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Genetic Variability and Heritability Study of Hot Pepper (*Capsicum Annuum* L.) Genotypes in Wolaita, Southern Ethiopia

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Abstract- Genetic variability, heritability and genetic advance study was conducted using 55 hot pepper genotypes with the objectives to identify the extent of genetic variability explained by genotypes and to assess the magnitude of heritability (broad sense) and expected genetic advance. The experiment was conducted during 2016-2018 at three locations in Wolaita, Southern Ethiopia using RCBD with three replications. The result illustrated the existence of sufficient genetic variability in growth, yield and quality characters. The fresh fruit yield ranged from 3151.43kg/ha to 43002.86kg/ha with a difference of 39851.43kg/ha. Similarly, the oleoresin content and dry weight depicted range of 1.44-10.20% and 489.83-7652.85kg/ha, respectively indicating ample variability for further improvement and selection of superior genotype. The PCV in percent ranged from 33.44 (for oleoresin) to 8.50 (branch number) and GCV ranged from 32.15 to 7.21 for same traits which is an indication for broad genetic base and these traits are under the control of additive gene effects and, hence, there is a good scope for further improvement. Heritability (in broad sense) ranged from 60.39 (fruit number) to 92.39 (oleoresin content).

Keywords: genetic advance, heritability, hot pepper, variability, variety.

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Keywords: genetic advance, heritability, hot pepper, variability, variety.

I. INTRODUCTION

Hot pepper (*Capsicum annuum* L.), in the family *Solonaceae* (2n = 24), is an important spice and vegetable crop[13]. According to[7] pepper production covers the lion share 74.63% of all the area under vegetables production and contributes 41.43 % yield to vegetable sector in Ethiopia. The crop has been produced for long periods of time in the country for coloring purposes, paprika and *capsicum* oleoresins for export market. It has wide indigenous applications in Ethiopian culture due its medicinal, nutritional and mainly for its pungency and color. Moreover, the crop has significant value in its household income generation and hence contributes for food security of rural community in Ethiopia[26].

The genotypic variation in the population is due to genetic differences among individuals for a particular character. On the other hand, phenotypic character is the observable difference present in individual due to the effects of both genotype and environment[9, 23]. We must recognize that the variability observed in some characters is caused primarily by difference in the genes carried by the different individuals and that the remaining variability in the character is due primarily to differences in the environment to which individuals have been exposed [2, 15].

The presence of wide range of variability in any crop provides a better chance of selecting the desirable types[23]. Detection of genetic variation and determination of genetic relationship between plant populations are important to develop efficient strategies for conservation and utilization of plant genetic resources. Improvement in any crop is proportional to the magnitude of its genetic variability present in germplasm[17]. For successful improvement program, plant breeders require basic information on crop variation, which are due to genotype, environment and genotype x environment interactions (g x e)[1, 12].

Genetic variation in a crop population can be caused by domestication, segregation, germpasm collection, plant introduction, hybridization (intervarietal, distant, somatic), mutation, polyploidy, somaclonal variation and genetic engineering[2]. According to[11, 15] variability existing in a given set of germplasm is the sum total of heredity effects of the concerned genes, environmental influence and their interactions. This warrants the need to partition the observed variability into heritable and non-heritable components. These genetic parameters are measured as range, genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability in broad sense and genetic advance as a percentage of mean[4, 23, 32].

The significance of heritability is that it generates information regarding the proportion of genotypic variance from the total phenotypic variance. Given a higher heritability for a given trait, it means selection becomes easier and simultaneously response to selection will be greater [17, 18]. Previous studies have

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been done to estimate variance components, heritability and genetic advance in various pepper characters[9].

Heritability accompanied with genetic advance gives more relevant and useful information than heritability alone in predicting the effect of character for selecting the best individual among generations[17, 18]. In addition,[6] suggested that genetic coefficients of variation together with heritability estimates would give the best picture of genetic advance to be expected from selection. Therefore, traits that exhibited a high genotypic coefficient of variation, heritability and genetic advance as percent of the mean would be useful as a base for selection[8, 9].

Ethiopia has long history of producing hot pepper varieties for traditional house hold consumption, local and international markets in varieties of processed products such as oleoresins. Some scholars believe Ethiopia to be one of center of diversity in hot pepper germplasm due to diversity of cultivars growing in diverse agroecological zones in the country. In Ethiopia in general and in southern regions in particular, the crop is becoming high value cash crop and its demand is increasing from time to time. But to exploit the existing potential and to contribute for the growing demand of local, national and international markets, the attention given and research efforts done so far in the area is very low as compared to other crops. Thus, to address the existing critical gap for crop improvement the current research was designed with the following objectives:

1. To identify the extent of genetic variability explained by hot pepper genotypes studied.
2. To assess the magnitude of character heritability (broad sense) and expected genetic advances for selection.

II. MATERIALS AND METHODS

a) *Description of the Study Areas*

The field experiment was conducted at three different locations namely, Areka, Humbo and Wolaita Sodo university horticulture research and demonstration site in Southern Ethiopia for two years from 2016 to 2018.

b) *Treatments, Experimental Design and Field management*

The field experiment was done using 55 hot pepper genotypes out of which 45 were F$_1$ hybrids and the rest 10 were parental materials. Out of 10 parents, six were introduced from AVRDC (Asia) and four were Ethiopian released varieties. The 10 parents were crossed in half diallel mating design and produced the 45 F$_1$ hybrids.

The experimental design used at each location was RCBD with three replications. The continuous plots were used during field planting to minimize heterogeneity in soil variability. Seedlings were transplanted using plant spacing of 70 cm x 30 cm between rows and plants, respectively. Each plot consisted of four row and ten plants per row that accommodated 40 plants in each plot. Thus, the plot area was 2.8m x 3.0m = 8.4 m^2. There was 1m distance between blocks and all other basic recommended horticultural practices were employed uniformly for all plots as per the recommendation of Melkasa Agricultural Research Center (MARC).

Table1: Basic information of Hot pepper genotypes used during the experiment

Sr. No.	Genotype	Origin	Code
1	Melkaawaze	Ethiopia	G1
2	Marakofana	Ethiopia	G$_2$
3	Melkashote	Ethiopia	G$_3$
4	Melkazala	Ethiopia	G$_4$
5	AVPP9813	Asian	G$_5$
6	AVPP0206	Asian	G$_6$
7	AVPP0514	Asian	G$_7$
8	AVPP0512	Asian	G$_8$
9	AVPP0105	Asian	G$_9$
10	AVPP59328	Asian	G$_{10}$
11-55	F$_1$-Hybrids	Cross/hybrids	G11- G55

c) *Data Collected*

Data were collected from representative randomly selected ten plants taken from central two rows of each plot for growth, yield and quality parameters.

Plant height [cm], Plant canopy width [cm], Stem diameter [cm], Branch number per plant, Number of fruits per plant, Fruit length [cm], Fruit width [cm], Fruit weight [g], Fruit wall thickness [mm], Number of seeds per fruit, Total Fruit yield [kg/ha], Total fruit dry weight [kg/ha], and Oleoresin content[w/w%].

d) *Statistical Analysis*

i. *Estimation of variability parameters*

The variance components were estimated from the mean square in the combined analysis of variance. Where:

ϭ^{2}e (Error variance component) = MSe

ϭ^{2}g$_e$ (Variance component of GXE interaction) = $\frac{MSge-MSe}{r}$

ϭ^{2}g (variance component of genotype) = $\frac{MSg-MSge}{re}$

Phenotypic variance of the means for genotypes over locations and replications, ϭ^{2}p, was estimated as:

$$\sigma^2_p = \sigma^2_g + \frac{\sigma^2_{ge}}{e} + \frac{\sigma^2_e}{re}$$

Where: ϭ^{2}p-phenotypic variance

ϭ^{2}g - genotypic variance

ϭ^{2}ge- variance due to genotype by environment interaction

ii. *Coefficient of variation*

Genotypic and phenotypic coefficients of variation were calculated as the ratio of their standard deviation to the mean of the character expressed in percentage [28].

1. Phenotypic coefficient of variation

$$PCV\% = \frac{\sigma P_i}{\overline{Xi}} \times 100$$

2. Genotypic coefficient of variation

$$GCV\% = \frac{\sigma G_i}{\overline{Xi}} \times 100$$

where,

σP_i, and σG_i were the phenotypic, genotypic and environmental standard deviations for i^{th} characters, respectively.

$\overline{Xi}$ = Mean of i^{th} character

iii. *Heritability and Expected genetic advance*

Heritability in broad sense (H) was calculated as the ratio of genotypic variance to the phenotypic variance[3]. The heritability estimates was calculated as follows:

$$H(h^2 b) = \frac{\sigma^2 g}{\sigma^2 p} \times 100$$

where,

$H(h^2_b)$ = Heritability in broad sense

$\sigma^2 g$ = Genotypic variance

$\sigma^2 p$ = Phenotypic variance

In a typical experiment where g accessions are evaluated at L environments, with r replications per locations *Heritability* on genotypic mean basis can be expressed as:

$$\frac{\sigma^2_g}{\sigma^2_g + \frac{\sigma^2_{gL}}{L} + \frac{\sigma^2}{rL}}$$

Where: $б^2$ = the experimental error variance

$б^2 g_L$ = the genotype by environment interaction variance

$б^2 g$ = the total genotypic variance [16].

iv. *Expected genetic advance*

Expected genetic advance was estimated as suggested by [3].

$$GA = K \times \sigma p \times H$$

Where,

K = Selection differential expressed in standard unit (2.06 at 5% selection intensity)

σp = Phenotypic standard deviation calculated as square root of phenotypic variance

H = Heritability in broad sense

GA = Expected genetic advance

Genetic advance expressed as percentage of mean (GAM) = $\frac{expected\ GA}{Grand\ mean} \times 100$

For categorizing the magnitude of different parameters, the following limits were used:

PCV, GCV and ECV <10% = Low; 10-20% = Moderate; >20% = High[27];

Genetic advance (GA) <15% = Low; 15-30% = Moderate; >30% = High

Heritability <60% = Low; 60%-80% = Moderate; > 80% = High[18].

III. RESULTS

a) *Variability Study*

Variability in means, ranges, genotypic variance (σ^2_g), phenotypic variance ($\sigma^2 p$), phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability in broad sense (h^2_b), genetic advance (GA) in absolute units and as percent of the mean (GAM) were employed to assess the variability existed on genotypes studied. The result illustrated significant ranges in variability in growth, yield and quality characters. The fresh fruit yield ranged from 3151.43kg/ha to 43002.86kg/ha with a difference of 39851.43kg/ha. Similarly, the oleoresin content and dry weight depicted range of 1.44-10.20% and 489.83-7652.85kg/ha, respectively which clearly indicates the existing variability in potential for breeding, further improvement and selection of superior genotype (Table 2).

The percentage values of PCV ranged from 33.44(for oleoresin) to 8.50(branch number) and GVC ranged from 32.15 to 7.21 for same traits. High PCV were recorded for traits oleoresin (33.44), fresh fruit yield (24.44), fruit number per plant (23.39) and dry weight (21.61) and that of high GCV were recorded for oleoresin (32.15) and fresh fruit yield (21.72) (Table 2).Moreover moderate PCV estimates were noticed by traits canopy width (11.01), stem diameter (11.30), fruit length (10.79), fruit diameter (11.88), skin thickness (10.81) and seed number per fruit (14.47) while moderate GCV values were recorded by fruit number (18.17), fruit diameter (10.85), seed number per fruit (12.62) and fruit dry weight (18.07) substantiating the variability in studied genotypes.

b) *Heritability and Genetic Advance*

Broad sense heritability (H_b%) for traits ranged from 60.39 for fruit number per plant to 92.39 for oleoresin content. Results indicated that characters showed heritability greater than 60% which explained their moderate to high heritability. According to the current investigation traits with high heritability in order of magnitude were oleoresin content (92.39), fruit diameter (83.48), fruit length (80.96) and fresh fruit yield (78.94) (Table 2).

Genetic advance as percent of the mean (GAM) that could be expected from selecting the top 5% of the genotypes, varied from 12.13 % for plant height to 63.33% for oleoresin content. Traits with high GAM values in the order of magnitude include oleoresin content (63.33), fresh fruit yield (39.80), dry fruit weight (31.18), fruit number per plant (29.13) and seed number per fruit (22.69) (Table 2).

Table 2: Variability and heritability of 12 traits studied for 55 hot pepper genotypes, 2016 to 2018

Traits	Mean	Min	Max	Range	σ^2_g	σ^2_P	GCV%	PCV%	H_{bs} (%)	GA	GAM
PH	54.38	17.33	115.20	97.87	15.53	23.57	7.25	8.93	65.87	6.60	12.13
CW	40.79	16.00	86.20	70.20	15.32	20.15	9.59	11.01	76.00	7.04	17.26
BN	5.46	2.00	10.10	8.10	0.15	0.22	7.21	8.50	71.87	0.69	12.61
SD	3.83	1.90	9.00	7.10	0.15	0.19	9.95	11.30	77.63	0.69	18.09
FN	40.61	6.75	174.00	167.25	54.47	90.19	18.17	23.39	60.39	11.83	29.13
FL	88.09	10.90	149.85	138.95	73.12	90.31	9.71	10.79	80.96	15.87	18.02
FD	13.66	8.45	32.21	23.75	2.20	2.63	10.85	11.88	83.48	2.79	20.46
TIC	1.43	0.48	3.27	2.79	0.02	0.02	9.17	10.81	72.03	0.23	16.06
SN	75.59	22.25	146.01	123.76	90.98	119.68	12.62	14.47	76.01	17.15	22.69
OL	5.53	1.44	10.20	8.76	3.16	3.42	32.15	33.44	92.39	3.50	63.33
YLD	11087.69	3151.43	43002.86	39851.43	5797002.14	7343179.28	21.72	24.44	78.94	4413.05	39.80
DW	2275.38	489.83	8142.68	7652.85	169111.81	241754.34	18.07	21.61	69.95	709.54	31.18

PH=Plant height; CW= Canopy width; BN=Branch number; SD=Stem diameter; FN= Fruir number; FL= Fruit length; FD= Fruit diameter; TIC= Pericarp thickness; SN= Seed number; OL= Oleoresin content; YLD=fresh fruit yield; DW= Dry weight.

IV. DISCUSSION

The current investigation confirmed the existence of sufficient genetic variability for many of the horticultural traits studied on 10 parents and 45 F_1 hybrids of hot pepper genotypes. In line with current findings, earlier authors Krishna *et al*[19]; Vani *et al*[31]; Ukkund *et al.*[30]; Sharma *et al.*[25]; Munshi *et al.*[22] noticed almost same findings.

In the table 2, result revealed that the greater proportion of phenotypic variance was explained by genotypic variance and thereby contributed for high heritability of character confirms the greater contribution of genetic variability for phenotypic variability that further gives opportunity for selection and improvement. The phenotypic coefficient of variation (PCV) was higher than the genotypic coefficient of variation (GCV) for all the characters and the difference between PCV and GCV was narrow indicating the little influence of environment on the expression of these characters and considerable amount of genetic variation was observed for all the characters. These results were supported by earlier observations of Munshi *et al.*[22], Krishnamurthy *etal.*[20], Sandeep *et al.*[24]. In line with the current finding Vijaya *et al.*[32] reported high PCV and GCV for dry fruit yield per plant followed by number of fruits per plant. Manju and Sreelathakumary[21] reported the highest PCV and GCV for these characters. Again high estimates of PCV and GCV were reported for number of fruits per plant (40.50 and 37.77 %), dry fruit weight (40.75 and 37.77 %), and yield per plant (30.81 and 26.43%) by Janaki *et al.*[17]. This indicates the existence of wide range of genetic variability, broad genetic base, less environmental influence and these traits are under the control of additive gene effects and hence, there is a good scope for further improvement of these characters through simple selection. Moreover, there were traits which depicted moderate PCV and GCV values like canopy width, stem diameter, fruit length, and fruit diameter. In line with the current finding, Sharma *et al.*[25] reported moderate PCV in pericarp thickness; Devi[9] reported moderate PCV and GCV values for fruit length and width; Afroza *et al.*[5] reported moderate PCV and GCV for fruit length, fruit diameter, flesh thickness and number of fruits per plant.

High heritability was observed in some traits like oleoresin content, fruit diameter, fruit length and fresh fruit yield that can be attributed to greater role of additive and additive x additive gene action, which can be exploited by following simple selection. Dhaliwal *et al.*[10] noticed high heritability for red ripe fruit yield, plant height, fruit length, and fruit width indicating that these characters were less influenced by the environment and improvement by selection is relatively easier and rewarding. Krishna *et al.*[19] reported same finding for fruit length, fruit number and fresh fruit yield. Yatung *et al.*[33] observed high heritability for all the characters ranged between 68.47 and 98.44%.

High heritability coupled with high genetic advance as per cent of mean was observed for most of the characters indicating the predominance of additive gene action and hence direct phenotypic selection for improvement is useful with respect to these traits in hot pepper genotypes studied. Consistent with the current results, earlier workers noticed high heritability coupled with high genetic advance for fresh fruit yield, plant height, fruit length and fruit width (Dhaliwal *et al.*[10]); for all yield and quality related characters (Vijaya *et al.*[32]; Gupta *et al.*[14]) for fruit diameter and average dry fruit weight; Suryakumari *et al.*[29] for number of seeds per fruit;(Krishna *et al.*[19]) for total fruit yield and fruit number.

V. CONCLUSION

The result illustrated significant ranges of variability in growth, yield and quality characters indicating ample variability for further improvement and selection of superior genotypes. The difference between PCV and GCV was narrow indicating the little influence of environment on the expression of these characters and considerable amount of genetic variation was observed for all the characters. Broad sense heritability explained moderate to high heritability in all characters. High heritability coupled with high GAM was observed for most of the characters indicating the predominance of additive gene action and hence direct phenotypic selection for improvement is useful with respect to these traits in hot pepper genotypes studied. Therefore, using different varieties at different agroecological regions is crucial to exploit the potential variability existing among hot pepper genotypes.

Significance statement

Ethiopia is endowed with diverse agroecology to accommodate varieties of hot pepper to grow for local and international markets. Thus, identifying and assessing the existing and newly introduced hot pepper varieties for yield and quality has significant importance for production and productivity in the area.

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