-E	1831
229694	Benishangul Gumuz	Metekel	Dibate	-	-	1640
229695	Benishangul Gumuz	Metekel	Dibate	-	-	1650
229696	Benishangul Gumuz	Metekel	Dibate	-	-	1700
229697	Benishangul Gumuz	Metekel	Dibate	-	-	1440
229698	Benishangul Gumuz	Metekel	Dibate	-	-	1520
229699	Amhara	Misrak Gojam	Bibugn	11-07-00-N	37-44-00-E	1850
229700	Amhara	Misrak Gojam	Bibugn	11-06-00-N	37-44-00-E	1830
229701	Amhara	Misrak Gojam	Hulet Ej Enese	11-05-00-N	37-46-00-E	1940
Melka Fana						

The rare research site is located at 9 o26' N latitude, 42 o3' E longitudes at an altitude of 1980 m.a.s.l. The mean annual rainfall is 760 mm [30]. The mean annual temperature is 16 °C. The mean relative humidity is 50%, varying from 20 to 81%. The soil of the experimental site is alluvial type with an organic carbon content of 1.15%, total Nitrogen content of 0.11%, available Phosphorus content of 18.2 mg kg soil-1, the exchangeable Potassium content of 0.65 cmolc kg soil-1, pH of 8.0 and percent sand, silt, and clay content of 62.92, 19.64, and 17.44, respectively [39].

Planting materials used for this study shown in Table I below comprised 20 genotypes among which 19 were treatment tests with landrace genotypes maintained at EBI (Ethiopia Biodiversity Institute) and the other genotypes was Marako fana (improved variety) used as check varieties which were obtained from Fedis Agricultural Research Center.

The experimental design was a randomized complete block design (RCBD) with three replications. Seeds of each genotype were sown in April 2023 on a seedbed size of 7.8m×2m with a total seed bed area of 15.6m2 (each genotype was sown on two rows of 2m long) [25]. Transplanting to the actual field was done when the seedlings attained 20 to 25 cm height and or 40 days after sowing. Each seedling genotype was planted on a plot size of 1.5 m x 2m (with a total plot size of 3 m2) and the distance between plots and between replication was 0.7m and 1m respectively. Each plot within a replication consists of four rows and each row contains fivplants with a total of 20 plants per plot. The Seedlings were spaced 50 cm between plants and 70 cm between rows. The experimental plots will be fertilized with 200 kg/ha DAP as a side dressing during the transplanting operation in addition, 100 kg/ha UREA, half of it during the transplanting and half of it 15 days after transplanting will be applied [16].

III. EXPERIMENTAL PROCEDURE

A. Land Preparation

Larger clods were broken into small particles and finally attained into a desirable tilth to ensure proper growing conditions. Recommended doses of well-decomposed cow dung, manure, and chemical fertilizers were applied and mixed well with the soil of each plot. Proper irrigation and drainage channels were also prepared around the plots. Each unit plot was prepared keeping 5cm height from the drains. The bed soil will be made friable and the surface of the bed be leveled.

B. Planting

In April 2023, seeds of 19 landrace genotypes and 1 check, totaling 20 genotypes, were sown on a seed bed. The bed was initially covered with dry grass for 20 days, followed by the application of raised shade to shield the seedlings from intense sunlight until they were ready for transplanting. After 55 days of seeding, robust and healthy seedlings were carefully selected and transplanted into the well-prepared field. Each hole received one seedling, and after planting, the bases of the seedlings were covered with soil and firmly pressed by hand. Four days before planting capsicum seedlings, a mixture of well-decomposed cow dung, TSP, and other fertilizers was applied to the plots and thoroughly incorporated into the bed soil. During the final bed preparation, one-fourth of both Urea and MP fertilizers were applied. The remaining Urea and MP were top-dressed in three equal installments, 30, 45, and 60 days after planting.

C. Irrigation

During the initial phase of planting seed on the seed bed, irrigation was used. After that semi-irrigation was used based on the availability of rain.

D. Cultural practices

Mulching, weeding, cultivation, watering, and earthing-up were done at the appropriate time to facilitate root, to control disease infestation, and to control waterlogging. Integrated Weeding and hoeing were done to improve soil structure and reduce competition of weeds and earthing-up was done as required to prevent exposure of roots to direct sunlight.

Harvesting: Harvesting of fruits was started at 75 DAP and continued up to 25 DAP with an interval of 25 days. Harvesting was done usually by hand. Five plants from each row or plot left the plants growing at both ends of each row to avoid edge effects, were harvested to estimate fruit yield and other yield-related parameters.

IV. DATA COLLECTION

Quantitative (12) morphological data was collected according to the descriptor for Capsicum [22]. At harvest, 10 guarded plants were randomly taken from each plot to measure quantitative morphological character. Some of the characters were measured before harvest. The sampling was done in such a way that the border effects were completely avoided. For this purpose, the outer two lines and the end of the middle rows were excluded.

The following quantitative morphological data was collected:

- **Plant Height (PH):** Length in centimeters of the central axis of the stem, measured from the soil surface up to the tip of the stem, and the average was recorded. Recorded when in 50% of the plants the first fruit has begun to ripen.
- **Days to 50% Flowering (DFL):** Number of days from transplanting to when 50% of plants in a plot open the flower.
- **Days to 50% Fruiting (DF):** Number of days from transplanting until 50% of the plants bear mature fruits at the first and second bifurcation. Recorded on mature fruits.
- **Number of Flowers Per Axil (NFLA):** the number of flowers counted per axil recorded on fully open flower.
- **Days to First Harvest (DH):** Number of days from transplanting to first harvest.
- **Number of Fruits Per Plant (NFP):** Average number of chili fruits, counted at harvest on 10 sample plants of each plot.
- **Fruit Length (FL):** The average length of five chili fruits was measured in centimeters on 10 plants of each plot.
- **Fruit Width (FW):** Measured at the widest point. Average fruit width of 10 ripe fruits.
- **Fruit Weight (FWT):** Average fruit weight of 10 ripe fruits of the second harvest.
- **Number of Seeds Per Fruit (NSF):** Average of at least 10 fruits selected from 10 random plants.
- **1000-Seed Weight [g] (TSW):** The weight of 1000 seeds is in measured each plot.
- **Yield Per Plot [Kg] (FYPP):** The weights of total fruits harvested in each plot from all central row plants were recorded to estimate yield per plot.

A. Data Analysis

i. Descriptive Statistics

The mean value of each character understudy was summarized using Microsoft Excel and subjected to analysis of variance following the procedure described by [19] and [35].

B. Estimation of Genetic Parameter

i. Genotypic and Phenotypic Coefficient of Variation

The phenotypic and genotypic variability of each quantitative trait was estimated as phenotypic and genotypic variances and coefficients of variation. Phenotypic and genotypic components of variance were estimated by using the formula given by [12] and [7]. Genotypic and phenotypic coefficient of variation was computed according to [9] and [10]

Genotypic variance (σ^2g)
Where, σ^2g = genotypic variance
Mg= mean square of genotype
Me = mean square of error
r = number of replications
Phenotypic Variance ($\sigma 2p$) = $\sigma^2g + \sigma^2e$
Where, σ^2g = Genotypic variance
σ^2e = Environmental variance
σ^2p = phenotypic variance

[41] classified the PCV and GCV estimates as follows:

Low, <10%
Moderate, 10-20%
High, >20%

ii. Heritability

The broad sense heritability (H2) was estimated for all characters as the ratio of genotypic variance to the total or phenotypic variance as suggested by [20] and [27]

$H2 = (\sigma 2g/\sigma 2p) \times 100$

Where, H2 = heritability in a broad sense

σ2p = phenotypic variance

σ2g = Genotypic variance

According to [17] and [34] heritability estimates in cultivated plants can be placed in the following categories.

Low, <30%

Moderate, 30-60%

High, >60%

iii. Genetic Advance (GA) and Genetic Advance as a Percent of the Mean (GAM)

The genetic advance will be estimated according to [24] and [2]:

$GA = K * SDp * H2$

Where, GA = Genetic advance

SDp = Phenotypic standard deviation on a mean basis;

H2 = Heritability in the broad sense.

k = the standardized selection differential at 5% selection intensity (K = 2.063).

$GAM = [GA/PMC] \times 100$

Where GAM = Genetic advance as percent of mean

GA = Genetic advance

PMC = Populations mean character to be evaluated

The GA as a percent of the mean will be categorized as low, moderate and high as suggested by [24] as follows.

0 - 10% = Low

10 – 20 = Moderate

>20 = High

V. RESULT AND DISCUSSION

A. Range, Mean, CV (%), and Standard Deviation of 20 Genotypes

Table-II: Range, Mean, CV (%) and Standard Deviation of 20 Genotypes

Characters	Mean Sum of Square			CV
	Replication (r-1) = 2	Genotype (g-1) = 19	Error (r-1)(g-1) = 38	
Plant height	3.870965	90.317731**	18.273535	8.28
Days to flowering	0.772667	162.967579**	3.983895	2.92
Days to fruiting	25.443167	95.409158**	30.003342	5.75
Number of flowers per plant	0.686502	256.378658^{ns}	220.75880	25.21
Days to harvest	30.444435	87.358707^{ns}	52.892260	4.61
Fruit length	10.1051667	8.4525965**	3.6770965	26.62
Fruit width	16.219852	105.109612**	25.990246	30.04
Fruit weight	1.8435050	43.4944404^{ns}	27.084161	30.78
Number of fruit per plant	77.516667	175.483333**	56.499123	31.47
Number of seed per fruit	1163.26667	2854.51228**	380.61754	13.01
Thousand seed weight	8.92381500	5.19725754**	2.2551746	26.35
Yield per plot	2.37049833	0.12476307**	0.02261254	25.33

CV (%) = coefficient of variation, SD = standard deviation and SE = standard error PH: Plant height, DFL: Days to 50% flowering, DF: Days to 50% Fruiting, NFLA: Number of flower per axil, DH: Days to first harvest, FBP: Fruit bearing period, NFP: Number of fruits per plant, FL: Fruit length, FW: Fruit width, FWT: Fruit weight, NSF: Number of seed per Fruit, TSW: 1000-seed weight.

The mean performance of 20 hot pepper genotypes for 12 quantitative traits was detailed in Supplimentary material submitted along with these articles. Table II presents the mean, range, coefficient of variation (CV), and standard deviation values for these traits.

Notably, accession 20206 exhibited the tallest plant height (64.27), while accession 229694 displayed the shortest (42.4). Days to fifty percent flowering ranged from 55 (accession 28337) to 83.33 (accession 20207), with a mean of 68.72.

Likewise, fruit-related traits showcased considerable variation, with accession 229694 recording the shortest fruit length (4.5cm) and accession 229699 registering the longest (11.17cm). Fruit width ranged from 8.33cm to 31.4cm, while fruit weight ranged from 11.25g to 24.88g. Accession 229697 boasted the highest fruit number per plant (42.67), contrasting with M/fana (12.67), which had the lowest. Fruit yield per plot ranged from 0.26kg/plot (accession 229696) to 0.91kg/plot (accession 28337), with a mean of 0.5935 kg/plot.

Approximately 40% of the genotypes outperformed the population mean. The findings align with similar studies conducted by [3] and [37] reflecting wide-ranging means for various traits and affirming the potential for pepper improvement.

B. Analysis of Variance (ANOVA)

Analysis of variance (ANOVA) was conducted for fruit yield per plot and other yield-related traits, revealing highly significant ($P \leq 0.01$) mean squares for all traits except for days to harvest and fruit weight. The result of analysis of variance was presented in Table III.

The coefficient of variation was notably high for the number of fruit per plant (31.47) and lowest for days to fifty percent flowering (2.92), underscoring substantial variability among the accessions.

Table-III: Analysis of Variance for Different Characters in Hot Pepper Genotypes

Traits	PCV	GCV	h2(%)	GA	GAM (%)
Plant height	12.60	9.499	56.79	7.61	14.77
Days to flowering	10.98	10.59	93.01	14.48	21.08
Days to fruiting	7.56	4.91	42.08	6.24	6.57
Number of flower per plant	25.88	5.83	5.07	1.59	2.71
Days to harvest	5.08	2.14	17.83	2.95	1.87
Fruit length	31.84	17.50	30.22	1.43	19.86
Fruit width	42.64	30.26	50.36	7.51	44.30
Fruit weight	33.69	13.81	16.80	1.98	11.68

** Denotes significant at 1% level of probability ns: non-significant

C. Estimate of Genotypic and Phenotypic Coefficient of Variation

Table IV presents a comprehensive overview of variability concerning environmental, phenotypic, and genotypic factors, alongside heritability, genetic advancement, and coefficient variations. Across traits, a notable trend emerges: the phenotypic coefficient of variation (PCV) consistently outweighs the genotypic coefficient of variation (GCV), underscoring the profound influence of environmental factors. Particularly striking are the high PCV and GCV values for yield per plot, number of fruit per plant, and fruit width, indicating substantial potential for enhancement through selective breeding. This divergence between PCV and GCV values across traits highlights the intricate interplay between environmental dynamics and genetic variability. Moreover, moderate to high heritability estimates underscore the reliability of these findings.

Studies by [44] and [43] corroborate these observations, reinforcing the robustness of the reported trends.

The classification of PCV and GCV into three ranges by [42] underscores these findings, delineating low, moderate, and high categories [46]. Particularly noteworthy is the pronounced PCV observed for a range of traits, including fruit width, yield per plot, fruit weight, and thousand seed weight, among others [47]. This trend is echoed by moderate PCV values for plant height and days to flowering, while days to fruiting and days to harvest exhibit low PCV [48].

The high genotypic coefficient of variation for yield per plot, fruit width, and number of fruit per plant, juxtaposed with moderate GCV for other traits, further solidifies the potential for targeted breeding efforts.

Similarly, studies by [3] on hot pepper validate the findings regarding the number of fruits per plant and yield per plant, providing additional support for the observed trends.

The discernible differences between GCV and PCV underscore the considerable role of environmental factors in shaping trait expression. This discrepancy is particularly pronounced for traits such as fruit length, fruit weight, and thousand seed weight, indicative of the substantial environmental influence on these traits. In contrast, traits such as days to flowering and days to fruiting exhibit minimal variation between GCV and PCV, suggesting a lesser impact of environmental factors.

Overall, the ample genetic variability observed across traits holds promise for targeted selection processes, facilitating the enhancement of desired traits and the development of improved cultivars**.**

D. Estimate of Heritability (%)

Heritability refers to the proportion of phenotypic variance attributable to genotype, indicating the heritable genetic component transmitted to subsequent generations. Broad-sense heritability, encompassing genotypic variance relative to total variance within a non-segregating population, offers insights into the potential effectiveness of selecting hybrids for desired traits [6] and [21]. Traits with elevated broad-sense heritability suggest substantial genetic variances with minimal environmental influence, facilitating effective selection. Conversely, traits with low heritability pose challenges in selection due to the predominant impact of environmental factors [23]. Alongside heritability estimates, genetic coefficients of variability, as proposed by [10] provide valuable indications of the expected enhancement achievable through selection.

In this study, Broad-sense heritability (H2) ranged from 5.07 for the number of flowers per plant to 93.01 for days to flowering as shown in Table IV. Categorization of heritability percentages as low, moderate, and high revealed high heritability estimates for days to flowering, number of seeds per fruit, and yield per plot. In contrast [28], and [26] reported varying heritability levels for traits such as the number of branches, number of fruits per plant, fruit length, and primary branch per plant [40] and [36]. High heritability for different traits suggests a significant proportion of phenotypic variance attributed to genotypic variance, supporting reliable selection based on phenotypic expression [29].

Conversely, plant height, days to fruiting, fruit length, fruit width, number of fruit per plant, and thousand seed weight exhibited moderate heritability estimates. Additionally, low broad-sense heritability estimates were noted for traits such as the number of flowers per plant, days to harvest, and fruit weight, consistent with findings by Vijaya et al. [44] and [37].

E. Estimate of Genetic Advance and Genetic Advance % of the Mean

Genetic advance is the measure of improvement that can be achieved by practicing selection in a population [13]. Therefore, genetic advance is a useful indicator of progress that can be expected as a result of exercising selection on a population [42]. The genetic advances as a percent of the mean (GAM) at 5% selection intensity are presented in Table IV. It ranged from 1.87 for days to harvest to 49.94 for yield per plot.

[24] categorized The GA as a percent of the mean as follows Low= 0-10 %, Moderate= 10-20%, and High ≥20. The result of the present study indicated that the highest genetic advance as a percent of mean (GAM) at 5% selection intensity was recorded for yield per plot followed by fruit width, number of fruit per plant, days to flowering, and number of seeds per fruit. This study was supported by the result of [40] and [4] for dry yield per plant.

The low genetic advance was recorded for days to harvest, number of flowers per plant, and days to fruiting. The result of [3] is similar to these findings for days to fruiting. This is due to low PCV and GCV values of variability. This shows the importance of genetic variability for improvement through selection [44].

Table-IV: Estimate of Genetic Parameters

Traits	PCV	GCV	h2(%)	GA	GAM (%)
Plant height	12.60	9.499	56.79	7.61	14.77
Days to flowering	10.98	10.59	93.01	14.48	21.08
Days to fruiting	7.56	4.91	42.08	6.24	6.57
Number of flower per plant	25.88	5.83	5.07	1.59	2.71
Days to harvest	5.08	2.14	17.83	2.95	1.87
Fruit length	31.84	17.50	30.22	1.43	19.86
Fruit width	42.64	30.26	50.36	7.51	44.30
Fruit weight	33.69	13.81	16.80	1.98	11.68
Number of fruit per plant	41.48	26.64	41.24	8.34	35.30
Number of seed per fruit	23.15	19.15	68.42	49.00	32.68
Thousand seed weight	31.53	17.37	30.34	1.12	19.73
Yield per plot	39.87	31.07	60.71	0.29	49.94

Heritability (H%), genetic advance (GA), genetic advance as percent mean

(GAM), phenotypic and genotypic coefficients of variation. Underlined and bolded are the maximum and minimum value respectively.

Heritable variation can be determined with greater accuracy when heritability is studied along with genetic advance. Since the estimates of heritability does not indicate the amount of progress expected from the selection, they are most meaningful when accompanied by estimates of genetic advance. Genetic advance is affected by factors like the intensity of selection, heritability, and phenotypic variance. High genetic advance coupled with high heritability is an indication of more additive gene action [13]. In the present study, high genetic advance coupled with high heritability was obtained for yield per plot, number of seeds per fruit, number of fruit per plant, fruit width, and days to flowering. In line with the results of these studies was [23] for the number of fruits per plant [44], the number of fruit per plant and yield per plot. These offer opportunities for selection, and Indicate the predominance of additive gene action and hence direct phenotypic selection is useful with respect to these traits.

VI. CONCLUSIONS

The current study revealed that yield per plot, number of fruits per plant, and fruit width exhibited high values of phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), and high heritability, along with significant genetic advance as a percentage of the mean. These findings suggest the predominance of additive gene action and a lesser influence of environmental factors on the expression of these traits, indicating the potential for improvement through selection. Furthermore, this implies the feasibility of enhancing these traits through selective breeding.

In conclusion, accession 28337 is recommended for yield per plot, accession 229697 for number of fruits per plant, and accession 229695 for fruit width based on the study's results. Additionally, the following suggestions and recommendations are proposed:

A. The study observed high phenotypic and genotypic coefficients of variation, as well as significant genetic advance coupled with high heritability for yield per plot, number of fruits per plant, and fruit width, indicating the potential for improvement through selection. Emphasis should be placed on selecting genotypes with a higher number of fruits per plant, as this trait showed a significant positive correlation with yield per plot, suggesting its usefulness in selecting productive genotypes.

B. While morphological characterization was conducted in this study, it is recommended to consider molecular analysis for similar accessions to complement the findings. This integration of morphological and molecular studies could provide a comprehensive understanding of genetic variability.

C. The study was conducted with 19 accessions and 1 check variety. To broaden the scope of research, it is advised to include more accessions and varieties from diverse environments for further investigation. This would enhance the robustness and applicability of the study's findings.

ACKNOWLEDGEMENT

The authors would like to express gratitude to the administrators of the Raare Research Station of Harmaya University and field data collectors for their cooperation.

DECLARATION STATEMENT

I must verify the accuracy of the following information as the article's author.

- **Conflicts of Interest/Competing Interests:** Based on my understanding, this article has no conflicts of interest.
- **Funding Support:** This article has not been sponsored or funded by any organization or agency. The independence of this research is a crucial factor in affirming its impartiality, as it has been conducted without any external sway.
- **Ethical Approval and Consent to Participate:** The data provided in this article is exempt from the requirement for ethical approval or participant consent.
- **Data Access Statement and Material Availability:** The adequate resources of this article are publicly accessible.
- **Authors Contributions:** The authorship of this article is contributed solely.

REFERENCES

1. Alebachew Molla Nibret. Genetic Diversity of Hot Pepper (Capsicum annuum) from Selected Areas of Ethiopia Using Inter Simple Sequence Repeats (ISSR) Marker. A Thesis Submitted to Applied Biology Program in Partial Fulfillment of the Requirement of the degree of Master of Science in Biology (Biotechnology) School of Applied Natural Science Office of Graduate Studies Adama Science and Technology University. 2018. https://www.jpmb-gabit.ir/article_35163_04971ac6a9c13cf839dd79c3651c3057.pdf
2. Allard RW. Principles of Plant Breeding. John Willey and Sons; 1960, New York. p. 485. https://www.wiley.com/en-us/Principles+of+Plant+Breeding%2C+2nd+Edition-p-9780471023098
3. Bekele B, Petros P, Oljira T, Andargie M. Genotypes performance and genetic variability studies in Hot Pepper (Capsicum annum L.). Trends in current biology; 2023. DOI: https://doi.org/10.14719/tcb.2863
4. Belay F, Abate B, and Tsehaye Y. Genetic diversity studies for morphological traits of hot pepper (Capsicum annuum L.) genotypes in Central Zone of Tigray Region, Northern Ethiopia. Academic Journals Vol. 14(33), pp. 1674-1684, October, 2019. ISSN: 1991-637X. DOI: https://doi.org/10.5897/AJAR2019.14256
5. Belay Fasikaw and Tsehaye Yemane. Variability, Association and Path Coefficient Analysis of Green Pod Yield and Yield Components of Hot pepper (Capsicum annuum L.) Landraces at Mereb Lehke, Northern Ethiopia. Vol. 12(1), pp. 58-69, January-March 2020 Article Number: 2C6A83763304 ISSN 2006-9758. DOI: https://doi.org/10.5897/JPBCS2019.0840
6. Bhagyalakshmi, P. V., Shankar, C. R., Subbramanyam, D. and Babu, V. G. Heterosis and combining ability studies in chillies. Indian Journal of Genetics and Plant Breeding; 1990, 51 (4): 420-423. https://www.isgpb.org/journal/index.php/IJGPB/article/view/3013
7. Birhanu Habtie & Tiegist Dejene. Multivariate Analysis and Traits Association in Hot Pepper (Capsicum annuum) Landraces of Ethiopia. International Journal of Research Studies in Agricultural Sciences (IJRSAS), 2020; 6(10), pp. 42-51, DOI: https://doi.org/10.20431/2454-6224.0610005
8. Birhanu H, Tiegist D, Yigzaw D. Morphological Characterization of Hot Pepper (Capsicum annuum.L) Land Races of Ethiopia for Qualitative Characters", International Journal of Research Studies in Science, Engineering and Technology, vol. 4, no. 9, pp. 4-9 2017. https://ijrsset.org/pdfs/v4-i9/2.pdf
9. Burton, G.W. Quantitative inheritance in grasses. Proceedings of 6th International Grassland Congress;

1952. 1: 227-283. https://www.sciepub.com/reference/171425

10. Burton GW, De Vane EH. Estimating heritability in tall fescue (Fistvea arundiancea) from the replicated clonal material. Agriculture Journal; 1953. 1953;45: 284-291. DOI: https://doi.org/10.2134/agronj1953.00021962004500100005x
11. Cabral N.S.S., Medeiros A.M., Neves L.G., Sudré C.P., Pimenta S., Coelho V.J., Serafim M.E. and Rodrigues R. Genotype x environment interaction on experimental hybrids of chili pepper. Genetics and Molecular Research 16 (2): 2017 gmr16029551. DOI: http://dx.doi.org/10.4238/gmr16029551
12. Cochran, W. G., and Cox, G. M. Experimental Designs. pp. 127-131. cooperation, Ministry of agriculture, Government of West Bengal. (online) https://www.scirp.org/reference/referencespapers?referenceid=2430179
13. Comstock, R. E., and H. F. Robinson. The components of genetic variance in populations of biparental progenies and their use in estimating the average degree of dominance. Biometrics (1952): 254-266. DOI: https://doi.org/10.2307/3001412
14. CPI (Chile Pepper Institute) publication. New Mexico State University. 2007. https://cpi.nmsu.edu/
15. CSA. Area and Production of Crops (Private Peasant Holding, Meher Season). Addis Ababa. pp; 2006. 14-63. https://catalog.ihsn.org/index.php/catalog/7377/related-materials
16. EARO (Ethiopian Agricultural research Organization). Released crop varieties and their recommended cultural practices. Progress report. Addis Ababa, Ethiopia. https://www.scirp.org/reference/referencespapers?referenceid=746429
17. Falconer DS, Mackay TFC. An Introduction to quantitative genetics. Ed, 4.Printice; 1996. DOI: https://doi.org/10.1093/genetics/167.4.1529
18. Fekadu Moges. and Dandena, G. Status of Vegetable Crops in Ethiopia.Ugandan Journal of Agriculture; 2006. 12(2): 26-30. https://www.researchgate.net/publication/238077742
19. Gomez, K. A and Gomez, A. A. Statistical procedure for an agricultural research, 2nd edition. John Wily and Sons, USA. Pp: 680. https://www.wiley.com/en-us/Statistical+Procedures+for+Agricultural+Research%2C+2nd+Edition-p-9780471870920
20. Hanson, C. H., Robinson, H. F. and Comstock, R. E. Biometrical studies of yield in segregating population of Korean lespedse. Agronomy Journal; 1956. 48, 267-282. DOI: https://doi.org/10.2134/agronj1956.00021962004800060008x
21. Ibrahim, M., Ganiger, V.M., and Yenjerappa, S.T. Genetic variability, heritability, genetic advance and correlation studies in chilli. Karnataka J Agril Sci; 2001, 14:784-787. https://ijrpr.com/uploads/V3ISSUE6/IJRPR5396.pdf
22. IPGRI. Descriptors for Capsicum (Capsicum sp.). Rome, Italy. https://cgspace.cgiar.org/items/ef0f3bcd-4878-4025-90ed-098a4c1b2918
23. Janaki, M., Naram, L., Naidu, C., Ramana, V., and Rao, M. P. Assessment of Genetic Variability, Heritability and Genetic Advance for Quantitative Traits in Chilli (Capsicum annuum L.). International Quarterly Journal of Life Science; 2015, 10(2): 729-733. https://www.researchgate.net/publication/329337346
24. Johnson, H.W., Robinson, H.F. and Comstock, R.E. Genotypic and phenotypic correlations in soybeans and their implication in selection. Agronomy Journal; 1955. 47: 477-483. DOI: https://doi.org/10.2134/agronj1955.00021962004700100008x
25. Kahsay Y. Evaluation of Hot Pepper Varieties (capsicum species) for Growth, Dry pod Yield and Quality at M/Lehke District, Tigray, Ethiopia. International Journal of Engineering Development and Research. © 2017 IJEDR | Volume 5, Issue 3 | ISSN: 2321-9939. https://rjwave.org/ijedr/viewpaperforall.php?paper=IJEDR1703022
26. Khurana, D. S., Singh, P. and Hundal, J. S. Studies on genetic diversity for growth, yield and quality traits in chilli (Capsicum annum L.). Indian Journal of Horticulture; 2003, 60 (3): 277-282. https://www.ijcmas.com/9-12-2020/Chandan%20Kumar%20Mondal,%20et%20al.pdf
27. Lush, J.L. Inter-size correlation regression of offspring on dairy as a method of estimating heritability of characters. In: Proceedings American Society of Animal Production; 1940. 32: 293-301. https://www.sciepub.com/reference/127208
28. Manju, P. R. and Sreelathakumary, I. Genetic Variability, Heritability and Genetic Advance in Hot Chilli (Capsicum Chinense Jacq.). Journal of Tropical Agriculture; 2002, 40: 4-6. https://jtropag.kau.in/index.php/ojs2/article/view/65
29. Maurya, A. K., Kushwaha, M. L., and Singh, B. K. Genetic Studies in Chilli (Capsicum annuum L.). International Journal of Science & Technology; 2015, 2321 – 919. https://www.researchgate.net/publication/318431594
30. Mishra B.B., H.G. Kidan, K. Kibret, M. Assen and B. Eshetu. Soil and land resource inventory at Alemaya University research farm with reference to land evaluation for sustainable agricultural management and production: Synthesis of working papers, Soil Science Bulletin. Alemaya University, Ethiopia. https://www.scirp.org/reference/referencespapers?referenceid=3587017
31. Pandit, M. K and Adhikary, S. Variability and Heritability Estimates in Some Reproductive Characters and Yield in Chilli (Capsicum annuum L.). International Journal of Plant and Soil Science; 2014 3 (7): 845-853. DOI: https://doi.org/10.9734/IJPSS/2014/7236
32. Purseglove, J.W. (1968). TropicaL crops, Dichotyledons. John Wiley and Sons, New York. Vol. 2: 524-530. https://www.scirp.org/reference/referencespapers?referenceid=1815301
33. Rehima Mussema (2006). Analysis of Red pepper Marketing. The case of Alaba and Siltie in SNNPRS of Ethiopia. A Thesis submitted to Department of Agricultural Economics School of Graduate studies Haramony University. P: 1-8. https://cgspace.cgiar.org/items/1b6af7f9-96bf-424e-ab76-c8bf172949ad
34. Robinson, H.F. Quantitative genetics in relation to breeding of the centennial of mendalism. Indian Journal of Genetics; 1966. 26, 171-187. https://eurekamag.com/research/014/630/014630275.php
35. SAS Institute. SAS software. SAS Institute INC., Cary. NC. USA. https://www.sas.com/en_in/home.html
36. Sreelathakumary, I. and Rajamony, L. Variability, heritability and genetic advance in chilli (Capsicum annuum L.). Journal of Tropical Agriculture; 2015, 42(1-2): 35-37. https://jtropag.kau.in/index.php/ojs2/article/view/112
37. Shimeles Aklilu, Bekele Abebie, Dagne Wogari and Adeferis TW. Genetic Variability and Association of Characters in Ethiopian Hot Pepper (Capsicum Annum L.) Landraces. Journal of Agricultural Sciences. 61(1): 19-36. DOI: https://doi.org/10.2298/JAS1601019A
38. Shumbulo A, Nigussie M, Alamerew S. Correlation and Path Coefficient Analysis of Hot Pepper (Capsicum annuum L.) Genotypes for Yield and its Components in Ethiopia. Adv Crop Sci Tech; 2017, 5: 277. DOI: https://doi.org/10.4172/2329-8863.1000277
39. Simret Burga. Influence of inorganic nitrogen and potassium fertilizers on seed tuber yield and size distribution of potato (Solanum tuberosum L.). An. M. Sc Thesis Presented to the School of Graduate Studies of Haramaya University, Ethiopia. 65p. https://www.ajol.info/index.php/eajsci/article/view/125431
40. Singh, Y., Sharma, M. and Sharma, A. Genetic Variation, Association of Characters, and their Direct and Indirect Contributions for Improvement in Chilli Peppers, International Journal of Vegetable Science; 2009, 15(4): 340-368. DOI: https://doi.org/10.1080/19315260903004158
41. Sivasubramaniah, S and Menon, M. Heterosis and inbreeding depression in rice. Madras Agricultural Journal; 1973. 60: 11-39. https://www.sciepub.com/reference/127212
42. Sood, S., Sood, R., Sagar, V. & Sharma, K. C. Genetic Variation and Association Analysis for Fruit Yield, Agronomic and Quality Characters in Bell Pepper. International. Journal of Vegetable Science; 2009, 15 (3): 272-284. DOI: https://doi.org/10.1080/19315260902875822
43. Verma, S. K., Singh, R. K. and Arya, R. R. Genetic variability and correlation studies in chillies. Progressive Horticulture; 2004, 36(1): 113-117. https://www.plantarchives.org/20-1/686-690%20(5697).pdf
44. Vijaya, H.M., Gowda, A.P. M. and Nehru, S. D. Genetic variability, correlation coefficient and path analysis in chilli (Capsicum annuum l.) genotypes. Environmental Life Science; 2014, 7 (3): 175- 178. https://aaj.net.in/wp-content/uploads/2024/06/2008_article_552-7.pdf
45. Zhang, Z., Lu, A. and D'arcy, W. G. Capsicum annuum Linnaeus, Special Plant, Flora of China,17, 313–313. 200. DOI: https://doi.org/10.1155/2014/540868
46. Kindie, B., & Abdala, T. (2024). Review of Plant Genetic Resources, Utilization and Conservation of Genetic Resources. In International Journal of Basic Sciences and Applied Computing (Vol. 10, Issue 9, pp. 6–11). DOI: https://doi.org/10.35940/ijbsac.i0514.10090524
47. Muthulakshmi, P. (2019). Genetic Algorithm – A Sensible Evolutionary Optimization Technique. In International Journal of Innovative Technology and Exploring Engineering (Vol. 8,

Issue 9, pp. 2805–2809). DOI: https://doi.org/10.35940/ijitee.i8651.078919

48. blessie, Dr. E. C., & Gnanapriya, S. (2019). Robustious Feature Selection Based Genetic Algorithm (RFS-GA) For Cross Domain Opinion Mining. In International Journal of Recent Technology and Engineering (IJRTE) (Vol. 8, Issue 2, pp. 6267–6279). DOI: https://doi.org/10.35940/ijrte.b3199.078219

AUTHOR'S PROFILE

Abdurazak Sufiyan, (MSc.) is a Geneticist and Researcher at Ethiopia Biodiversity Institute, Harar Biodiversity Center. He obtained his first degree in Applied Biology (BSc.) from Addis Ababa University in 2017 and second Degree in Genetics (MSc.) from Haramaya University in 2023. He has six and half years experience and working on conservation of biodiversity, Genetic resources and diversity conservation.