World Journal of Agricultural Sciences 5 (3): 361-368, 2009
ISSN 1817-3047

Nature of Gene Action of Some Quantitative Traits in Chickpea (*Cicer arietinum* L.)

A.C. Deb and M.A. Khaleque

Department of Genetic Engineering and Biotechnology, University of Rajshahi, Rajshahi-6205, Bangladesh

Abstract: Nine agronomic characters were performed in the study as follow: first flower (DFF), number of primary branches at first flower (NPBFF), number of secondary branches at first flower (NSBFF), plant height at maximum flower (PHMF), plant weight just after harvest (PWH), number of pods per plant (NPd/P), pod weight per plant (PdW/P), number of seeds per plant (NS/P) and seed weight per plant (SW/P) of P_1, P_2, F_1, F_2 and F_3 generations of chickpea (*Cicer arietinum* L.). Scaling test revealed that in cross 1 for NPBFF, PHMF, PWH, PdW/P and NS/P, in cross 2 for NPBFF, PWH and PdW/P and in cross 3 for PHMF, PWH, NPd/P, PdW/P, NS/P and SW/P additive-dominance model was found to be adequate. Analysis of components of variation revealed that dominance component (H) expressed positive values in 11 cases and negative in 16 cases, whereas additive component (D) exhibited positive values in 17 cases and negative in 10 cases. Genetic advance (GA) and genetic advance expressed as percentage of mean (GA%) were low in majority of the characters and crosses. Heritability both in broad (h^2_b) and narrow (h^2_n) senses were found to be low in majority cases. But in some cases these values were high.

Key words: Chickpea · Additive-dominance model · Heritability and Genetic advance

INTRODUCTION

Pulse crops (food legumes) are the second most planted crops in Bangladesh after rice, reflecting the importance of pulses as a source of protein in Bangladeshi diets. The dominant pulse crops are lathyrus, lentil, chickpea, black gram and mungbean. Among the pulses, chickpea (*Cicer arietinum* L.) is the third most important food legume grown in 11 m ha with 9 million ton production (http://apps.fao.org). It is grown in over 45 countries in all continents of the world. It provides a high quality protein to the people in developing countries. People in the developed countries consider it as a health food. Green leaves/twigs of chickpea are used in preparing a nutritious vegetable in countries of South Asia. These are also used as high protein fodder mixed with cereal leaves. Chickpea Stover is fed to the cattle/goats as a nutrient-rich supplement to their major cereal fodder in the lean season. Successful breeding program for yield improvement in chickpea requires information on (a) the fundamental nature of gene action and interactions involved in the inheritance of grain yield and its components and (b) the efficiency of such genetic patterns in the selection process. The far and foremost duty of a breeder in Bangladesh is to develop high yielding varieties suitable in our climate. Since yield is a complex character depending upon a number of other characters and their interactions, knowledge about the associations of these characters with yield will greatly help a breeder in his selection work with more precision and accuracy. For this, crossing and breeding between exogenous and endigenous germplasm and selection of progenies from the advance generation may give rise to varieties suitable to our environments.

Geneticists and breeders are interested in the estimation of gene effects in order to formulate the most advantageous breeding procedures for the improvement of the quantitative characters. Estimation of additive and dominance components is important for the improvement of yield and its components. In this context, the present research work was undertaken to study the scaling test, estimation of heritability, genetic advance and genetic advance expressed as percentage of mean of nine yields and yield components in a population having advanced generations of chickpea (*Cicer arietinum* L.).

MATERIALS AND METHODS

Three parent plant materials for this research work were collected from Regional Agricultural Research Station, Ishurdi, Pabna, Bangladesh are as follows:

Corresponding Author: A.C. Deb, Department of Genetic Engineering and Biotechnology, University of Rajshahi, Rajshahi-6205, Bangladesh

Serial No.	Ac. No.	Lines
1	6	Nobin
2	31	RBH-228
3	42	ICC-4918

The material consisted of three inter-lines crosses of chickpea: RBH-228 × ICC-4918 (cross 1), RBH-228 × Nobin (cross 2) and Nobin × ICC-4918 (cross 3) where Nobin and RBH-228 considered as high yielder and ICC-4918 considered as stable line. The experiment was conducted in the Rabi season in the Botanical Research Garden of Rajshahi University. Parents, F_1s, F_2s and F_3s were derived from the above inbred lines. Replicated rows of all the four generations in three crosses were designed in a single randomized block. Seeds of three different lines and crosses were grown in three plots having different rows with the number of hills depending on the availability of seeds. The size of each plot was 120 × 160 cm. and the spaces between hill, row and plot were 30, 40 and 125 cm, respectively. Different rows with five hills were considered for both individual lines and generations. Seeds of the parents and different generations derived from them were sown randomly in different plots.

Statistical Analysis: The collected data were analyzed following the biometrical techniques as developed by Mather [28] based on the mathematical model of Fisher [6] and those of Allard [1], Hayman [9] and Mather and Jinks [29]. The methods in details are given bellow:

Analysis of Components of Mean:

I) Mather's Scaling Test: For testing the presence or absence of epistasis, scaling test was done following Mather [28] and Hayman and Mather [10]. In the present investigation, only two scales (C and D) were used. The two different scales and the formulae for the computation of its standard error are given below:

I. Scales:

$$C = 4\ \bar{F}_2 - 2\ \bar{F}_1 - \bar{P}_1 - \bar{P}_2$$

and

$$D = 4\ \bar{F}_3 - 2\bar{F}_2 - \bar{P}_1 - \bar{P}_2$$

Standard Error of Scales:

$$\text{S.E. of } C = [16\ V(\bar{F}_2) + 4V(\bar{F}_1) + V(\bar{P}_1) + V(\bar{P}_2)]^{1/2}$$

and

$$\text{S.E. of } D = [16\ V(\bar{F}_3) + 4V(\bar{F}_1) + V(\bar{P}_1) + V(\bar{P}_2)]^{1/2}$$

Where, VP_1, VP_2, VF_1, VF_2 and $V F_3$ are the variances of $\bar{P}_1$, $\bar{P}_2$, $\bar{F}_1$, $\bar{F}_2$ and $\bar{F}_3$ populations, respectively.

II) Joint Scaling Test: Joint scaling test was done based on 3-parameter model for five generations. For testing the adequacy of additive-dominance model weighted least square technique was done as proposed by Cavaili [4].

Analysis of the Components of Variation: Based on the additive (D) - dominance (H) model variances of different generations under study can be written following Mather and Jinks [29].

$$V_{F2} = \frac{1}{2}D + \frac{1}{4}H + E_1$$

$$\bar{V}_{F3} = \frac{1}{4}D + \frac{1}{8}H + E_1$$

$$V\bar{F}_3 = \frac{1}{2}D + \frac{1}{16}H + E_2$$

Where,

V_{F2} = Variance of F_2 family
$\bar{V}_{F3}$ = Mean variance of F_3 families and
$V\bar{F}_3$ = Variance of F_3 family means.

The non-heritable components of variation in a generation were found out from the variance of non-segregating generations as follows:

$$E_1 = {}^1/_4\ V_{P1} + 1/_4\ V_{P2} + {}^1/_2\ V_{F1}$$

Heritablity: Heitability was calculated in two different ways following Mather [28] as follows:

I) Broad Sense Heritability (h^2_b): It is expressed as the ratio of the genetic variance over the (expected) phenotypic variance of F_2 generation as follows:

$$h^2_b = \left(\frac{1}{2}D + \frac{1}{4}H\right) / \left(\frac{1}{2}D + \frac{1}{4}H + E_1\right)$$

Where, D, H and E are the estimates of components of variation.

II) Narrow Sense Heritability (h^2_n): It is expressed as the ratio of fixable heritable variation (D) over the (expected) phenotypic variance of the F_2 generations as follows:

$$h^2_n = \frac{1}{2}D / \left(\frac{1}{2}D + \frac{1}{4}H + E_1\right)$$

Genetic Advance (GA): It was calculated as per the following formula:

$$GA = K \times \sigma_P \times h^2_b$$

Where,

K = The selection differential in standard units in the present study and it was 2.06 at 5% level of selection [26].

σ_P = Standard deviation of the phenotypic variance of F_2

h^2_b = Heritability in broad sense.

Genetic Advance Expressed as Percentage of Mean (GA%): It was measured by the following formula:

$$GA\% = \frac{GA}{\overline{X}} \times 100$$

Where, $\overline{X}$ = Grand mean for a respective character.

RESULTS AND DISCUSSION

In the analysis of the components of means viz. m, [d] and [h], first Mather's [28] scaling test was done to see whether additive-dominance model was adequate or not. Mather's [28] scaling test for C and D were done for all the characters in all the three different crosses separately and are presented in Table1. Table showed that in cross 1 characters such as NPBFF, PWH, PWd/P and NS/P were non-significant for C and D and other characters viz. DFF, NSBFF, PHMF, NPd/P and SW/P were significant for the same. In cross 2 most of the characters were found to be significant for C and D except NPBFF, PWH and PdW/P which were non-significant for C and D. While, in cross 3 most of the characters were non-significant for C and D except DFF, NPBFF, NSBFF where these were significant. Non-significant C and D indicated that the additive-dominance model was adequate for their respective characters and crosses. Singh [44] found adequacy of additive-dominance model in chickpea for days to flower only in cross BGM-417 × Ponaflair. Shahid [39] made a result from Mather's [28] scaling test on wheat and observed that additive-dominance model was inadequate for most of the cases. Joint scaling test of Cavalli [4] is more effective than any other test in detecting the adequacy of model, since it uses information from of all the generations available from each cross at a time.

In the absence of epistasis the data fit with the 3-paramenter model in which m measures a constant (base population mean), [d] and [h] estimate the algebraic sum of the additive and dominance effects, respectively. The values of m, [d] and [h] were calculated in terms of 3-parameter model. The χ^2- test was done to test the goodness of fit of the observed generation means with that of the expected means based on the 3-parameter estimate. Following Cavalli's [4] joint scaling test, the χ^2-values were obtained for each of the characters as shown in Table (1). In this Table χ^2-values were found to be non-significant for NPBFF, PHMF, PWH, PdW/P and NS/P in cross 1, for NPBFF, PWH and PdW/P in cross 2 and PHMF, PWH, NPd/P, PdW/P, NS/P and SW/P in cross 3. It exhibited the presence of only additive-dominance relationship in the inheritance of these characters and crosses. This result of the present investigation indicated that with only the additive-dominance relationship for those characters and crosses would likely help in doing successful breeding plan easily for the development of potential lines in chickpea. Shahid [39] observed that almost all the characters in all the crosses except Aghrani × FM-32 (4) for harvest index, fertile tillers/plant, spikelets/ear and grains/ear, where 3-parameter model was satisfactory to explain the genetic differences. Similar results were obtained by different workers such as Islam [17] in eggplant for different characters and crosses viz. YP and HT in cross 1; PS in cross 2; FW, TF and YT in cross 3; PS and PB in cross 4

Table1: Gene action of nine quantitative characters in three crosses of chickpea

Crosses		DFF	NPBFF	NSBFF	PHMF	PWH	NPd/P	PdW/P	NS/P	SW/P
Cross 1	C	17.91± 3.18*	1.85±1.38	1.94±1.41	12.47±6.26*	0.90±20.23	132.96±26.84*	8.56±5.61	25.74±33.01	12.92±4.08*
	D	11.85±2.76*	-1.31±1.37	-5.32±0.94*	-0.39±3.97	-12.92±1.19	-8.32±18.31*	-1.38±3.46	32.22±23.43	-2.38±2.60
	χ^2	15123.57***	2.0847	33.7059***	5.2292	4.4354	24.6584***	3.9215	4.9830	9.2282***
Cross 2	C	39.55±3.48*	0.05±1.17	-7.41±1.34*	-30.63±3.78*	-18.38±11.03	-151.21±24.97*	-7.93±5.57	-172.79±31.90*	-22.27±3.31*
	D	-24.31±3.29*	-0.61±1.58	-2.39±1.30	-1.83±4.73	-2.10±10.19	56.31±34.37	-2.67±5.25	28.83±36.12	2.59±3.78
	χ^2	338.0254***	0.1040	32.1773***	66.6106***	5.1056	41.0318***	3.6341	33.1336***	46.2570***
Cross 3	C	-23.69±3.07*	-8.00±1.30*	-1.37±1.44	4.98±7.28	3.46±17.73	-19.07±40.00	-1.79±7.97	-48.09±39.00	-6.15±4.55
	D	-19.85±2.43*	-6.40±1.01*	-3.37±1.17*	-9.42±8.30	7.24±19.53	-12.11±41.09	-1.63±6.57	-19.73±40.28	0.99±4.70
	χ^2	93.9871***	72.2609***	14.7361***	1.3964	0.6460	0.3917	0.2156	2.1461	1.8577

* and *** indicates significant at 5% and 0.1% levels, respectively

Table 2: Estimates of component of genetic variations (D, H and E) of nine quantitative characters in three crosses of chickpea

Crosses		DFF	NPBFF	NSBFF	PHMF	PWH	NPd/P	PdW/P	NS/P	SW/P
Cross 1	D	387.7406	-36.1308	14.0552	672.4056	-7473.2674	-5255.7166	-318.5666	-11740.1916	-168.4948
	H	-1040.0811	170.6528	-126.8421	-854.2213	50422.6998	37899.2976	2332.0709	82336.5219	1206.1919
	E	239.9500	20.3334	49.0333	593.8330	1620.1063	7770.5832	287.9267	9216.7161	139.6600
Cross 2	D	711.4570	-6.2306	6.7934	640.2648	766.3906	12024.5478	117.5958	14286.0150	116.2638
	H	-2453.4699	-22.4970	-115.9471	-1770.0479	-8874.1642	-54598.5153	-188.3939	-79368.1168	-752.4398
	E	311.4390	21.5390	40.1895	244.4046	2520.6372	12976.5554	339.3846	19344.4222	204.1020
Cross 3	D	57.6210	9.2850	8.6868	1056.9512	-103.9716	-2528.8398	-184.0326	830.8510	35.7614
	H	-388.5312	-81.5931	-54.4219	-1285.5620	7415.8021	7702.0917	2266.3931	22852.5851	373.1952
	E	134.3223	18.5058	14.8116	231.7148	860.2388	5756.7280	86.1408	5274.1778	54.0614

Table 3: Estimates of heritability, genetic advance (GA) and genetic advance express as percentage of (GA) mean of nine quantitative characters in three crosses of chickpea

Crosses		DFF	NPBFF	NSBFF	PHMF	PWH	NPd/P	PdW/P	NS/P	SW/P
Cross 1	H^2_b	-0.3806	0.5475	-1.0137	0.1712	0.8455	0.4684	0.6216	0.6149	0.6088
	H^2_n	1.1155	-0.4021	0.2886	0.4692	-0.3562	-0.1798	-0.2337	-0.2453	-0.2360
	GA (b)	-10.3362	7.5601	-10.3046	9.4400	178.3820	166.6598	33.4320	195.9521	23.6947
	GA(n)	30.2934	-5.5523	2.9337	25.8718	-75.1504	-44.7810	-12.5693	-78.1705	-9.1852
	GA% (b)	-13.9754	319.6930	-380.2435	19.2535	895.0462	224.8210	340.4481	347.5560	253.6906
	GA%(n)	40.9656	-235.2123	108.2546	52.7673	-377.0717	-60.4087	-127.9969	-138.6493	-98.3426
Cross 2	H^2_b	-4.7880	-0.6828	-1.7528	-1.0029	-2.6782	-1.4304	0.0333	-1.9109	-1.7535
	H^2_n	6.6121	-0.2434	0.2327	2.6253	0.5592	1.1261	0.1675	1.0749	0.7843
	GA (b)	-72.3457	-5.0322	-13.7965	-22.8218	-144.4268	-215.3093	1.2853	-320.8971	-31.0994
	GA(n)	99.9074	-1.7938	1.8316	59.6998	30.1559	169.5049	6.4653	180.5078	13.9101
	GA% (b)	-88.3989	-112.5772	-1242.927	-58.1151	-717.4704	-487.0027	11.7594	-630.5701	-594.6348
	GA%(n)	122.0765	-40.1298	165.0090	152.0239	149.8058	383.4085	59.1519	354.7019	265.9675
Cross 3	H^2_b	-1.0352	-5.7294	-1.6690	0.4719	0.6769	0.5279	0.8464	0.5375	0.6728
	H^2_n	0.4365	1.6882	0.7827	1.2044	-0.0195	-0.1037	-0.1641	0.0364	0.1082
	GA (b)	-21.8432	-19.5723	-8.0994	20.3634	71.9469	120.0879	41.2873	118.2362	17.8161
	GA(n)	7.3052	5.7671	3.7983	51.9722	-2.0726	-23.5899	-8.0048	8.0071	2.8652
	GA% (b)	-28.8397	-633.4078	-710.4737	44.0671	371.0516	319.6377	617.1495	325.1722	68.0570
	GA%(n)	9.6450	186.6375	333.1842	112.4696	-10.6890	-62.7892	-119.6532	22.0217	423.1853

and PB, FW and TF in cross 5 and Uddin [48] in wheat for EL in cross 1, 3, 5, 7and 8; for FEN/P in cross 1, 2, 3, 4, 5, 7and 8; for SN/E in cross 1, 2, 5 and 6; for KN/E in cross 3 and 4 and for Y/P in cross 1, 2, 3, 4 and 5. Rahman [37] also observed that additive-dominance model was adequate for LL4, LLS, LW5, LV4 CW, PW and PV in *Philosamia ricini*. Again, the rest of the characters in the present investigation such as DFF, NSBFF, NPd/P and SW/P in cross 1, for DFF, NSBFF, PHMF, NPd/P, NS/P and SW/P in cross 2 and DFF, NPBFF and NSBFF in cross 3 were found to be significant indicated inadequacy of the additive-dominance model. Inadequacy of the model showed that in the inheritance of these characters with the additive-dominance gene effects, non-allelic interaction and linkage may be a part. Significant χ^2-values were noted by Uddin [48] in wheat, Islam [17] in eggplant and Rahman [37] in *Philosamia ricini* for different characters and crosses.

Components of variation (D, H and E) were computed on the basis of additive-dominance model are presented in Table (2). During the calculation of components of variation, environmental variation (E) was found out as the mean of P_1, P_2 and F_1 variances and the values for D (additive variation) and of H (dominance variation) was estimated from the variances of F_2 and F_3 generations. Having only three parameters (D, H and E) a perfect fit of solution was possible and thus neither the standard deviation of the estimates or test of the goodness of fit could be done.

The estimates of H component were negative in a number of cases such as for DFF, NSBFF, PHMF, in cross 1 for DFF, NPBFF, NSBFF, PHMF, PWH, NPd/P, PdW/P, NS/P and SW/P in cross 2 and for DFF, NPBFF, NSBFF and PHMF in cross 3. These results corroborate with the findings of Moll [30], Lindsey [25] and Williams [50] in maize, Joarder and Eunus [18] and Joarder [19] in mustard,

Samad [38] in rapeseed, Husain [16] in chilli and Nahar [31] in sugarcane. The magnitude of D was negative in few cases viz. for NPBFF, PWH, NPd/P, PdW/P, NS/P and SW/P in cross 1, for NPBFF in cross 2 and for PWH, NPd/P and PdW/P in cross 3. The rest of the characters in these crosses additive component were positive and had considerable amount of D values indicated that additive component of variation was important in the present investigation.

Similar results were reported by Paul [35] and Samad [38] in rapeseed; Joarder [20] in mustard; Hogarth [12, 13], Wu [51], Hogarth [14], Skinner [45], Hogarth and Kingston [15] and Nahar [31] in sugarcane and Husain [16] in chilli. On the other hand, H and D were found to be negative for NPBFF in cross 2. Negative estimates of components of variation, however might arise from sampling errors [28] and/or genotype-environment interaction [11]. These values are to be considered either as zero or as very small but positive [28]. Negative estimates of D and H have been recorded in *Solidago sempervirens* L. [8] in N*icotiana rustica* L. [28]; in coriander [43]; in *Brassica campestris* L. [19]; in rice [23]; in jute [36] and in wheat [39]. Walton [49] reported importance of additive and dominance genetic variation for grain yield and its component traits in wheat.

Heritability estimates both in broad and narrow senses (Table 3) were found to be low in majority cases. However, in some cases these values were high. The inconsistent magnitude of narrow sense heritabilities (h^2_n), in most of the cases indicated that the genetic progress under selection for the characters studied would be slow. As these traits are controlled by polygenes the low heritatability values might be effected due to high large sampling variance and which is actually occurred in the present material. In contrast, high magnitude of broad sense heritabilities (h^2_b) observed, which were mostly uniform for PWH, PdW/P, NS/P and SW/P in cross 1 and for PWH, PdW/P and SW/P in cross 3. Stuber [46] reported that flowering days were highly heritable, whereas grain yield, number of fertile tillers and plant height were less heritable. However, Ketata [22] noted heritability estimates to be high for heading dates, moderately high for kernel weight, moderate for plant height and tiller number and low for spikelets per ear and grain per ear, though many authors gave contrasting reports. Paroda and Joshi [34] estimated poor narrow sense heritability for spikelet per plant. Gill [7] found grains per ear as a poorly heritable character. Plant height and 100-grain weight were also reported to be highly heritable [42, 2, 20]. Biological yield was considered as poorly heritable traits by Paroda and Joshi [34] and Shamsuddin [40]. Sharma [41] reported low heritabilities for most of the traits in one population and for number of grains, number of leaves and ear-lengths in another population in pearl millet. Cambel and Kondra [3] noted that heritability estimates were generally low for most of the characters in oilseed. Olsson [32] also reported low estimates of heritability for yield on a single plant basis in the same plant. Laosuwan [24] also in the same plant found low broad sense heritability for number of leaves. Deb [5] obtained low heritability for all the characters except 100-SW/P in chilli. Nahar [31] and Husain [16] also recorded low narrow and broad sense heritabilities for all the characters in sugarcane and chilli, respectively. Shahid [39] also estimated low to moderate broad and narrow sense heritabilities in most of the cases in wheat.

Nevertheless, higher magnitude of broad sense heritabilities in the present materials indicated the preponderance of more non-additive genetic variation than the additive genetic variation in the inheritance of those characters (PWH, PdW/P, NS/P and SW/P in cross 1 and for PWH, PdW/P and SW/P in cross 3).

Genetic advance was calculated both for broad sense and narrow sense heritabilities for all the characters and are shown in Table (3). In cross 1 the highest genetic advance in broad sense was calculated for NS/P followed by PWH, NPd/P and PdW/P, while the highest GA in narrow sense calculated as 30. 2934 for DFF followed by PHMF. The highest GA for both broad and narrow senses was recorded for PdW/P and NS/P, respectively in cross 2. Cross 3 expressed the highest GA in broad sense for NPd/P followed by NS/P and PWH with the values of 120.0879, 118.2362 and 71.9469, respectively. While, in the same crosses highest genetic advance in narrow sense was 51.9722 for PHMF.

Genetic advance expressed as percentage of mean was calculated in different crosses for all the characters and are presented in Table (3). In the present study, in cross 1 the highest GA% in broad sense was calculated for PWH followed by NS/P, PdW/P, NPBFF and SW/P. While, the highest GA% in narrow sense was observed for NSBFF followed by PHMF and DFF. The highest GA% was recorded both for broad and narrow sense as 11.7594 and 383.4085 for PdW/P and NPd/P, respectively in cross 2. In cross 3 the highest GA% in broad sense was expressed by the character PdW/P followed by PWH, NS/P and NPd/P with the values of 617.1495, 371.0516, 325.1722 and 319.6377, respectively.

On the other hand, the highest GA% in narrow sense was recorded for SW/P followed by NSBFF, NPBFF and PHMF in the same cross. The characters viz. CH, CD, TC, MCC, FB, RSP and CYC showed lower values of GA recorded by Nahar [31] in sugarcane. In the present research materials, genetic advance expressed as percentage of mean (GA%) in some cases showed the highest value. Majid [27] studied black gram and found the highest GA and GA% for the number of pods per plant. Nahar [31] also obtained the highest GA with GA% for leaf area in sugarcane suggesting that the direct selection for the character would be effective for the improvement of yield. However, heritability estimates along with the genetic gain is usually more useful than heritablity values alone in predicting the resultant effect from selecting the best individuals as was indicated by Swarup and Chaugale [47] in sorghum and Johnson [21] in soybean. The high heritability and high genetic gain are the indication of additive gene effects [33].

Importance of dominance genetic variation was also found in the analysis of components of variation where dominance effects though negative was found to be large than the additive effect. But in self-pollinated crops like chickpea, it is difficult to fix dominance effect in improving lines or strains. Therefore, selection practice would likely to be effective from advance generation where genetic variation within a hybrid population becomes largely dominant and in that case pure line selection following pedigree method may be used to achieve effective genetic progress [23]. In this regard the characters like PWH, PdW/P, NS/P and SW/P in cross 1 and PWH, PdW/P and SW/P in cross 3 may likely give fruitful result since they showed high broad sense heritability and adequacy of the additive-dominance model. Therefore, non-significant inbreeding depression in the present materials supported this view that selection from the advance generation would likely be effective.

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