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Genetic analysis of some yield attributes in Indian mustard (*Brassica juncea* L.)

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The present investigation on *Brassica juncea* L. genotypes is an attempt to study variations and to generate variability through hybridization and also to obtain genetic information on some yield attributes for selection in segregating generations. Eight promising genotypes were selected and crossed in all possible combinations under complete diallel system. Data was recorded for seed yield and some important yield attributes. Analysis of variance showed significant differences for all the traits and therefore further analyzed using Hayman's approach, which showed existence of both additive and dominance gene effects governing all the traits. However, estimates for genetic components of variation revealed that additive effects were more important for seeds per siliqua and 1000-seed weight indicating possibility of selection for these traits in early segregating generations. Dominance effects were more prominent with presence of over-dominance for plant height, number of primary branches per plant, number of siliqua per plant, siliqua length and seed yield per plot, thus suggesting that selection could be effective in latter generations. Only siliqua length showed the presence of directional dominance, while asymmetrical distribution of dominant genes among the parents was identified for all the traits.

Key words: Indian mustard, genetic analysis, gene action, yield attributes, complete diallel.

INTRODUCTION

Brassica group of crops are the second largest contributors to the vegetable oil after cotton seed in Pakistan. Cultivars of *Brassica juncea* perform better than those of *Brassica napus* during production in lower-rainfall marginal growing environments. It shows higher seedling vigour, improved heat and drought tolerance and pod-shatter resistance relative to *B. napus* (Kirk and Oram, 1978; Woods et al., 1991; Burton et al., 1999; Oram et al., 1999). It was also observed that mustard cultivars had more seed and dry matter production than rapeseed under semi-arid conditions (Chauhan and Bhargava, 1984), and better performer than *Brassica campestris* and *B. napus* for seed yield under the conditions of Islamabad, Pakistan (Munir, 1978).

In Pakistan, existing *B. juncea* varieties are low-yielding. There is great potential for improvement of seed yield in this crop, although adequate time is required to develop varieties with higher per unit area seed yield. Specific requirements of a crop regarding climate, soil and cultivation practices are important, but it is mainly the genetic stability of a crop, its yield potential and quality of the marketable product that determines the cultivation and use of a particular oilseed crop (Wittkop et al., 2009). It is required to hybridize present high yielding and widely-adapted cultivars by selecting desirable genotypes in segregating generations to develop varieties with these improved seed yield in Pakistan. Information regarding additive genetic variance, dominance variance,

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environmental component of variation, proportion of positive and negative genes, distribution of genes among the parents, maternal and reciprocal effects, ratio of dominant and recessive genes and average degree of dominance can be obtained through the diallel analysis.

The understanding of the relative contribution of the genetic components that control the variation is of great importance for any improvement in a trait under a breeding program.

In the present study, an attempt was made to derive some information on the various genetic mechanisms which govern the inheritance of various parameters in Indian mustard (*B. juncea* L.) by making diallel crosses. The diallel analysis technique was used to understand the inheritance mechanism of different plant characters to ascertain the genetic basis of variation of various characters. This technique provides information regarding gene action and genetic components of variance to carry out effective selection in segregating generations.

MATERIALS AND METHODS

Parental materials

The experimental material comprised a of total eight promising genotypes of *B. juncea* L. namely S-9, KJ-119, BARD-1, BRS-2, 95102/51, NIFA RAYA, UCD-8/4 and UCD-6/23 obtained from the National Agricultural Research Centre (NARC), Islamabad, Barani Agricultural Research Institute (BARI), Chakwal and Nuclear Institute for Food and Agriculture (NIFA), Peshawar.

Development of F_1 hybrids

Four rows of eight Indian mustard genotypes of 5 m length were sown in the research area of BARI, Chakwal, maintaining plant to plant and row to row distances 30 and 90 cm, respectively during rabi season of 2006 to 2007. Normal agronomic practices were applied in the field. At the flowering, these eight genotypes were crossed in all possible combinations under complete diallel system through hand emasculations and controlled pollinations. Kraft paper bags were used for avoiding contaminations. Pollinations to emasculated florets were repeated once after two days for maximum seed setting.

The seeds of F_1 crosses and selfed parents were sown under a randomized complete block design with three replications in the rabi season of 2007 to 2008 in the field. Row to row distance of 75 cm and plant to plant distance of 25 cm were maintained, respectively. Each row was 5 m long accommodating about 19 plants. Diammonium phosphate (DAP) fertilizer at 75 kg and urea at 60 kg per hectare at the time of sowing was applied to provide the nutrients. The crop was managed to avoid insect pests and irrigation was carried out when it was necessary to avoid drought stress. All other standard agronomic practices were followed as recommended for Indian mustard crop.

Data recoding

The data was recorded on five randomly selected plants of each genotype per replication and then average was calculated for plant height (cm), number of primary branches per plant, number of siliquae per plant, siliqua length (cm), seeds per siliqua, 1000-seed weight (gm) and seed yield per plot (g).

Data analysis and fulfillment of diallel assumptions

The data collected from 64 genotypes for yield attributes were subjected to analysis of variance following Steel and Torrie (1980) to determine the significance of difference among various genotype means. The characters showing significant genotypic differences were further genetically analyzed using Hayman-Jinks diallel analysis model. The validity of genetic information derived by diallel crossing depends upon the fulfillment of certain assumptions (Hayman, 1954a). Purity of parental material was assured when seed was obtained from the sources; it was maintained in a proper way by selfing at the respective research stations and therefore, almost homozygous. Indian mustard behaves cytogenetically as diploid. Multiple allelism might be present at certain loci controlling quantitative traits, but Hayman (1960) reported that it did not disturb measure of dominance seriously. Reciprocal differences were removed by taking the mean of direct and reciprocal crosses for all the traits.

The adequacy of simple additive-dominance model was determined by using two scaling tests – that is the analysis of regression coefficient test and the uniformity of W_r and V_r test (t^2) as described by Singh and Chaudhary (2004). The assumptions of the genetic model were considered adequate if the regression coefficient (b) deviated significantly from zero, but not from unity (Mather and Jinks, 1982). The second test for the adequacy of the additive-dominance model consisted of analysis of variance of ($W_r + V_r$) and ($W_r - V_r$). If dominance is present, the values of ($W_r + V_r$) must change from array to array. If there is non-allelic interaction (epistasis), (Wr-Vr) will vary between arrays. The values of (Wr - Vr) are expected to be constant if additive-dominance model with independent distribution of genes is adequate. The traits qualifying both the tests were considered fully adequate for additive-dominance model. If only one test validated the data set, the model was considered as partially adequate.

Hayman's analysis (additive –dominance model)

By using this model, variance was partitioned into additive (a), non-additive (b), maternal (c) and reciprocal effects other than maternal (d) components. Non-additive component (b) is further divided into b_1, b_2 and b_3. Significant results for component indicated the prevalence of additive gene action, while significance of b revealed presence of dominance effects. Significance of component 'c' indicated the presence of maternal effects and 'd' showed the presence of reciprocal differences other than 'c'. Significant values for b_1 indicated unidirectional dominance, b_2 showed asymmetrical distribution of genes and b_3 pointed out specific type of gene action. Significant value for dominant gene action (b) suggested that further analysis of data was adequate for the estimation of dominance ratio. After proving the adequacy of genetic model, the genetic components of variation were estimated as described by Hayman (1954b).

Graphic analysis

F_1 values were set out in the diallel tables and crosses were arranged in arrays. By plotting covariance (Wr) of each array against its variance (Vr), information on gene action, diversity among parents, presence or absence of epistasis, degree of dominance and distribution of dominant and recessive genes among the parents was obtained. The limiting parabola was

Table 1. Mean squares for analysis of variance of different yield traits in Indian mustard.

SOV	df	Plant height	Number of primary branch	Number of siliquae per plant	Siliqua length	Number of seeds per siliqua	1000-seed weight	Seed yield per plot
Replications	2	3.40	0.63	3634.40	0.02	2.22	0.01	9153.94
Genotypes	63	818.77**	4.85**	17593.76**	2.59**	9.33**	0.54**	176559.50**
Error	126	6.77	0.48	1424.80	0.03	0.86	0.03	20260.21

****,** significant at 1% probability level.

Table 2. Adequacy of the data to additive-dominance model for various yield traits in Indian mustard.

Character	Analysis of variance of array		Joint regression analysis	
	Wr + Vr	Wr - Vr	b_0	b_1
Plant height	160.88**	1.78	2.46*	-0.16
No. of primary branches	4.52**	0.78	3.47*	0.85
No. of siliquae per plant	6.98**	2.12	2.94*	0.91
Siliqua length	133.83**	2.90	2.55*	-0.03
No. of seeds per siliqua	3.09	7.79**	3.51*	0.39
1000-seed weight	5.68**	1.68	4.55**	1.48
Seed yield per plot	8.74**	4.63**	3.78**	0.46

****, * ,** significant at 1 and 5% probability level, respectively.

constructed by plotting Vr (Wr × Vr) points. The different arrays were fitted within the limits of the parabola using the individual variance and covariance as their limiting points. Array nearest to the point of origin possessed most dominant genes, while the array that lay farthest, possessed most recessive genes. The regression line was calculated from the mean of variance (Vr) and the mean of covariance (Wr). The slop and the position of the regression line were fitted to the array points. If the line of a unit slope (b = 1) passed through the origin then complete dominance was indicated. In case, it cuts the axis below the origin, there was over dominance and if it touched the axis above the origin, it indicated partial dominance.

RESULTS

The success of the plant breeder lies in the steady improvement of genetic architecture of crop plant for the synthesis of superior genotypes showing promise of increased production per unit area. To achieve this, knowledge of the genetic mechanism of the control of various parameters is the first pre-requisite. In the present study, an attempt was made to derive some information on the various genetic mechanisms which govern the inheritance of various parameters in Indian mustard (*B. juncea* L.) by making diallel crosses. The diallel analysis technique was used to understand the inheritance mechanism of different plant characters to ascertain the genetic basis of variation of various characters. This technique provided information regarding gene action and genetic components of variance to carry out effective selection in segregating generations.

Analysis of variance and tests of adequacy

The data collected from 64 genotypes (eight parents, 56 F_1 crosses) was subjected to analysis of variance following Steel and Torrie (1980) to determine the significance of difference among various genotypes. All the characters showed significant genotypic differences (Table 1) and therefore further analyzed using Hayman-Jinks diallel analysis model. The adequacy of simple additive-dominance model was determined by using results for two scaling tests- the analysis of regression coefficient test and analysis of variance of Wr + Vr and Wr – Vr, which showed that assumptions of additive-dominance model were considered fully adequate for all the traits except for number of seeds per siliqua for which it was partially adequate but can be further analyzed (Table 2).

Hayman’s analysis of variance and estimation of genetic components

Hayman’s analysis of variance (Table 3) showed the presence of both additive and dominance gene effects in governing all the traits. However, estimates for genetic components of variation (Table 4) indicated that additive effects were more important for seeds per siliqua and 1000-seed weight as value of D was greater than H_1 and H_2, while dominance effects were more prominent for plant height, number of primary branches, number of siliquae per plant, siliqua length and seed yield per plot. Value of H_1 was greater than H_2 indicating frequency of gene

Table 3. Mean squares from Hayman's analysis of variance for various yield attributes in 8 x 8 diallel of Indian mustard.

Source of variation	df	Mean square	Re-tested against 'c'	Re-tested against 'd'	Mean square			Re-tested against 'c'	Re-tested against 'd'	Mean square
		Plant height			No. of primary branches	No. of siliquae per plant	Siliqua length			No. of seeds per siliqua
a	7	2180.5*	4.1*	-	21.12**	79558.2**	6.79**	3.78	-	41.59**
b_1	1	1288.3		6.1*	2.54	7118.0	4.01**		5.50*	7.56
b_2	7	875.5**		4.1**	2.38**	7343.2**	2.70**		3.70**	1.81
b_3	20	1035.8**		4.9**	5.71**	20908.1**	3.23**		4.43**	3.95**
b	28	1004.7**		4.7**	4.77**	17024.4**	3.1**		4.29**	3.55**
c	7	532.4**			1.24	3868.3	1.80**			13.33**
d	21	212.2**			0.76	2273.3	0.73**			4.97**
Blocks	2	3.4			0.63	3634.4	0.02			2.22
B x a	14	5.2			0.51	2160.0	0.04			1.43
B x b_1	2	19.5			0.63	852.9	0.01			0.54
B x b_2	14	8.6			0.51	916.8	0.03			0.52
B x b_3	40	4.5			0.52	1482.9	0.02			0.69
B x b	56	6.1			0.52	1318.9	0.02			0.64
B x c	14	11.5			0.39	1206.2	0.04			0.64
B x d	42	6.7			0.44	1393.9	0.03			1.05
Block interaction	126	6.8			0.48	1424.8	0.03			0.86

Source of variation	df	Re-tested against 'c'	Re-tested against 'd'	Mean square	Re-tested against 'd'	Mean square	Re-tested against 'c'	Re-tested against 'd'
				1000-seed weight		Seed yield per plot		
a	7	3.12	-	3.47**	-	666329.9**	6.1*	-
b_1	1		1.52	0.03	0.34	307007.4		4.1
b_2	7		0.36	0.13	1.55	104815.4**		1.4
b_3	20		0.80	0.32**	3.69**	153274.2**		2.0
b	28		0.71	0.26**	3.04**	146650.0**		1.9
c	7			0.08		108962.4**		
d	21			0.09**		75714.5**		
Blocks	2			0.01		9153.94		
B x a	14			0.03		21721.47		
B x b_1	2			0.04		37440.25		
B x b_2	14			0.03		10952.87		
B x b_3	40			0.02		17627.08		
B x b	56			0.02		16666.15		
B x c	14			0.02		24162.19		
B x d	42			0.03		23264.53		
Block interaction	126			3.47		20260.21		

****, *,** significant at 1 and 5% probability level, respectively.

distribution in the parents was unequal, and it was also supported by the ratio of $H_2/4H_1$ (<25) showing asymmetrical gene distribution at the loci in the parents showing dominance for all the traits. The F value was positive showing the presence of higher number of dominant genes than recessives and it was confirmed by the high value of KD/KR except for seed weight, for which negative F value indicated presence of higher number of recessive genes than dominants.

For all the studied traits, the positive sign of h^2/H_2 indicated that the dominance of genes was directional to the parent with higher value. Significance of h^2 indicated the presence of dominance effects due to heterozygous loci for plant height, siliqua length, number of seeds per siliqua and seed yield. Estimate of narrow sense heritability was high for number of seeds per siliqua and 1000-seed weight, but was low for plant height and siliqua length. Component of variance due to

Table 4. Estimates of genetic components of variation for yield attributes in Indian mustard.

Genetic component	Plant height	Number of primary branch	Number of siliquae per plant	Siliqua length	Number of seed per siliqua	1000-seed weight	Seed yield per plot
D	242.85 ± 51.96*	2.11 ± 0.22*	8149.4 ± 850.7*	0.70 ± 0.15*	5.15 + 0.23*	0.193 ± 0.02*	66915.3 + 7677.6*
H_1	884.13 ± 119.45*	3.44 ± 0.50*	12182.1 ± 1955.5*	2.74 ± 0.35*	2.21 + 0.53*	0.189 ± 0.04*	110160.9 + 1764.6*
H_2	666.50 ± 103.92*	2.94 ± 0.43*	10619.9 ± 1701.3*	2.01 ± 0.31*	1.92 + 0.46*	0.16 ± 0.04*	87723.3 + 15355.1*
F	279.18 ± 122.76*	0.89 ± 0.51	3172.9 ± 2009.8	0.81 ± 0.36*	2.03 + 0.55*	-0.07 ± 0.05	35080.8 + 18141.6
h^2	187.16 ± 69.69*	0.32 ± 0.29	878.4 ± 1141.0	0.58 ± 0.21*	1.01 + 0.31*	0.001 ± 0.26	42574.9 + 10297.8*
E	1.68 ± 17.66	0.12 ± 0.07*	364.8 ± 289.2	0.01 ± 0.05	0.22 + 0.01*	0.01 ± 0.01	5021.7 + 2609.9
$(H_1/D)^{1/2}$	1.91	1.28	1.22	1.97	0.65	0.99	1.28
$H_2/4H_1$	0.19	0.21	0.22	0.19	0.22	0.21	0.20
KD/KR	1.86	1.39	1.38	1.82	1.86	0.70	1.51
h^2/H_2	0.28	0.11	0.08	0.28	0.52	0.01	0.49
h^2_{ns}	0.35	0.50	0.52	0.35	0.71	0.75	0.50

*Significant value of variance (if it exceeds 1.96 after dividing by its standard error). Environmental variance (E); additive variance (D); variation due to dominant effect of genes (H_1); variation due to dominant effect of gene correlated with gene distribution (H_2); over all dominant effect of heterozygous loci (h^2); relative frequency of dominant to recessive alleles (F); mean degree of dominance (H_1 / $D^{1/2}$); proportion of genes with positive and negative effect in the parents (H_2 / $4H_1$); proportion of dominant and recessive genes in the parents (KD/KR); the number of groups of genes which control the character and exhibit dominance (h^2/H_2); narrow- sense heritability ($h^2{}_n$).

environment was significant only for number of primary branches and number of seeds per siliqua, thus indicating involvement of environmental effects in the expression of these traits. Degree of dominance $(H_1/D)^{1/2}$ was smaller than 1 for number of seeds per siliqua and 1000-seed weight indicating partial dominance, and graphical analysis of data (Figures 1 to 7) also showed that the regression line intercepted traits. Meanwhile, over dominance was observed for the rest of the traits.

High values for narrow sense heritability for some traits indicated the good potential of genotypes for selection for these traits. The distribution of array points on the regression line indicated that genotype UCD-6/23 being closed to the point of origin, contained maximum dominant genes for number of seeds per siliqua, 1000-seed weight and seed yield. Genotype 95102/51 possessed maximum dominant genes for siliqua length and plant height. KJ-119 and BARD-I contained maximum dominant genes for number of primary branches and number of siliqua per plant, while UCD-8/4 possessed maximum recessives for plant height and could be further utilized for developing short statured genotypes to avoid lodging problem.

DISCUSSION

The success of the plant breeder lies in the steady improvement of genetic architecture of crop plant for the synthesis of superior genotypes showing promise of increased production per unit area. To achieve this, knowledge of the genetic mechanism of the control of various parameters is the first pre-requisite. Singh et al. (2008) observed that both the D and H components were important in genetic control of plant height. Thakral et al. (2000) found over dominance for all the yield related traits. Shweta et al. (2007b) also reported the presence of over-dominance for number of primary branches in F_2 generation, while Shweta et al. (2007a) identified predominance of non-additive gene action. All these evidences therefore support the present results. However, Rai et al. (2005) contradicted by reporting partial dominance for number of primary branches, and this contradiction might be due to the difference in environmental conditions under which experiments were conducted.

On the other hand, Rai et al. (2005) supported the present findings by reporting over-dominance and low estimates for narrow-sense heritability for siliqua length, while Shweta et al. (2007a) reported that dominant genes were more frequent than recessive ones and found predominance of non-additive gene action for plant height, seed yield and its components. Over dominance with

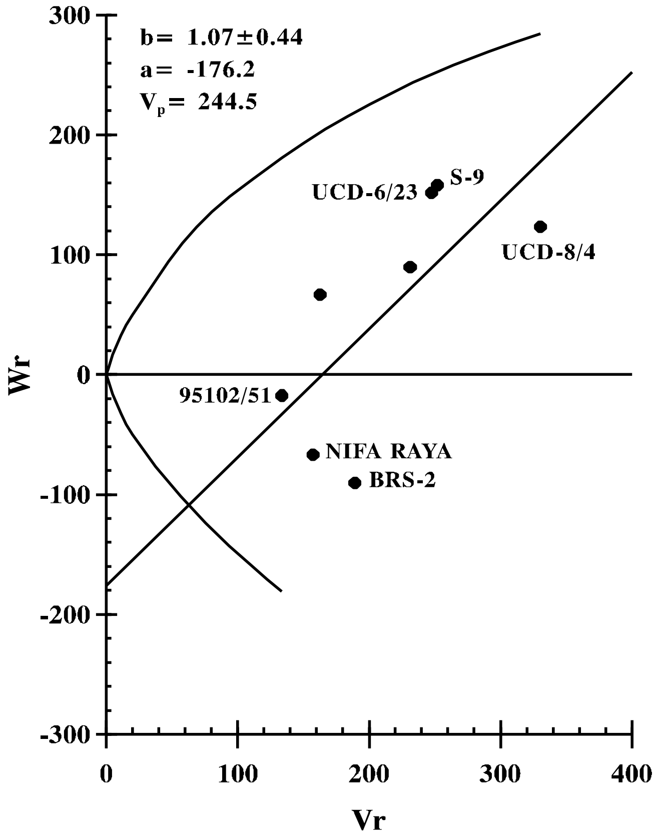

Figure 1. Vr/Wr graph for plants' height.

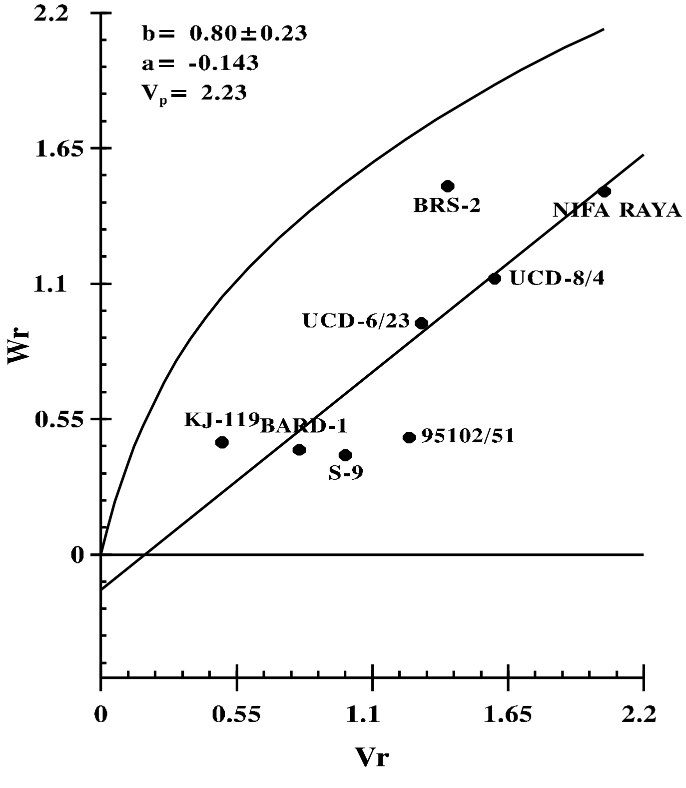

Figure 2. Vr/Wr graph for number of primary branches/plant.

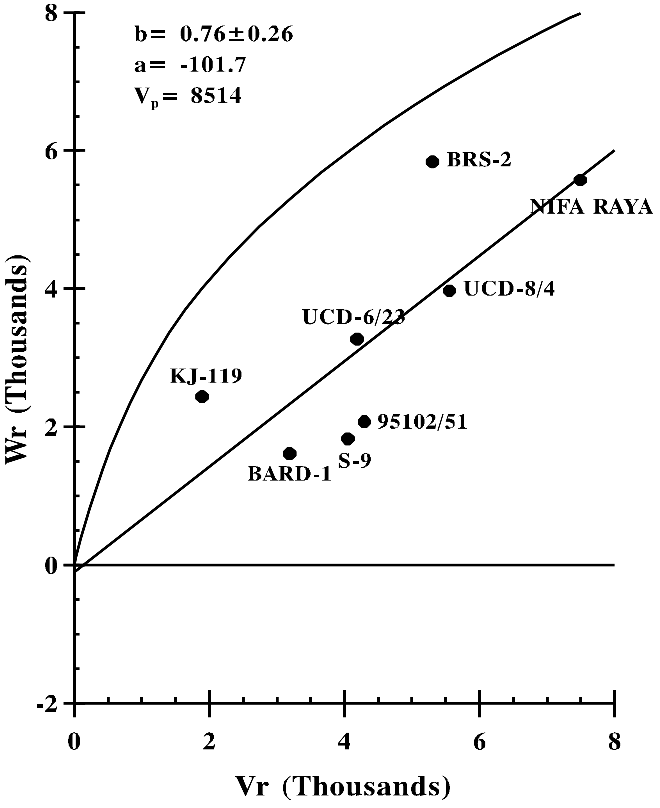

Figure 3. Vr/Wr graph for number of siliqua/plant.

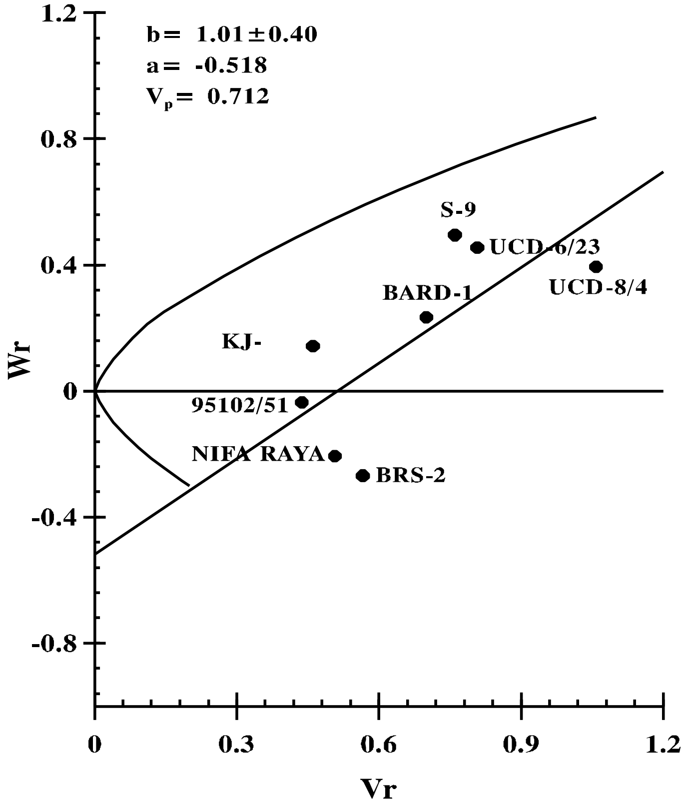

Figure 4. Vr/Wr graph for siliqua length.

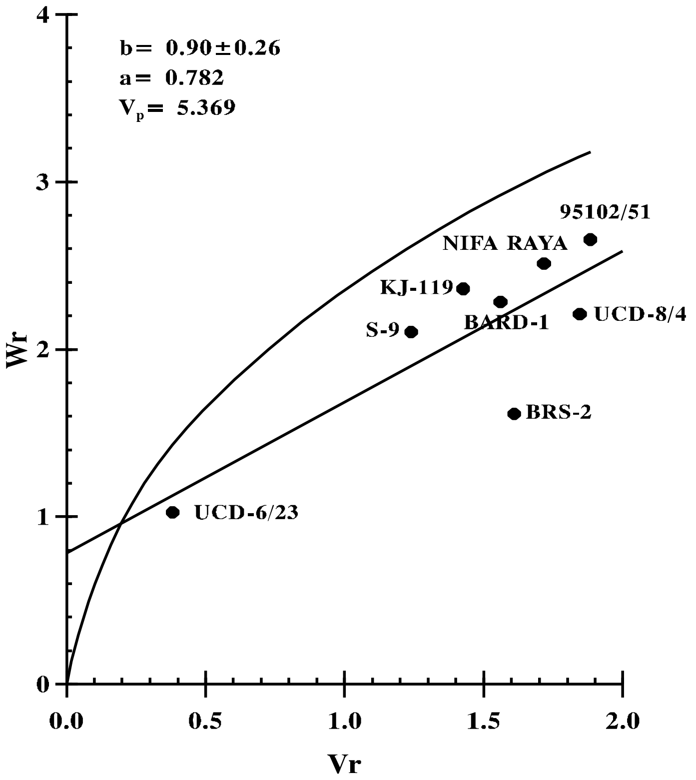

Figure 5. Vr/Wr graph for number of seeds/siliqua.

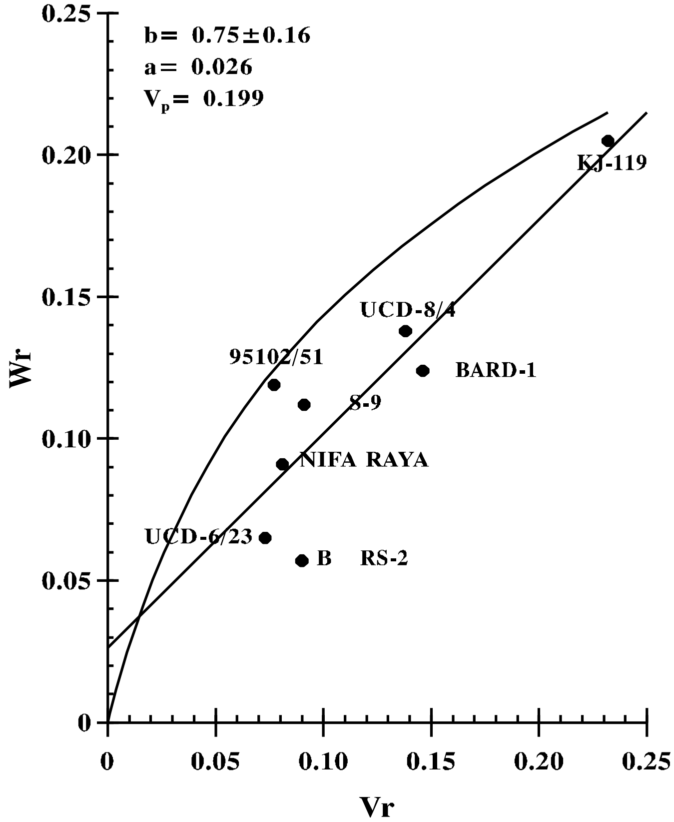

Figure 6. Vr/Wr graph for 1000-seed weight.

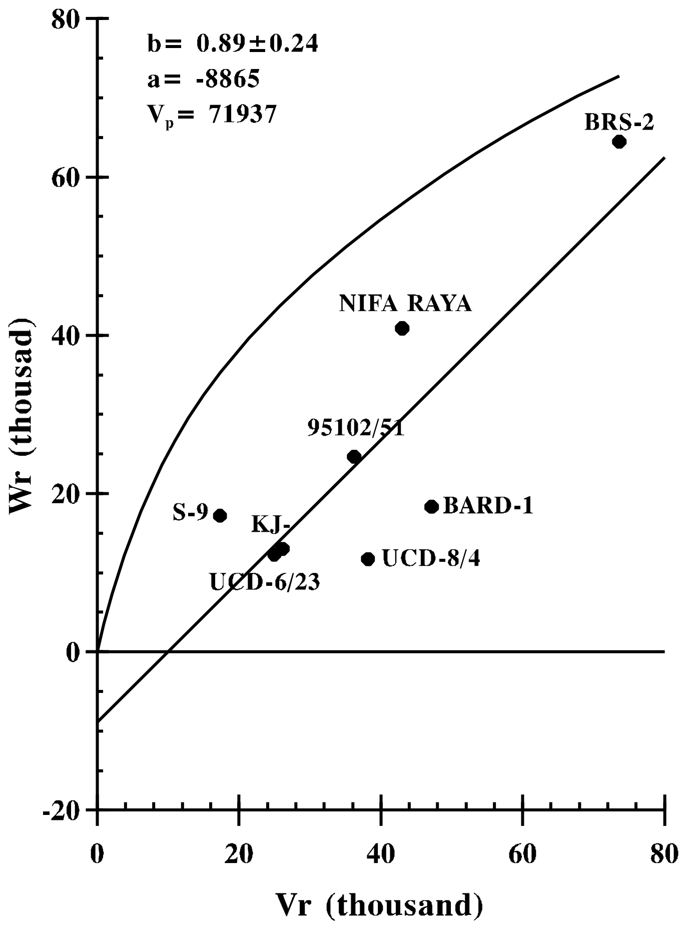

Figure 7. Vr/Wr graph for seed yield per plot.

non-additive gene action was reported by Shweta et al. (2007b) for number of siliquae on main raceme. Due to more prominent role of non-additive effects and presence of over-dominance, it was suggested that selection might be delayed up to late segregating generations for all the traits except for 1000-seed weight and seeds per siliqua. Since presence of over-dominance was detected in plant height, number of primary branches per plant, number of siliquae per plant, siliqua length and seed yield per plot from the present investigations, non-additive gene action might be due to over-dominance and not due to epistasis.

Rai et al. (2005) found over-dominance for 1000-seed weight and it was at variance to the present findings. However, Thakral et al. (2000) described that additive component was more important for 1000-seed weight and similar result was observed in the present study. The contradiction might be due to the differences in genetic material used for studies and not due to environmental factors as variance due to environment was non-significant in the present study, thus indicating the absence of environmental effects in controlling this trait. Singh et al. (2008) indicated that both the D and H components were important in genetic control of the number of seeds per siliqua. Rai et al. (2005) also found prevalence of partial dominance along with high estimates of narrow-sense heritability for seeds per siliqua and thus our present results were in agreement with previous findings. Some differences in findings were natural as results indicated that component of variance due to environment was significant for seeds per siliqua.

Conclusion

From the results of the present study, it is suggested that due to more prominent role of non-additive effects and presence of over-dominance, selection could be delayed up to late segregating generations for all the traits except for 1000-seed weight and seeds per siliqua. Also, due to more effective role of additive effects and absence of over-dominance, selection could be effective in early segregating generations only for seeds per siliqua and 1000-seed weight. Information regarding maximum and minimum collection of dominant and recessive genes in different genotypes for a specific trait might be of significant value for future utilization as donor parents. Thus, the present investigations contributes significantly to ascertain genetic control mechanism of various yield-related attributes to accelerate the selection and breeding program of high yielding Indian mustard genotypes in Pakistan.

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