TRENDS IN CURRENT BIOLOGY
ISSN 2584-2080 (online)
Vol 1(1): 01–06
https://doi.org/10.14719/tcb.2863

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RESEARCH ARTICLE

Genotypes performance and genetic variability studies in Hot Pepper (*Capsicum annum* L.)

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ARTICLE HISTORY

Received: 11 August 2023
Accepted: 25 September 2023

Available online
Version 1.0 : 01 October 2023
Version 2.0 : 22 February 2024

Additional information

Peer review: Publisher thanks Sectional Editor and the other anonymous reviewers for their contribution to the peer review of this work.

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CITE THIS ARTICLE

Bekele B, Petros Y, Oljira T, Andargie M. Genotypes performance and genetic variability studies in Hot Pepper (*Capsicum annum* L.). Trends in Current Biology. 2023; 1(1): 01-06. https://doi.org/10.14719/tcb.2863

Abstract

Pepper (*Capsicum* sp.) is one of the most widely used food worldwide. To assess the magnitude and extent of genetic variability among some chili accessions and varieties, and their contributions to yield, a field experiment was conducted using 30 genotypes during the off-season period from November 2016 to May 2017 under irrigation. The experiment was conducted using an RCBD design with three replicates. Analysis of variance (ANOVA) showed highly significant differences for all traits tested, except for fruit girth, pedicel length, and plant height. Primary branch per plant, dry fruit yield per plot, fruit length, stem width, and number of fruits per plant all had high GCV (genotype coefficient of variation) and PCV (phenotypic coefficient variation) values among the yield components, along with high heritability and genetic advance as a percentage of the mean. For all traits, the phenotypic coefficient of variation was higher than the genotypic coefficient of variation, indicating an environmental influence on these traits. High heritability, along with high genetic advance as a percentage of mean, was observed for primary branch per plant, stem width, fruit length, number of fruits per plant, and dry fruit yield per plot, implying the potential for crop improvement in chilli through selection.

Keywords

Capsicum annuum, genetic advance, heritability

Introduction

Pepper (*Capsicum* sp.) is one of the most widely used food worldwide. It's center of origin was Mexico and Central America (1). Moreover, it was considered the first spice to be used by human beings (2). The genus Capsicum comprises approximately 20 species. The cultivated species of capsicum all had 2n=24 chromosomes. Within *C. annuum*, a tremendous range in the size, shape, and mature color of fruits has been selected to form the basis for the types used in commerce throughout the world. There are numerous cultivated varieties of Capsicum spp. that are adapted to various agroclimatic conditions (3). Diverse hot pepper genotypes have been widely grown in the tropics and typical tropical climates of Ethiopia over centuries. Although hot pepper has been cultivated for centuries in a typical tropical climate in Ethiopia, the yield has remained very low owing to limited improvement work on the crop (4). Data on the level of genetic diversity of a germplasm collection increases the efficiency of efforts to improve a species (5). Hence, this study was carried out assess the magnitude and extent of the genetic variability.

Materials and Methods

2.1. Study Area Description

A field experiment was conducted at Dire Dawa, Ethiopia, located at $9^0 6'$N latitude and $41^0\ 8'$ E longitude, at an altitude of 1197 m above sea level. The area receives mean annual rainfall of 520 mm. It experiences 14.5-21.6 and 28.1-34.6 ˚C mean minimum and maximum temperature ranges, respectively (6). The soil property of the experimental site is a sandy loam (7) with an average pH of 8.12 and organic matter, total nitrogen, and available phosphorus contents of 1.5%, 0.15% and 15.6 mg/kg, respectively, in the 0–30 cm soil depth(8). The map of the study area is given in fig.1. below

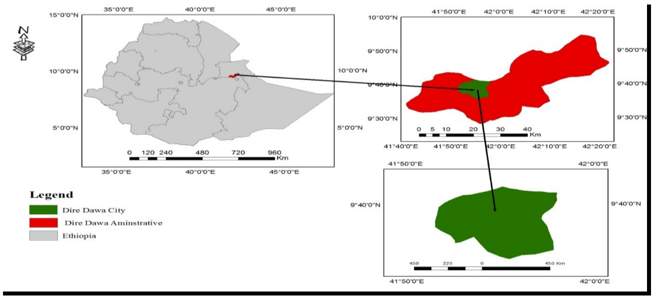

Figure 1. Location of the Study Area

2.2. Experimental Materials

In this study, four chili varieties and twenty-Six chili accessions were evaluated during the off-season period from November 2016 to May 2017.

2.3. Treatment and Experimental Design

The trial was laid out as a randomized complete block design (RCBD) with three replications. Each plot size was 1.5 m x 2.8 m (with a total plot size of 4.20 m^2) and the distance between plots was 1m. Each plot within a replication consisted of four rows, and each row contained five plants, with a total of 20 plants per plot. Transplanting to the actual field was performed when the seedlings attained a height of 20–25 cm or at 40 days after sowing. Seedlings were spaced 30 cm apart between plants and 70 cm between rows. The experimental plots were fertilized with 200 kg/ha DAP as a side dressing during the transplanting operation in addition to 100 kg/ha UREA, half of it during the transplanting, and half 15 days after transplanting (9).

2.4. Data Collection

Data were collected as per Descriptors for Capsicum of (10). Ten plants were collected per plot, which means that the two middle rows were collected for data collection.

1. Days to 50% flowering (DF): The number of days from transplanting to when 50% of the plants in a plot open the flower.

2. Days to maturity (DM): The number of days from transplanting to when the plants in a plot change the color of their fruit from green to red and are ready for harvest.

3. Plant height (PH): The length in centimeters of the central axis of the stem was measured from the soil surface up to the tip of the stem, and the average was recorded.

4. Internode Length (IL): Length of each Internode on the main stem was measured in centimeters and added together, and then divided by the number of internodes on the sample plant to obtain the average length of internodes for each plot.

5. Number of fruits per plant (NFP): Average number of chili fruits, counted at harvest on 10 sample plants of each plot.

6. Fruit length (FL): Average length of five chili fruits was measured in centimeter on 10 plants of each plot.

7. Fruit girth (FG): The average fruit girth of five chili fruits was measured in centimeters on 10 plants in each plot. This was determined by wounding a thread around the fruit circumference at the widest point and then placing it on a ruler to obtain the readings.

8. Pedicel length (PL): The average pedicel length of five chili fruits was measured in centimeter on ten plants in each plot. This was performed by placing the ruler at the point of pedicel attachment to the fruit and reading at the tip of the pedicel.

9. Dry Fruit yield per plot (DFY): Weights of total dry fruits harvested from each successive harvest (three rounds) were recorded and summed to estimate yield per plot in kilograms.

10. Stem width (SW): Average stem width of ten plants was measured in centimeter at the widest point of the stem for each plot.

11. Number of primary branches per plant (PB): number of primary branches from ten plants was taken and averaged over the total number of plants from which data were collected.

12. Days to first fruit set (FS): Number of days from transplanting to when the first fruit was set.

2.5. Statistical Data Analysis

2.5.1. Analysis of variance

The mean value of each character under study was summarized and subjected to analysis of variance following the procedure described by (11) and using SAS Software version 9.1.

2.5.2. Estimation of genetic parameters

Genotypic and phenotypic coefficients of variation were used to measure variability in a given population (12).

Genotypic and phenotypic variances were computed based on the expected mean sum of squares from the ANOVA (Analysis of variance) table as follows:

$$\text{Genotypic variance } (\sigma^2 g) = \frac{Msg\text{-}Mse}{r}$$

$$\text{Phenotypic variance } (\sigma^2 p) = \sigma^2 g + \sigma^2 e$$

$$\text{Environmental variance } (\sigma^2 e) = \text{Error mean square}$$

Where, Msg = Mean sum of squares due to genotypes
Mse = Mean sum of squares due to error
r = Number of replications

The phenotypic and genotypic coefficients of variation were determined as described by (12).

Phenotypic coefficient of variance (PCV)

$$\text{PCV (\%)} = \frac{\sqrt{(\text{phenotypic variance of genotypes})}}{\text{General mean of character}} \times 100$$

Genotypic coefficient of variance (GCV)

$$\text{GCV (\%)} = \frac{\sqrt{(\text{Genotypic variance of genotypes})}}{\text{General mean of characters}} \times 100$$

The genetic components GCV and PCV were categorized as suggested by (13) as follows:0–10%, low; 10–20%, moderate; and high, >20%.

The broad-sense heritability (h^2bs) was estimated by following the procedure suggested by (14), as indicated below.

$$\text{Heritability} = \frac{Vg}{Vp} \times 100$$

where Vp is the phenotypic variance, and Vg is the genotypic variance of the respective accessions.

Heritability percentages were categorized as demonstrated by (15) as follows: 0–30%, low; 30–60%, moderate; and high, > 60%.

The expected genetic advancement resulting from the selection of 5% superior individuals was calculated according to the formula described by (13).

$$\text{GA} = \text{H} \times \sigma p \times k$$

where H is the broad-sense heritability, σp is the phenotypic standard deviation, and k is 2.06 (selection differential at a 5% selection index).

Genetic advance as percent mean (GAM) was calculated to compare the extent of predicted advances of different traits under selection using the formula:

$$\text{GAM (\%)} = \frac{\text{Genetic advance}}{\text{General mean of the character}} \times 100$$

Genetic advance values were categorized as low (0–10%), moderate (10–20%), and high (>20%) broad-sense heritability

Results

3.1. Mean performance of Genotypes

The mean dry fruit yield per plot recorded in this study was 0.618 kg/plot. The lowest and highest dry fruit yields per plot were obtained for accession 229697 (0.279 kg/plot) and 9098 (0.966 kg/plot), respectively. The highest fruit number per plant was obtained for variety 'V.AVPP.0411' and the least for accession'9099' with a mean value of 48.26. The fruit length varied from 4 cm in V-Unknown-2, 9086, 9099, and 9082' to 11 cm in V.AVPP.0411.

The highest plant height at maturity was recorded for V. AVPP.0411, and the lowest plant height was obtained at 229697. The mean plant height recorded in this study was 49.9 cm. The present study indicated that the lowest number of primary branches per plant at maturity was obtained for 9099 and the highest for V. AVPP.0411. The mean population for this trait was 7.53. The average number of days to first fruiting was 61, while accession 9107 was early fruiting, and accession 9086 took the longest days to first fruiting. In general, the overall performance of the genotypes showed that approximately 43.3% of the genotypes yielded higher yields than the population mean (0.618 kg/plot).

Similar findings to those of the present study were reported by (16), (17), and (18), who reported a wide range of means for fruit number, plant height, yield per plant, number of primary branches per plant, days to 50 percent flowering, dry fruit yield per plant, fruit length, fruit width, and pedicel length. The range and mean values in this study generally indicated that there was enough variation among the tested accessions for most of the traits examined and their significant potential for pepper improvement.

Table 1. Minimum, maximum, mean values and SE of mean performance of genotypes for the 12 quantitative traits of the chili accessions and varieties

Traits	**Minimum**		**Maximum**		**Mean**	**SE**
	Score	**Accession**	**Score**	**Accession**		
DF	33	9099	45	9101	38.1	2.3
FS	50	9107	68	9086	61	2.47
PB	3	9099	14.5	V.AVPP.0411	7.53	0.849
SW	3.5	229697, 9099	9.3	9098, V.AVPP.0411	6.64	0.73
FG	3.6	230799	6.8	9107	5.39	0.685
DM	120.6	9104	156	V.AVPP.0411	136.4	6.78
FL	4	V-Unknown-2, 9086, 9099, 9082	11	V.AVPP.0411	7.17	0.65
PL	2.5	9098, 229697, 9097, 9094 9102, 238486, 9083	3.83	9104	2.92	0.31
PH	41	229697	62.16	V.AVPP.0411	49.9	6.26
NFP	33.3	9099	70	V.AVPP.0411	48.26	4.62
IL	2.7	V.AccNo.223654	8.1	V.Acc No.223631	5.17	0.74
DFY	0.279	229697	0.966	9098	0.618	0.09

where DF: Days to 50 percent flowering, FS: Days to first fruit set, PB: Primary branch per plant, SW: Stem width, FG: Fruit girth, DM: Days to maturity, FL: Fruit length, PL: pedicle length, PH: Plant height, NFP: number of fruits per plant, IL: Internode length, and DFY: Dry fruit yield per plot.

3.2. Analysis of variance (ANOVA)

Analysis of variance (ANOVA) was performed for dry fruit yield per plot and other yield-related traits, as outlined by (11). Table 2 presents the results. Analysis of variance revealed highly significant ($P \leq 0.01$) mean squares for all traits except for days to 50 percent flowering, which was significant at ($P<0.05$) and fruit girth, pedicel length, and plant height, which were not -significant. Highest coefficients of variation were observed for dryfruit yield per plot (25.5) and the least one is for days to first fruit setting (seven). The highly significant differences indicate the existence of large variability among the accessions.

3.3. Estimates of genotypic and phenotypic coefficient variation

A greater phenotypic coefficient of variation (PCV) than the genotypic coefficient of variation (GCV) was observed for all traits. Similar results on chili have been reported by (19) and (18). This indicated that the apparent variation was not only due to genotypes, but also due to the influence of the environment.

PCV and GCV values were categorized as low, moderate, and high values, as indicated by (20), as follows Low = 0-10%, Moderate = 10-20%, high > 20. A high phenotypic coefficient of variation was observed for the primary branches per plant, followed by fruit dry weight per plot, fruit length, stem width, number of fruits per plant, plant height, and fruit girth. On the other hand, relatively moderate values were observed for pedicel length followed by days to fifty percent flowering and days to maturity. A low phenotypic coefficient of variation was noted on the days to the first fruit set.

The genotypic coefficient of variation was highest for primary branches per plant, followed by fruit dry weight per plot, fruit length, stem width, number of fruits per plant, and internode length. On the other hand, a relatively lower genotypic coefficient of variation was observed for plant height, followed by days to maturity, days to 50 percent flowering, pedicel length, days to first fruit set, and stem width.

High phenotypic and genotypic coefficients of variation were obtained for the primary branch per plant, stem width, fruit length, number of fruits per plant, internode length, and fruit dry weight per plot. The high GCV and PCV values of these traits suggest the possibility of improving these traits through selection. Similar findings on chili were reported by (21) for yield per plant, fruit weight, fruit per plant, and fruit length (21) and (22) for dry fruit yield per plant.

The difference between PCV and the corresponding GCV values was relatively higher for fruit girth, plant height, pedicel length, and internode length, indicating a greater influence of the environment on the traits. However, this difference was moderate for fruit dry weight per plot, stem width, and days to 50 percent flowering, and comparatively low for number of fruits per plant, primary branch per plant, days to maturity, days to first fruit setting, and fruit length. This small difference indicates that the environment has a minimal influence on the expression of these traits. In addition, the presence of sufficient genetic variability for observed traits may facilitate the selection process (Demewez *et al.*, 2014). Therefore, selection based on the phenotypic performance of the traits would be effective to bring considerable improvement in improving these traits.

3.4. Estimates of heritability

Heritability is the portion of phenotypic variation that is transmitted from parent to progeny. The higher the heritable variation, the greater the possibility of fixing characters by selection. Hence, heritability studies are of foremost importance to determine whether the observed variation for a particular character is due to the genotype or environment (23). (12) suggested that genetic coefficients of variability, along with heritability estimates, would provide a reliable indication of the expected degree of improvement through selection. Broad sense heritability (h^2), a measure of the genotypic variance's cumulative contribution to the phenotypic variation ranged from 3.86 for fruit girth to 85.62 for primary branches per plant (Table 3). According to (15), the heritability percentage was divided into three categories: low (0–30%), moderate (30–60%), and High≥60%.

Accordingly, high heritability estimates were obtained for primary branches per plant, followed by fruit

Table 2. Mean squares from analysis of variance for the 12 quantitative characters of chili accessions and varieties.

Source of variation	Df	DF	FS	PB	SW	FG	DM	FL	PL	PH	NFP	IL	DFY
Rep	2	18.30	17.68	1.44	0.678	0.278	2.5	0.478	0.0058	128.1	27.9	1.05	0.0116
Accession	29	38.44*	49.83**	40.75**	12.25**	1.58	495.6**	18.58**	0.4065	171.5	513**	5.25**	0.190**
Error	58	16.44	18.33	2.16	1.59	1.41	138	1.27	0.2927	117.7	64	1.66	0.0248
CV (%)	_	10.5	7.0	19.5	19	22.0	8.6	15.7	18.5	21.8	16.6	24.9	25.5

where ** and * indicate significant differences at the 1% and 5% levels, respectively. df: degree of freedom DF: Days to fifty percent flowering, FS: Days to first fruit set, PB: Primary branch per plant, SW: Stem width, FG: Fruit girth, DM: Days to maturity, FL: Fruit length, PL: Pedicel length, PH: Plant height, NFP: number of fruit per plant, IL: Internode length, DFY: Dry fruit yield per plot, Rep: replication and CV (%): coefficient of variance.

length, the number of fruits per plant, and stem width. Similar findings on chili were reported by (21), (24), (25) and (21) for the number of fruits per plant and fruit length, and (25) for primary branches per plant. A reliable selection might be done for these traits based on phenotypic expression since high heritability for various traits suggests that a significant amount of phenotypic variance has been attributed to genotypic variance. (26).

On the other hand, relatively moderate estimates of heritability was found for days to maturity followed by internode length, days to first fruit set and days to fifty percent flowering. Such results for chili were reported by (19) for days to 50 percent flowering. In addition, low broad-sense heritability estimates were obtained for the fruit girth, pedicel length, and plant height. These findings show that a greater part of the phenotypic variation was attributable to genotypic variance, allowing for the reliable selection of most features based on phenotypic expression. In contrast to the current study, (21) reported low heritability for primary branches per plant.

3.5. Estimates of genetic advance

Genetic advancement is a measure of genetic gain under selection and expression as a percentage of the means (27). Hence, genetic advancement is a useful indicator of progress that can be expected as a result of exercising selection in a population (28). The genetic advances as a percentage of the mean (GAM) at 5% selection intensity are presented in Table 3. It ranged from 1.79 for fruit girth to 90.65 for primary branch per plant.

GAM of the mean was categorized as low, moderate, and high, as described by (13) as follows: Low= 0-10 %, Moderate= 10-20% and High≥20. At 5% selection intensity, the maximum genetic advancement as a percentage of mean (GAM) was recorded for primary branches per plant, followed by fruit dry weight per plot, fruit length, stem width, number of fruits per plant, and internode length. Similar findings to the present study on chili were reported by (25) for dry yield per plant, internode length (21) for fruit per plant and fruit length, and (18) for number of fruits per plant, fruit length, dry fruit yield per plant, and number of branches per plant.

Low genetic advances were observed for fruit girth, pedicel length, plant height, days to 50 percent flowering, and days to first fruit set. (3) reported similar results in chili for days to 50 percent flowering. This was brought on by the low PCV and GCV values of the variability. This demonstrates the significance of genetic variability for progress via selection (18).

The effectiveness of selection depends on the genetic advancement of the character selected, along with heritability (21). In the present study, high genetic advancement coupled with high heritability was obtained for primary branches per plant, fruit length, number of fruits per plant, stem width, and dry fruit weight per plot. Similar findings were obtained by (3) for the number of fruits per plant and fruit length, (23) for the number of primary branches per plant, number of fruits per plant, fruit length, (18) for the number of primary branches, number of fruits per plant, fruit length, and dry fruit yield per plant. These offer opportunities for selection and indicate the predominance of additive gene action; hence, direct phenotypic selection is useful with respect to these traits (23).

Conclusion

In conclusion, this study indicated that significant variability exists among C.annuum genotypes tested for agronomic traits. As a result, there are chances to choose the best genotypes of C.annuum to employ in improvement efforts. ANOVA showed presence of strongly significant variation among the testsed traits and further it is clearly seen that high range values was observed almost in all traits studied. High PCV along with GCV were obtained for branh per plant, yield per plot, and fruit length. Further high heritability were exhibited by branch per plant and fruit length. Hence, considering those trait for future improvement program is highly recommende.

Table 3. Estimates of Phenotypic (σ2p) and Genotypic variance (σ2g), Phenotypic coefficient of variation (PCV) and Genotypic Coefficient of variation (GCV), Broad sense heritability (H%), Expected genetic advances (GA) and Genetic advance as percent of mean (GAM)

Traits	(σ^2 p)	(σ^2g)	(σ^2e)	PCV%	GCV%	H%	GA	GAM%
DF	23.77	7.33	16.44	12.6	6.98	30.85	3.09	8.00
FS	28.83	10.50	18.33	8.8	5.30	36.42	4.03	6.60
PB	15.02	12.86	2.16	51.5	47.7	85.62	6.83	90.65
SW	5.14	3.55	1.59	34.2	28.3	69.09	3.23	48.65
FG	1.47	0.06	1.41	22.45	4.40	3.86	0.10	1.79
DM	257.2	119.2	138	11.76	7.99	46.35	15.3	11.23
FL	7.04	5.77	1.27	36.9	33.5	81.96	4.47	62.4
PL	0.33	0.04	0.29	19.6	6.70	11.47	0.14	4.65
PH	135.63	17.93	117.7	23.3	8.50	13.22	3.17	6.36
NFP	213.67	149.67	64	30.3	25.4	70.05	21.10	43.7
IL	2.86	1.20	1.66	32.7	21	41.89	1.46	28.2
DFY	0.08	0.06	0.02	45.8	37.2	68.95	0.40	65

where DF: Days to 50 percent flowering; FS: Days to first fruit set; PB: Primary branch per plant; SW: Stem width; FG: Fruit girth; DM: Days to maturity; FL: Fruit length; PL, pedicle length; PH: Plant height; NFP, number of fruits per plant; IL: Internode length; DFY: Dry fruit yield per plot.

Acknowledgements:

This study is part of the thesis done by Bantayehu Bekele at haramaya university in partial fulfillment for master of science in Genetics (http://ir.haramaya.edu.et/hru/bitstream/handle/123456789/969/Bantayehu%20Bekele.pdf?isAllowed=y&sequence=1).

Authors' contributions

Conceptualization: Bantayehu Bekele, Yohanes Petros.

Data curation: Bantayehu Bekele.

Formal analysis: Bantayehu Bekele,

Investigation: Bantayehu Bekele.

Methodology: Bantayehu Bekele, Yohanes Petros, Tamiru Oljira, Mebeasilassie Andargie.

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Disclosure of interest

There is no conflict of interest

Funding

No funding was received

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