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Genetic Components and Heritability of Yield and Yield Related Traits in Hot Pepper

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Abstract: The yield of hot pepper has remained low in typical tropical climate of Ethiopia mainly due to lack of genetic information and limited improvement work. Twelve genotypes of the crop were crossed in half-diallel fashion to estimate genetic components of variation and the resultant 78 progenies (66 F_1 and 12 parental selfs) were evaluated using Randomized Complete Block Design at Melkassa Agricultural Research Center, Ethiopia during October 2004 to June 2005. Significant variation were obtained among the progenies for all the traits, namely dry fruit yield per plant, number of branches per plant, plant height, number of fruits per plant, days to maturity, fruit length and single fruit weight. For days to maturity and dry fruit yield per plant only dominant component, and for all other traits both dominance and additive genetic components were significant. Over-dominance governed expression of majority of the traits except plant height. Unequal distributions of genes with positive and negative effects among the parents were revealed for the entire traits. and indicated a need of caution in selecting hot pepper parents for breeding purposes. Proportions of dominant to recessive genes were positive and more than unity except for fruit length (0.73) and signified that the parents mostly carried dominant genes with positive effects. Expression of number of fruits per plant, days to maturity and dry fruit yield per plant were insensitive to environment influences. Broad sense heritability ranged from 0.85 to 0.96 and signified the observed variation to be genotypic in origin. Heterosis and pedigree methods with recurrent selection would facilitate simultaneous exploitation of the genetic components for improvement of hot pepper.

Key words: additive gene, *Capsicum* spp. L., gene action, over-dominance

INTRODUCTION

Diverse hot pepper (*Capsicum annuum* L. var. *annuum*) genotypes have been widely grown in tropics and typical tropical climate within Ethiopia (between 3° and 18° North latitude; 48° east of longitude) over centuries. More than 100,000 tones (annual average) of dry fruit of hot pepper are produced in the country and used for export for worldwide market but substantial amount are consumed locally as spice which exceeds the volume of all other spices put together in the country. Nowadays there is serious shortage of dry fruits both for export and local markets partly due to very low productivity (0.4 t dry fruit yield/ha) of the crop.

In fact, though hot pepper has been cultivated for centuries in typical tropical climate within Ethiopia but the yield has remained very low due to limited improvement work on the crop. However, in the past three decades, diverse genotypes (more than 300) of the crop have been introduced from different regions of the world and local collections have also been made in the country. The genetic improvement of hot pepper is also lacking in the country due to non availability of requisite genetic information. It is well recognized that the knowledge and understanding of the genetic basis of economic traits is important to enhance the progress in breeding new varieties of the crop.

The diallel analysis techniques[20] have been found to be the useful tools to obtain precise information about the types of gene actions involved in the expression of various traits and to predict the performance of the progenies in the latter segregating generations. Cross breeding and selection of improved strains in succeeding generations would enable to sort out ideal genotypes of chilli for which knowledge of its genetics is of priority importance[4]. Earlier investigator[11] suggested the use of at least ten parents

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for reasonably accurate estimation of the genetic components of variation. The present study was, therefore, aimed at estimating the genetic components of variation for fruit yield and associated traits using progenies of twelve elite inbred lines of hot pepper genotypes of diverse origins which included nine Asian and three Ethiopian genotypes.

MATERIALS AND METHODS

Genetic Material and Crossing Techniques: The seed material of the entire test genotypes were obtained from the worldwide and local Ethiopian germplasm collections maintained at Melkassa Agricultural Research Center (MARC), Ethiopia by Horticulture Research Division. The genotypes are quite diverse with respect to their regions of evolvement including nine Asian, namely, PBC 972 (Malaysia), PBC 602 (Taiwan), PBC 223 (Korea), ICPN9#16 (Malaysia), PBC 731 (Korea), PBC 535 (Indonesia), PBC 580 (Sri Lanka), ICPN10#5 and ICPN10#6 (Taiwan); and three local Ethiopian ('Marekofana', 'Bakolocal' and 'Marekoshote') inbreed lines of hot pepper. The parents from all the genotypes, involved to produce F_1 seeds, were considered as homozygous because they were selfed for eight generations during 1995 to 2002 in Ethiopia.

During December to January 2003, crossing was done among the twelve parents in all possible combinations in a half-diallel fashion to fit Griffing's Method 2, Model I - fixed effect analysis[8]. Single flower caging (50 mesh net of 0.78 x 0.26 hole size) was used to effect the required mating as well as prevent chance out-crossing. The crossed seeds were harvested during April to May, 2004. Subsequently, the harvested seeds of all the twelve selfed parental lines and their 66 F_1 crosses were sown on seedbed at the end of August 2004 and transplanted to the field in October 2004.

Description of Study Site and Field Planting: The study was conducted at MARC, Ethiopia (8°24'N latitude, 39°12'E longitude, altitude of 1550 m above sea level, average annual rainfall of 763 mm, annual mean maximum and minimum temperatures of 26-29°C and 11-16°C, respectively), during October 2004 to June 2005. The testing location represented major hot pepper producing areas having typical tropical climate. Hence, the genotypes were expected to express their full genetic potentials for the traits under consideration. Details of the site were described by earlier work[7].

The experiment was conducted in Randomized complete block design (RCBD) with three replications using plot size of 4.2 m x 4 m with four rows to accommodate 56 plants per plot. Intra-row spacing of 0.3 m and inter-row spacing of 1 m were maintained for all the experimental units.

Data Collection and Analysis of Variance: Seven traits were recorded on each plant from the middle two rows (24 plants) by excluding single border plant on each side of the row and the mean values were used to represent each experimental unit. The traits recorded were number of branches per plant (count), plant height (cm), number of fruits per plant (count), days to maturity (count from days of transplanting), dry fruit yield per plant (g), fruit length (cm) and single fruit weight (g).

Analysis of variance was performed based on mean values of 78 progenies for each trait as prior suggestion[27].

Assumptions of Diallel Analysis and Procedures for Testing the Adequacy: The validity of information from a group of genotypes obtained from the diallel cross method was based on the following assumptions[10,3]. (1) Diploid segregation of chromosomes, (ii) Homozygosity of parents, (iii) Absence of reciprocal effects, (iv) Absence of epistasis, (v) No multiple allelism, (vi) Independent distribution of genes among the parents. To fulfill the assumptions of absence of epistasis, no multiple allelism and independent distribution of gene distribution, data were subjected to three tests[26] of the validity of the hypothesis viz. size of Vr and Wr or t^2 values, b values and uniformity of Wr + Vr and Wr - Vr , all related to Vr and Wr statistics. The uniformity of Wr, Vr indicates the validity of assumptions[11] and was tested using t^2 test. The second test was the joint regression analysis of Wr and Vr. The regression co-efficient (b = wr.vr) is expected to be significantly different from zero and not from unity, failure of this test means the presence of epistasis or the genes are not independent[20]. The third test was using Wr + Vr and Wr - Vr based on diallel theory[10, 20, 12] that states consistency of Wr + Vr over arrays in absence of non-additive genetic variation but shows differences due to dominance. In the absence of non-allelic gene interaction and with independent distribution of gene among parents, Wr - Vr is constant over arrays and serve to indicate the adequacy of additive dominance model. If certain types of non-allelic interaction are

present, Wr + Vr and /or Wr - Vr must change from array to array. Failure of these three tests completely invalidates the additive-dominance model. However, if one fulfills the assumptions, the additive-dominance model is considered to be partially adequate.

The estimates of t^2 and regression co-efficient 'b' were based on the following formula[27]:

$t^2 = (n - 2)/4[(d^2Vr - d^2Wr)^2/(d^2Vr \times d^2Wr) - Cov^2 (Vr, Wr)]$
$b = bwr.vr = Cov (Wr, Vr)/V_{ar} (Vr)$
For testing Ho: b = 0, t = (b-0)/S.E. (b)
For testing Ho: b = 1, t = (1-b)/S.E. (b)

Where
V_r = variance of one array (r^{th} array) = 1/n-1[sum of squares of the crosses involving a particular parent - C.F.]
W_r = the covariance between parents and their off-springs in one array (r^{th} array)
d^2Vr = 1/n-1[Sum of squares of the crosses involving a particular parent - C.F.]
$d^2Wr = 1/(n-1)[\sum Wr_i^2 - (\sum Wr_i)^2/n]$
$Cov^2 (Vr, Wr) = 1/n-1[(\sum Vr, Wr - \sum Vr \sum Wr /n]$
n = number of parents
$C_{ov} (Wr, Vr) =[\sum Vr, Wr - \sum Vr \sum Wr /n]/(n-1)$
$V_{ar} (Vr) =[\sum Vr^2 - (\sum Vr)^2/n]/(n-1)$
$S.E. (b) =[d^2Wr - b Cov (Wr, Vr)/d^2Vr(n - 2)]^{1/2}$
C.F. = (sum of all the 'n' crosses involving a particular line)^2/number of crosses

Estimation of Genetic Components of Variance: Various components of variation viz. D (variation due to additive effect), H_1 (variation due to the dominant effect of the genes), H_2 (variation due to dominant effect of genes correlated for gene distribution where $H_2 = H_1[1 - (u - v)^2]$, u = proportion of positive genes in parents and v = proportion of negative genes in parents, such that u + v =1), F (relative frequency of dominant and recessive alleles over the arrays; if F was positive, dominant alleles are more frequent than the recessive and if F is negative vice-versa is correct), h^2 (overall dominance of heterozygous phase in all crosses), E (environmental variance), $(H_1/D)^{1/2}$ (mean degree of dominance), $H_2/4\ H_1$ (proportion of genes with positive and negative effects in the parents), $[(4DH_1)^{1/2}+F]/[(4DH_2)^{1/2}-F]$ (proportion of dominant and recessive genes in the parents), h^2/H_2 (the number of groups of genes which control the character and exhibit dominance), $h^2_{(n)}$ (heritability in narrow sense) and $H^2_{(b)}$ (heritability in broad sense) were estimated using earlier described procedures[10, 27]. The diallel cross method[9] was used for computing the components of genetic variance for the F_1 data where additive-dominance model fitted. The components of genetic variances were computed only for the traits which fitted to the additive-dominance model based on the following formulae[27]:

$D = V_{oL0} - E$
$H_1 = V_{oLo} - 4W_{oLo1} - 4V_{1L1} - (3n - 2)E/n$
$H_2 = 4V_{1L1} - 4V_{oL1} - 2E$
$h^2 = 4(M_{L1} - M_{Lo})^2 - 4(n - 1)E/n^2$
$F = 2V_{oLo} - 4W_{oLo1} - 2(n - 2)/n$

Where
$V_{oLo} = V_p$ = variance of parental array = 1/n-1[Sum of squares of the parental mean - C.F.]
$V_{1L1} = \grave{V}_r$ = mean of variance of the array = $1/n\sum Vri$
$W_{oLo1} = \grave{W}_r$ = mean covariance between parents and their off-springs in one array (r^{th} array) = $1/n\sum Wri$
$V_{oL1} = \grave{V}_m$ = variance of the mean of the arrays = 1/n-1[Sum of squares of the array mean - squares of total array mean/n]
E = Me = the expected environmental component of variation for parents and F_1s data of individual environment
$(M_{L1} - M_{Lo})^2$ = the difference between mean of the parents and mean of their n^2 - n/2 progenies
Vri =[(Sum of squares of i th array) - 1/n(total of i th array)^2]/(n - 1)
Wri =[sum of product of (i th array x non-recurrent parent) - 1/n (parental total x total of i th array)]/(n - 1)

Estimation of Standard Errors and T Values for the Main Components: Standard errors (SE) for respective components were calculated as the square roots of the product of the variance or common multiplier (C) and specific multiplier (s^2)[10] for each of the statistics as:
$SE(D) = (s^2_D \times C)^{½}$
$SE(H_1) = (s^2_{H1} \times C)^{½}$
$SE(H_2) = (s^2_{H2} \times C)^{½}$
$SE(h^2) = (s^2_{h2} \times C)^{½}$
$SE(F) = (s^2_F \times C)^{½}$
$SE(E) = (s^2_E \times C)^{½}$

Where
$C = (1/2)[Var(Wr - Vr)] = ½[1/n-1\{\sum(Wri - Vri)^2 - [\sum(Wri - Vri)]^2 / n\}]$
$s^2_D = (n^5+n^4/n^5)$
$s^2_{H1} = (n^5+41n^4-12n^3+4n^2)/n^5)$
$s^2_{H2} = 36n^4/n^5$
$s^2_{h2} = (16n^4+16n^2-32n+16)/n^5$
$s^2_F = (4n^5+20n^4-16n^3+16n^2)/n^5$
$s^2_E = n^4/n^5$

All the significance level was determined by comparing computed 't' and Table 't' values at n-2 degrees of freedom, where the computed 't' = value of component/ S.E. of component.

Estimation of Heritability: Narrow sense heritability[$h^2_{(n)}$] and broad sense heritability[$H^2_{(b)}$] were obtained using the following formula[19] with minor modification to fit the analysis:

$$h^2_{(n)} = [(1/2)D + (1/2)H_1 - (1/2)H_2 - (1/2)F]/[(1/2)D + (1/2)H_1 - (1/4)H_2 - (1/2)F + E]$$

$$H^2_{(b)} = [(1/2)D + (1/2)H_1 - (1/4)H_2 - (1/2)F]/[(1/2)D + (1/2)H_1 - (1/4)H_2 - (1/2)F + E]$$

RESULTS AND DISCUSSION

Magnitude of genetic variability and heritability are necessary in systematic improvement of hot pepper for fruit yield and related traits. Total genetic variances were found to be highly significant (Table 1) for all the traits recorded and suggested availability of substantial genetic variation among the tested genotypes (66 F_1 and their 12 selfed parents). Thus tests for adequacy of additive-dominance model (Table 2) were applied for all the traits in which full adequacy of the model was obtained for plant height and partially adequate for all other traits except number of branches per plant for which all the three tests were inadequate. Further, separations of total genetic variance into its components of variation (Table 3) were performed and discussed for all the traits but for number of branches per plant added discussion would not be necessary. Actually the analysis of Vr, Wr graph might enable to conclude the genetics of the parents regarding this trait but not provided in this work. Earlier reports in other crop[5] indicated the importance of investigating genetic constituents and various ratios among them for improvement of yield and yield components.

The estimates of genetic components of variation (Table 3) showed significant variation both due to additive (D) and dominant (H_1) gene effects for plant height, number of fruits per plant, fruit length and single fruit weight while it was significant for dominant but non-significant for additive component with respect to days to maturity and dry fruit yield per plant. The results suggested existence of genetic potentiality in the tested genotypes both for intrapopulation improvement and development of hybrids with a need of biasness of a breeder toward heterosis breeding in case of development of early maturing high yielding variety. The D variation is the fixable genetic component that can be fixed by continuous selection of homozygous lines while the H_1 variation depends on the properties of heterozygotes and is, therefore, unfixable. In all the traits except plant height the dominant genetic component exceeded the expressed additive effects, a phenomenon called over-dominance, as indicated by more than unity values of $(H_1/D)^{1/2}$. Since over dominance is of primary importance for the above specified traits, the desirable procedure of improvement could be production of hybrids. However, an observed over-dominance might not be an index of real over-dominance[5], as degree of dominance might be biased due to linkage, epistasis or both[2]. Earlier reports[17,28,29,23,22,21,15] indicated the importance of dominance gene effect in the development of hybrid varieties in *Capsicum* species. Nevertheless, the lesser value of H_1 than D for plant height indicated partial dominance. Similar results were also reported by earlier investigators[1,4,24,25].

Unequal values of H_1 and H_2 for all the traits except for single fruit weight revealed asymmetrical distribution of genes with positive and negative effects in the parents as were supported by the values of $H_2/4$ H_1 which were different from 0.25. Such genetic variations among the parents with respect to the effects of the genes they were bearing and transmitting to their progenies could offer opportunities for *Capsicum* breeder for quick identification of parents which would carry genes with positive effects for traits of interest in an improvement program.

Estimates of overall dominance for all the recorded traits except for single fruit weight were significant and positive as indicated by h^2. The results suggested overall effects of the dominant genes in the F_1s were in enhancing direction for the traits under concern, which is advantage that could be utilized via hybrid seed production in hot pepper improvement program. Absence of similar overall-dominance effect due to heterozygous loci for single fruit weight suggested absence of directional dominance.

The relative frequencies of dominant alleles were indicated by F values (Table 3) to be positive for all the traits except fruit length. The results suggested availability of surplus dominant genes that might take part in the expression of the traits than recessive alleles. Values of $[(4DH_1)^{1/2}+F]/[(4DH_2)^{1/2}-F]$ for all the traits except for fruit length were greater than unity and suggested higher proportion of dominant genes in the parents, which might be the cause for higher frequencies of dominant alleles in the progenies. However, higher recessive genes in the parents might have played role in expression of fruit length as further supported by the negative value of F that indicated excess of recessive genes in the progenies.

Table 1: Mean squares from analysis of variance for 7 traits in 78 hot pepper progenies (12 parental selfs and their 66 F_1s) grown at Melkassa, Ethiopia during 2004/2005

Sources of variation	Number of branches per plant	Plant height	Number of fruits per plant	Days to maturity	Fruit length	Single fruit weight	Dry fruit yield per plant
Block (2)	0.060 ^{ns}	81.648 ^{ns}	88.894**	38.612***	11.646***	0.026 ^{ns}	89.215 ^{ns}
Genotypes (77)	3.737***	259.857***	439.146***	99.115***	6.087***	0.264***	1269.330***
Error (154)	1.066	30.765	23.731	4.637	0.51	0.042	141.594

Note: figures in parenthesis indicate degree of freedom, ^{ns} $p > 0.05$, ** $p < 0.01$, *** $p < 0.001$

Table 2: Tests of adequacy of additive-dominance model in 12 x 12 half diallel analysis for 7 traits of 78 hot pepper progenies (12 parental selfs and their 66 F_1s) grown at Melkassa, Ethiopia during 2004/2005

Traits	Joint regression	Test of t^2	Test for b =0	Test for b =1	Wr + Vr	Wr - Vr	additive-dominance model
Number of branches per plant	b=0.38±0.27	0.053^{ns}	-1.414^{ns}	2.287*	1.06 ^{ns}	1.06^{ns}	Inadequate
Plant height	b= 0.91±0.10	0.131^{ns}	-8.760*	0.922^{ns}	4.10**	0.67^{ns}	Fully adequate
Number of fruits per plant	b= 0.67±0.19	0.215^{ns}	-3.447*	1.718*	23.22***	8.63***	Partially adequate
Days to maturity	b= 0.11±0.08	32.503**	-1.326^{ns}	11.028*	17.29***	14.32***	Partially adequate
Fruit length	b= 0.64±0.26	0.025^{ns}	-2.473*	1.385^{ns}	1.50 ^{ns}	3.18**	Partially adequate
Single fruit weight	b= 0.79±0.22	0.057 ^{ns}	-3.583*	0.963^{ns}	5.34***	2.22 ^{ns}	Partially adequate
Dry fruit yield per plant	b= 0.09+ 0.12	13.439**	-0.724^{ns}	7.837*	5.59***	7.04***	Partially adequate

^{ns} $p>0.05$, * $p<0.05$, $^{**}p<0.01$, $^{***}p<0.001$

Table 3: Estimates of genetic and environmental components of variations along with their standard errors, ratios of genetic components and heritability estimates for 6 traits of 78 hot pepper progenies (12 parental selfs and their 66 F_1s) grown at Melkassa, Ethiopia during 2004/2005

Genetic components	Plant height	Number of fruits per plant	Days to maturity	Fruit length	Single fruit weight	Dry fruit yield per plant
D (additive component)	118.1±5. 6*	194.7±32.5*	10.2±11.7^{ns}	2.0±0.2*	0.1±0.0*	217.0±157.4^{ns}
H_1 (dominance component)	111.4±11.2*	358.5±65.0*	123.1±23.4*	2.3±0.4*	0.2±0.0*	1473.3±314.8*
H_2 (proportion of -/+ genes)	102.2±9.3*	312.7±54.1*	102.4±119.5*	2.1±0.3*	0.2±0.0*	1376.4±261.9*
h^2 (over all dominance effect)	43.5±6.2*	451.2±36.2*	84.1±13.0*	6.2±0.2*	0.0±0.0^{ns}	2201.6±175.0*
F (mean covariance of D and H_1)	12.0±12.7^{ns}	115.3±73.6^{ns}	12.6±26.5^{ns}	-0.7±0.4^{ns}	0.1±0.0*	202.5±356.7^{ns}
E (environmental component)	10.5±1.6*	6.5±9.0^{ns}	1.7±3.2^{ns}	0.2±0.0*	0.0±0.0*	47.0±43.6^{ns}
$(H_1/D)^{1/2}$ (mean degree of dominance)	0.97	1.36	3.47	1.07	1.29	2.61
$H_2/4$ H_1 (proportion of genes with ± effects)	0.23	0.22	0.21	0.23	0.21	0.23
$[(4DH_1)^{1/2}+F]/[(4DH_2)^{1/2}-F]$ (proportion of dominant and recessive genes)	1.11	1.56	1.43	0.73	1.73	1.44
h^2/H_2 (number of dominant genes blocks)	0.43	1.44	0.82	2.93	0.18	1.53
$h^2(n)$ (narrow sense heritability)	0.63	0.41	0.20	0.63	0.41	0.12
$H^2(b)$ (broad sense heritability)	0.89	0.96	0.96	0.92	0.85	0.9

^{ns} $p>0.05$, * $p<0.05$

The number of groups of genes which control the character and exhibit dominance as indicated by more than unity values of h^2/H_2 for number of fruits per plant, fruit length and dry fruit yield per plant suggested that the expression of these traits were governed by group of genes with dominant gene effects. However, for the other studied traits the values were less than unity and such result might not provide any valid interpretation concerning groups of genes exhibiting dominance[5]. Under estimation of such ratio could be resulted either when the dominance effects of all the genes concerned are not equal in size or distribution or when the distribution of genes is correlated[13], or when complementary gene interactions occur[16, 18].

Significant environmental component of variation coupled with high broad sense heritability were observed for plant height, fruit length and single fruit weight, suggesting the genotypes differ not only in their environmental sensitivity but also in their genotypic potential. The effects of environment for the expression of other studied traits was non-significant and the observed variation among the individuals of the population signified to be genotypic in origin as confirmed by elevated values of broad sense heritability. The results of the present study are in agreement with earlier findings[4, 25]. High broad sense heritability estimate indicates lesser influence of the environment in contrast to significant contribution of additive and non-additive variances in an expression of a trait[7]. High values for narrow sense heritability were observed for all the traits except for days to maturity and dry fruit yield per plant, suggesting the importance of additive genetic variation that could be useful in the improvement program of hot pepper for the traits under concern. However, narrow sense heritability were very

low versus very high broad sense heritability for days to maturity and dry fruit yield per plant, be a sign of the presence of dominance and suggested that selection based on individual plant will not give better progress in improvement of such trait. The viability of a breeding program aimed at developing hybrids depends on the existence of dominance effect, which is the interaction between allelic genes[6]. This is also in accordance with other earlier observations[14].

Conclusions: The results suggested the involvements and importance of both additive and dominant genetic components with predominance of dominance variance in the expression of all the studied traits except plant height. Further, narrow sense heritability was high for all the traits except for days to maturity and dry fruit yield per plant and indicated the importance of the fixable portion of genetic variation among the tested progenies. The over all genetic analysis suggested high role of dominant genetic variation that could be the cause for expression of heterosis. So, maximum improvement of dry fruit yield per plant can be achieved by hybrid breeding program rather than any selection efforts to develop pure line. However, improvement of other traits could be via selection of transgressive segregates and recombination. Thus, heterosis and pedigree breeding methods with recurrent selection would facilitate simultaneous exploitation of the obtained genetic components in hot pepper improvement program. Involvement of diverse elite genotypes of different origins along with elite local genetic materials would significantly contribute to enhance the improvement of hot pepper under tropical growing conditions. Further such studies, using local and worldwide genotypes of diverse origins, would enable to identify and generate useful genetic information and more appropriate breeding strategies that would facilitate the improvement of the crop.

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