Research Article

Genetic analysis of yield and yield related attributes in *Brassica napus*

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ABSTRACT

Diallel analysis in Rapeseed (*Brassica napus* L.) was carried out during 2011-2012 at The University of Agriculture, Peshawar to estimate the pattern of inheritance and heritability for important traits. During 2010-2011 four contrasting genotypes of *Brassica napus*. viz. G2, G4, G6 and G9 were crossed in a diallel manner and in the following season (2011-2012) all the F_1 hybrids along with parents were evaluated under field condition in a randomized complete block design. Highly significant ($P \leq 0.01$) differences were observed for plant height, primary branches plant⁻¹, seeds pod⁻¹, pods plant⁻¹, weight of 1000 seed, seed weight plant⁻¹. Additive-dominance model was fully adequate for plant height, primary branches plant⁻¹, pods plant⁻¹, seeds pod⁻¹, whereas for the rest of the traits it was partially adequate. Diallel analysis showed significant additive (a) and dominance (b) variances for all parameters. Genetic parameters estimation showed significant and higher magnitude of dominance component for all the studied traits. Graphical analysis showed overdominance for all of the parameters. The value of average degree of dominance for plant height (1.858), primary branches plant⁻¹ (4.355), pods plant⁻¹ (3.704), seeds pod⁻¹ (2.417), 1000 seed weight (3.995) and seed weight plant⁻¹ (1.852) also indicated the presence of overdominance gene action controlling these yield attributes, as it was greater than one. Low narrow (0.16-0.31) and broad (0.81-0.96) sense heritabilities were estimated for all the studied parameters, suggesting the low value of additive gene action and genetic potential for the improvement of such traits through selection in later generations.

Key words: Diallel analysis, Inheritance studies, Rapeseed.

Introduction

In Pakistan, shortage of edible oil is a great problem for many years due to the absence of high yielding varieties. Local production fulfill only 23% needs while the rest is imported from foreign countries [1]. This dependency on foreign import is increasing by 5% each year due to increase in population and per capita consumption as the standard of living rises [2]. Pakistan has made tremendous progress in many field crops such as wheat, cotton, etc, but not such satisfactory progress has been achieved in oil crops, as our country is facing a leviathan problem of edible oil shortage. The basic aim of all oil breeding programme is to boost yield in terms of oil Valuable decisions should be taken to enhance the yielding tendency of oilseeds crops by using genetically manipulated cultivars through intensive and extensive agriculture. Considering the edible oil problems and

needs, improvement and breeding requires serious work. The use of oilseed crops belonging to genus *Brassica* can play a significant role in fulfilling the production gap. Collectively *B. napus*, *B. rapa*, *B. campestris* and *B. jancea* are the third most important source of edible oil in the world after palm and soybean oil. Improvement can be made successful by evaluation of genetic behavior and producing genetic diversity in *B. napus*. According to Wang [3], about 2.3-2.5% improvement in seed produce in *B. napus* increases the oil content by one percent, so little efforts are needed to increase the oil yield Diallel is a Greek term used for all possible crosses of a group of males and females. According to Hayman [4, 5] diallel is the set of all possible crosses between many genotypes i.e. they may be individuals, clones, homozygous lines etc. The diallel cross method is a stable and systematic experiment to investigate

continuous variation. Genetic information of parental population is determined in early generation i.e. in 1st filial generation, so it saves time of breeder. Different methods are used for the analysis of data from a diallel cross [4-7]. The most commonly used diallel methods are Griffing and Hayman's approaches. The present study was conducted to describe the mechanism of gene action responsible for the expression and development of these traits in *Brassica napus* L. Such information would be helpful for future breeding programmes.

Material and Methods

Four contrasting *Brassica napus* genotypes i.e. G2, G4, G6 and G9 were crossed during growing season 2010-2011 in a full diallel fashion at experimental farm of Department of Plant Breeding and Genetics. For crossing 20-25 flowers of each plant of each genotype were selected, emasculated and covered with butter bags to control the flow of other plants pollens. At proper time when ovaries became ready to accept pollens, their stigmas were hand pollinated by shedding pollens of the desired genotype/parent. To obtain sufficient amount of seeds, at least 20 flowers were artificially pollinated for each direct and reciprocal cross. Separate harvesting and threshing was done for each cross at maturity.

During year-II (2011-2012), a randomized complete block design was used for the evaluation of all the 12 first filial generations ($G9 \times G2$, $G2 \times G9$, $G6 \times G2$, $G2 \times G6$, $G4 \times G2$, $G2 \times G4$, $G9 \times G6$, $G6 \times G9$, $G9 \times G4$, $G4 \times G9$, $G6 \times G4$, $G4 \times G6$) along with four parents (G2, G4, G6, G9) in three replications. There were four rows per genotype/cross of 5 meter length. The distance between rows was kept 30 cm. To get valid and conclusive results and reduce experimental error, cultural practices were performed uniformly for all genotypes.

Data regarding plant height (cm), primary branches plant⁻¹ (no), pods plant⁻¹ (no), seeds pod⁻¹ (no), 1000 seed weight (g) and seed weight plant⁻¹ (g) were recorded on all F₁ hybrids along with their parents. The data were analyzed following Steel and Torrie [8], analysis of variance (ANOVA) for null hypothesis of equality of means.

Additive-dominance model of Hayman [4, 5] is widely used technique to study the basis of genetic variation in early generations i.e. in F₁ and F₂, as well as nature and magnitude of genetic behavior. In this method total sum of square is portioned into different components such as a (additive), b (dominance/non-additive), c (maternal) and d (non-maternal reciprocal differences). The 'b' component is further divided into b₁, b₂ and b₃.

Significance of 'a' component means additive effects of gene and of item 'b' shows dominance effects of gene. Significance of b₁, b₂ and b₃ shows directional

dominance, asymmetrical gene distribution and specific effects of genes respectively, whereas 'c' shows presence of maternal effect and 'd' shows non-maternal reciprocal differences. After significance of 'b' component graphical analysis approach using Vr (variance) and Wr (covariance) is valid.

Testing Adequacy of the Additive-Dominance Model

To prove the additive-dominance adequate for the means of the studied parameter, the data were subjected to two tests. One test was t² test for the uniformity of Wr and Vr and the other test was the analysis of regression coefficient. For the fulfillment of all assumptions of diallel analysis, the result of the t² for the uniformity of Wr and Vr should be constant over arrays, whereas following Mather and Jinks [9] the analysis of regression coefficient for all parameters under study should be different significantly from zero, but not from unity.

Genetic Parameters

The genetic parameters such as D (additive variance), H₁ and H₂ (estimate of dominance and dominance $\times$ dominance interaction respectively), $(H_1/D)^{1/2}$ (average degree of dominance), $H_2/4H_1$ (the proportion of genes with positive and negative effects in the parents), F (dominant to recessive alleles frequency in parents), h² (over all dominance effect due to heterozygous loci), Dominant to recessive genes ratio in parents $(4DH_1)^{1/2} + F/(4DH_1)^{1/2} - F$, E (environmental effect), broad and narrow sense heritabilities were computed.

Results and Discussion

In this study the data on plant height, primary branches plant⁻¹, pods plant⁻¹, seeds pod⁻¹, 1000 seed weight and seed weight plant⁻¹ were analyzed in two steps. In the first step following Steel and Torrie [8], analysis of variance (ANOVA) was performed for null hypothesis of equality of means. Highly significant differences ($P \leq 0.01$) for all the studied traits were observed (Table-1). Then diallel analysis for different types of gene actions, broad and narrow sense heritability were carried out according to Hayman [4] for these traits. The results and discussion of the stated parameters are given below.

Plant height (cm)

Genotypes mean squares were highly significant (Table-1) for plant height therefore, diallel analysis was carried out. The values of 'a' and 'b' which represents additive and dominance gene effect, respectively were found highly significant (Table-2), indicating the effectiveness of both additive and dominance gene action for plant height.

The proportion of 'a' (12.52) was lower than 'b' (42.33) showing the greater importance of dominance for this trait. Similarly, Rao and Gulati [10] also

reported significant and higher magnitude dominant/non-additive component in plant height. Biranvand et al., [11] reported high and significant value of additive variance (a) component for this trait in chickpea. Both b_1 and b_2 (components of dominance which shows directional dominance deviation of genes and asymmetrical gene distribution among the parents, respectively) were significant, whereas the b_3 component (specific genes effect) was non-significant. The b_1 component (204.16) was greater than b_2 (15.90) and b_3 (1.07) indicating the greater role of directional dominance. Non-significance differences were found (Table-2) for both c (maternal effect) and d (reciprocal effect) (2.69 and 0.43, respectively) showing the independence of this trait from both maternal and reciprocal effects.

To prove the adequacy of additive-dominance model, as suggested by Mather and Jinks [9] two tests i.e. analysis of regression coefficient and uniformity of W_r and V_r (Table-3) were used. These tests suggested that additive dominance model is adequate. Table-4 shows the estimates of genetic components for plant height. Significant values were determined for both D (499.41) and H ($H_1=1724.13$, $H_2=1584.01$) indicating that the plant height was controlled by both additive and dominance gene effect. Average degree of dominance value (1.858) was greater than unity, indicating the presence of dominance. Farshadfar et al. [12] also reported both additive and dominant gene action in *B. napus* whereas; Sabaghnia et al. [13] reported the importance of dominance genetic variance for the expression of plant height. Inequality of H_1 (1724.13) and H_2 (1584.01) showed the unequal frequency of both positive and negative alleles. Singh and Chaudhry [14] stated that genes will be equally distributed when the ratio of $H_2/4H_1$ is 0.25 and for this trait it was (0.23) which is less than 0.25. F value (531.75), which indicates dominant with recessive allele's frequency in parents, was significant and positive showing the higher proportion of dominant alleles. Dominant to recessive genes ratio $(4DH_1)^{1/2} + F/(4DH_1)^{1/2} - F$ was 1.803, showing greater proportion and importance of dominant genes. The h^2 which measures overall dominant effect for heterozygous loci was significant (2916.96), showing its role in the expression of the plant height. The environmental component E effect (19.13) was also significant playing a role in the expression of this trait. The intercept of covariance (W_r) by variance (V_r) regression line was negative (Fig-1) for plant height, which indicated overdominance gene action and in this case H_1 was also greater than D, which supports overdominance. Farshadfar et al. [12] also reported similar results of overdominance type of

dominance for plant height in *B. napus*. High (0.95) broad sense heritability and low narrow (0.11) sense heritability (Table-4) was observed for plant height, showing higher contribution of dominance genetic variation as compared to additive genetic variation. Broad sense heritability estimates additive variation, dominant variation and variation which results from the interaction of both these, while narrow sense heritability estimates only additive variation. So for plant height higher proportion of heritable variation was of dominance nature. Rao and Gulati [10] also reported high broad sense heritability and low narrow sense heritability for the stated trait in *B. juncea*. Ali et al. [15] also reported similar result of high broad sense heritability for this trait in winter type rapeseed varieties.

Primary branches plant⁻¹

Since genotypic mean square was highly significant (Table-1) therefore, diallel analysis was carried out for primary branches plant⁻¹. The values of 'a' and 'b' were found highly significant for primary branches plant⁻¹ (Table-2) showing importance of additive and dominant gene action for primary branches plant⁻¹. The proportion of 'a' (10.81) was lower than 'b' (18.46) showing the lower proportion of 'a' to represent variation. Radovan et al. [16] reported that dominance has a greater role for primary branches than additive component. Meena et al. [17] reported the importance of non-additive gene action in chickpea, whereas Bicer and Sakar [18] found importance of both these types of gene action for primary branches in chickpea. Overall the component of dominance was highly significant and larger showing the dominance importance. b_1 component (91.50) which shows directional dominance deviation of genes was found highly significant and was responsible for a greater proportion of dominance than b_2 (4.46) and b_3 (2.96). The b_2 component of dominance was found significant and represented asymmetrical distribution of genes. Non-significance of the component b_3 indicated absence of specific genes effect. Non-significant values for both the c and d (0.30 and 0.68 respectively) were found (Table-2), that's why 'a' and 'b' components retesting was not done.

Analysis of regression coefficient and uniformity of W_r and V_r (Table-3) were used to prove the additive-dominance model to be adequate. The tests suggested this model to be adequate.

Table-4 shows the estimates of genetic components for primary branches plant⁻¹. Non-significant value of D (1.53) and significant value of H ($H_1=29.05$, $H_2=27.78$) was determined for primary branches plant⁻¹ showing more important role of dominance gene effects. Value of average degree of dominance (2.97) was found higher than one, indicating that for

this trait dominance is present. Radovan et al. [16] also reported higher and significant H component and non-significant value of D component for primary branches. Inequality of H_1 (29.05) and H_2 (27.78) showed presence of both positive and negative alleles with different frequencies. F value, was estimated non-significant and negative (-0.99), indicating the greater frequency of recessive genes. Ratio of dominant and recessive genes value (0.86) also supports this, as it is less than one. h^2 (53.87) value was significant, showing its role in the expression of the trait of primary branches plant^{-1} . The environmental component E effect (0.79) was also found significant to indicate its role in the expression of this trait.

Negative intercept of covariance (Wr) by variance (Vr) regression line (Fig-2) was observed, which indicated overdominance gene action and in this case H_1 was also greater than D which supports overdominance.

Low narrow sense heritability (0.19) and high (0.91) broad sense heritability (Table-4) was observed for primary branches plant^{-1} showed higher contribution of dominance genetic variation to this trait as compared to additive genetic variation. Rao and Gulati [10] reported low to medium narrow sense heritability for primary branches plant^{-1} . Sing et al. [19] reported similar results of high broad sense heritability in *B. campestris*. Deb and Khaleque [20] also found low narrow sense heritability and low broad sense heritability for primary branches plant^{-1} in chickpea.

Pods plant^{-1}

Genotypic mean square was highly significant (Table-1) for pods plant^{-1} therefore, diallel analysis was carried out. Highly significant results were found for a, b, b_1 , b_2 and b_3 (Table-2) suggesting the role of both additive and dominant types of gene actions for pods plant^{-1} . Farshadfar et al. [12] and Rameah et al. [21] also reported the role of both types of gene actions *B. napus*. The proportion of 'a' was lower than 'b' showing the lower proportion of 'a' to cause variation. In total dominance component was highly significant and larger showing the importance of dominance. The b_1 (42.85) component was responsible for a greater proportion of dominance than b_2 (19.51) and b_3 (5.78). Both b_2 and b_3 dominance components were also found highly significant, representing the absence of symmetry of genes and presence of specific genes effect respectively. Non-significant values were found for both c and d (1.02 and 1.49 respectively) whereas; Rameah et al. [21] reported significant maternal effect for pods plant^{-1} in *B. napus*.

To prove the additive-dominance model to be adequate, analysis of regression coefficient and

uniformity of Wr and Vr (Table-3) were used which suggested this model to be adequate.

Table-4 shows the estimates of genetic components for pods plant^{-1} . Non significant value of D (31886.36) and significant value of H ($H_1=437368.60$, $H_2=348443.60$) was determined for pods plant^{-1} showing more important role of dominance gene effects. Value of average degree of dominance (1.858) was found greater than one, which indicated the presence of dominance for this trait. Rao & Gulati [10] and Khan & Khan. [22] also noticed similar results in *B. juncea* and *B. napus* respectively. As per their findings, non-additive genetic action is more effective for yield contributing traits. Values of H_1 and H_2 were different. Inequality of H_1 and H_2 showed the presence of unequal frequencies of both positive and negative alleles. Non-significant value of F (531.75) was observed. Dominant to recessive genes value $(4DH_1)^{1/2} + F/(4DH_1)^{1/2} - F$ was 1.32, showing the presence of more dominant genes than recessive in parents for this trait. Rahman et al. [23] also noticed higher number of dominant genes in toria. The h^2 value (2916.96) was significant, showing its role in the expression of pods plant^{-1} . The environmental component E effect (19.13) was significant having a role in for the expression of pods plant^{-1} .

Negative intercept of covariance (Wr) by variance (Vr) regression line (Fig-3) was observed, which showed overdominance gene action and in this case H_1 (437368.60) was also greater than D (31886.36) which supports overdominance.

Lower narrow sense heritability (0.31) and high (0.93) broad sense heritability (Table-4) observed for pods plant^{-1} , showing higher contribution of dominance genetic variation as compared to additive genetic variation for this trait. So for pods plant^{-1} higher proportion of heritable variation was of dominance nature. Khan and Khan. [22] reported medium narrow sense heritability for pods plant^{-1} in *B. napus*, whereas Tahir et al. [24] and Mahmood et al. [25] reported high broad sense heritability for seeds pod^{-1} in canola and mustard respectively.

Seeds pod^{-1}

As genotypic mean square was highly significant (Table-1), so diallel analysis was carried out seeds pod^{-1} . As a result 'a' (12.0) and 'b' (14.92) were found highly significant for seeds pod^{-1} (Table-2), showing the importance of both additive and dominance gene action to control the stated trait in these genotypes of *B. napus*. Farshadfar et al. [12] and Rahman et al [23] also reported the role of both additive and dominant gene action for seeds pod^{-1} in *B. napus* and toria respectively. The proportion of 'a' was lower than 'b' showing the lower share of 'a' in the variation. Rahman et al [23] also reported

significant and higher value of 'b' component for seeds pod^{-1} in toria. Moreover they stated that dominance effect is more effective than additive effect. Overall dominance component was larger and highly significant for seeds pod^{-1} showing the importance of dominance gene effects. The b_1 (71.76) component was found highly significant and was responsible for a greater proportion of dominance than b_2 (3.72) and b_3 (3.31). The b_2 component of dominance which was found significant represented the absence of symmetry of genes and non-significance of the component b_3 showed the absence of specific genes effect. Values for both 'c' and 'd' (0.70 and 0.01 respectively) were non-significant therefore retesting was not needed. Rameah et al. [21] reported significant maternal effect for this trait in *B. napus*.

To prove the additive-dominance model to be adequate, analysis of regression coefficient and uniformity of W_r and V_r (Table-3) tests were performed. The findings suggested this model to be adequate.

Genetic components estimate are given in Table-4. The D component value (9.84) was non-significant and H value was significant for the trait of seeds pod^{-1} showing the more effective role of dominance gene effects for this trait in these genotypes. Value of average degree of dominance (2.417) was found greater than one, which indicated dominance presence for this trait. Inequality of H_1 (57.47) and H_2 (55.04) showed the unequal frequencies of both positive and negative alleles. Non-significant value of F (1.69) was observed. Dominant to recessive genes ratio $(4DH_1)^{1/2} + F/(4DH_1)^{1/2} - F$ value was 1.07, showing that more dominant genes are present than recessive in parents. Rahman et al. [23] reported contrasting result of higher number of recessive genes for this trait, i.e. the importance of recessive genes. The h^2 value was found significant for the trait of seeds pod^{-1} , showing its role in the expression of the trait of seeds pod^{-1} . The environmental component E effect (1.97) was also significant to show its role for the determination of this trait. Junsheng et al. [26] also reported significant role of environment in the expression of seeds pod^{-1} in rapeseed.

Negative intercept of covariance (W_r) by variance (V_r) regression line (Fig-4) was observed, which indicated overdominance gene action and in this case H_1 was also greater than D, which supports overdominance. Farshadfar et al. [12] also reported dominance gene action for this trait, but of partial dominance nature.

Low (0.25) narrow sense heritability and high (0.91) broad sense heritability (Table-4) was found for seeds pod^{-1} which indicated that greater proportion of

genetic variation for this trait was of dominance nature. Khan and Khan. [22] also reported low narrow sense heritability for this trait in *B. napus*, while Rao and Gulati [10] reported medium narrow sense heritability estimation in *B. juncea*. High broad sense heritability was reported by Fahimullah et al. [27] in *B. napus*.

1000 Seed weight

Genotypic mean square was highly significant (Table-1) for 1000-seed weight therefore, diallel analysis was carried out. As a result 'a' (4.30) and 'b' (7.80) were found significant and highly significant for 1000 seeds weight (Table-2) showing the importance of both additive and dominance gene action to control this trait. Similar results of both additive and dominant gene action for this trait in *B. napus* and toria respectively were observed by Farshadfar et al. [12] and Rahman et al. [23]. The proportion of 'a' was lower than 'b' showing the lower proportion of 'a' to represent variation. As per Junsheng et al. [26] majority of plant traits in rapeseed are controlled by both additive and dominance genes but both are not equal in effect. Overall dominance component was larger and highly significant for seeds pod^{-1} , which indicated the importance of dominance gene effects for this trait. Rahman et al. [23] also reported significant and higher value of 'b' component in toria. Moreover they also stated that dominance effect is more effective than additive for 1000 seed weight. The b_1 (5.50) component was highly significant and was responsible for a lower proportion of dominance than b_2 (13.18) and higher than b_3 (0.89). The b_2 component of dominance was highly significant indicating the absence of symmetry of genes and non-significance of the b_3 component showed the absence of specific genes effect. Values for both 'c' and 'd' (0.21 and 0.30 respectively) were non-significant. Rameah et al. [21] reported significant maternal effect for 1000-seed weight in *B. napus*.

To prove the additive-dominance model to be adequate two tests were used. Uniformity of W_r and V_r invalidated the additive-dominance model but the result of regression analysis suggested this model to be adequate, so we considered it partially adequate (Table-3).

Estimates of genetic components are given in table-4. The D component value (0.11) was found non-significant and H component value was found

Fig 1. W_r/V_r graph for plant height. 1, 2, 3 and 4 represent parental genotypes

Fig 2. W_r/V_r graph for primary branches plant^{-1} . 1, 2, 3 and 4 represent parental genotypes

Fig 3. W_r/V_r graph for pods plant⁻¹. 1, 2, 3 and 4 represent parental genotypes

Fig 4. W_r/V_r graph for seeds pod-1. 1, 2, 3 and 4 represent parental genotypes.

Fig 5. W_r/V_r graph for 1000 seed weight (g). 1, 2, 3 and 4 represent parental genotypes.

Fig 6. W_r/V_r graph for seed weight plant-1 (g). 1, 2, 3 and 4 represent parental genotypes.

Table 1. Mean squares for various parameters.

Character	Replication d.f=2	Genotype d.f=15	Error d.f=30
Plant height	191.404	1141.496**	55.577
Primary branches plant ⁻¹	2.075	24.024**	2.036
Pods plant ⁻¹	10726.0	342416.4**	26362.2
Seeds pod ⁻¹	11.271	51.707**	6.053
1000 seed weight	0.234	1.115**	0.273
Seed weight plant ⁻¹	816.076	912.549**	73.859

Table 2. Analyses of variance for various parameters in a 4 × 4 diallel cross of *Brassica napus* L.

Source of variation	df	Plant height	Primary branches plant ⁻¹	Pods plant ⁻¹	Seeds pod ⁻¹	1000 seed weight	Seed weight plant ⁻¹
A	3	12.52**	10.81**	19.29**	12**	4.30**	20.19**
B	6	42.33**	18.46**	18.82**	14.92**	7.80**	20.46**
b ₁	1	204.16**	91.50**	42.85**	71.76**	5.50**	99.57**
b ₂	3	15.90**	4.46*	19.51**	3.72*	13.18*	2.61ns
b ₃	2	1.07ns	2.94ns	5.78**	3.31ns	0.89ns	7.68**
C	3	2.69ns	0.30ns	1.02ns	0.70ns	0.21ns	0.10ns
D	3	0.43ns	0.68ns	1.49ns	0.01ns	0.30ns	0.57ns

Table 3. Tests for additive-dominance model to be adequate for 4×4 diallel crosses in *B.napus* L.

Parameters	Tests for adequacy of additive-dominance		
Parameters	Regression analysis b=0 b=1	uniformity of Wr and Vr	Remarks
Plant height	** NS	NS	Additive-dominance model was fully adequate.
Primary branches plant ⁻¹	** NS	NS	Additive-dominance model was fully adequate.
Pods plant ⁻¹	** NS	NS	Additive-dominance model was fully adequate.
Seeds pod ⁻¹	* NS	NS	Additive-dominance model was fully adequate.
1000 seeds weight	* NS	*	Additive-dominance model was partially adequate.
Seed weight plant ⁻¹	NS NS	NS	Additive-dominance model was partially adequate.

Table 4. Estimates of genetic components of various parameters in a 4 × 4 diallel cross of *Brassica napus* L.

Source of variation	Plant height	Primary branches plant ⁻¹	Pods plant ⁻¹	Seeds pod ⁻¹	1000 seed weight	Seed weight plant ⁻¹
D	499.41* ± 113.83	1.53 ^{ns} ± 1.76	31886.36 ^{ns} ± 25493.21	9.84 ^{ns} ± 5.82	0.11 ^{ns} ± 0.18	284.99* ± 102.36
H1	1724.13* ± 230.67	29.05* ± 5.95	437368.60* ± 91215.53	57.47* ± 13.54	1.79* ± 0.59	977.94* ± 188.46
H2	1584.01* ± 207.28	27.78* ± 5.57	348443.60* ± 71369.51	55.04* ± 12.48	1.25* ± 0.42	961.23* ± 179.30
F	531.75* ± 131.70	-0.99 ^{ns} ± 1.96	32962.05 ^{ns} ± 44498.66	1.69 ^{ns} ± 5.97	0.52 ^{ns} ± 0.36	68.56 ^{ns} ± 89.10
h2	2916.96* ± 415.05	53.87* ± 11.59	306648.30* ± 96509.63	104.63* ± 25.21	0.32 ^{ns} ± 0.35	1822.47* ± 359.16
E	19.13* ± 4.81	0.79* ± 0.21	9740.04* ± 2390.12	1.97* ± 0.49	0.09* ± 0.02	24.62* ± 6.27
(H1/D) ^{1/2}	1.858	4.355	3.704	2.417	3.995	1.852
H2/4H1	0.23	0.24	0.2	0.24	0.17	0.25
$\frac{(4DH1)^{1/2}+F}{(4DH1)^{1/2}-F}$	1.803	0.46	1.32	1.07	3.83	1.14
Heritability(ns)	0.115	0.197	0.312	0.252	0.147	0.306
Heritability(bs)	0.959	0.918	0.931	0.906	0.807	0.935

^{ns} shows non-significant.

* Value is significant, when after division by its standard error, exceeds 1.96.

significant showing the high important role of dominance gene effects for this trait of weight of 1000 seeds in these genotypes. Average degree of dominance value (3.995) was found greater than one which indicated the presence of dominance for this trait. Inequality of H_1 (1.79) and H_2 (1.25) explained the presence of unequal frequencies of both positive and negative alleles. F value (0.52) was non-significant. Dominant to recessive genes ratio was 3.83, which resulted that more dominant genes are present than recessive in parents. Rahman et al. [23] also reported higher number of dominant genes in toria for the mentioned trait, i.e the importance of dominant genes. The h^2 value (0.32) was non-significant showing its role absent in the expression of the trait of 1000 seed weight. The environmental component E effect value (0.09) was also found significant to indicate its role in the expression of this trait. Junsheng et al. [26] also reported significant result of environment in the expression of 1000 seed weight in rapeseed.

Negative intercept of covariance (Wr) by variance (Vr) regression line (Fig-5) indicated overdominance gene action and in this case H_1 (1.79) was greater than D (0.11) which also supports overdominance. Graphical evaluation of Farshadfar et al. [12] findings in *B. napus* also proved that overdominance is effective for 1000-seeds weight.

The estimates of narrow sense heritability were low (0.15) and broad sense were high (0.81) (Table-4) indicating that greater proportion of genetic variation for 1000 seed weight was of dominance nature. Khan and Khan. [22] also reported low narrow sense heritability for 1000 seed weight. Rao and Gulati [10] reported medium to high narrow sense heritability for weight of 1000 seeds in *B. juncea*. Fahimullah et al. [27] and Singh et al. [19] high broad sense heritability for 1000 seed weight.

Seed weight plant⁻¹

Genotypic mean square was highly significant (Table-1) therefore, diallel analysis was carried out. Highly significant values were found for both 'a' (20.19) and 'b' (20.46) (Table-2), showing the importance of both types of gene actions for controlling seed weight plant⁻¹ in these genotypes of *B. napus*. Farshadfar et al. [12] and Rahman et al. [23] also reported the role of both additive and dominant gene action for this trait in *B. napus* and toria respectively. The proportion of 'a' was found lower than 'b' showing the higher proportion of 'b' to represent variation and overall dominance component was larger and highly significant. Rahman et al. [23] also reported significant and higher value of 'b' component for the mentioned parameter in toria. Moreover they also stated that dominance effect is more important than additive for seed weight plant⁻¹.

The b_1 component (99.57) was found highly significant and was responsible for a greater proportion of dominance than b_2 (2.61) and b_3 (7.68). The b_2 component of dominance was non-significant showing the presence of symmetry of genes. Highly significance of the b_3 component represented the presence of specific genes effect. Non-significant values were estimated for both 'c' and 'd' (0.10 and 0.57 respectively), so retesting of a and b was not required.

To prove the additive-dominance model to be adequate two tests were performed. Uniformity of Wr and Vr indicated the additive-dominance to be adequate but regression analysis invalidated this model (Table-3), thus we considered it partially adequate.

Table-4 shows the estimates of genetic components. For both D (284.99) and H components significant values were obtained for seed weight plant⁻¹, showing that seed weight plant⁻¹ is under the control of both additive and dominance gene affects. The magnitude of H was higher than D. Average degree of dominance value (1.85) was found greater than one which showed the dominance presence for the mentioned trait. Values of H_1 (977.94) and H_2 (961.23) were equal showing the presence of both types of alleles in equal frequencies. F value (68.56) was non-significant and positive. Dominant to recessive genes ratio $(4DH_1)^{1/2} + F/(4DH_1)^{1/2} - F$ was 1.14, indicating that more dominant genes are present in parents. Rahman et al. [23] also reported higher number of dominant genes for seed weight plant⁻¹ trait in toria. h^2 value (1822.47) and environmental component E effect value (24.62) were significant showing their role in the expression of seed weight plant⁻¹.

Negative intercept of covariance (Wr) by variance (Vr) regression line (Fig-6) indicated overdominance gene action. In present study H_1 (977.94) was greater than D (284.99) which also supports overdominance. Farshadfar et al. [12] also reported the effectiveness of overdominance for seed weight plant⁻¹ in *B. napus*. Low (0.31) narrow sense heritability and high (0.93) broad sense heritability (Table-4) was estimated for seed weight plant⁻¹ showing the greater proportion of genetic variation was of dominance nature. Rao and Gulati [10] reported medium to low narrow sense heritability for seed weight plant⁻¹. Tahir et al. [24] also found high broad sense heritability for this trait in canola.

Conclusion

Among parental genotypes, G6 excelled for yield and yield contributing traits whereas among F1 hybrids, performance of G4 × G6, G6 × G4 and G6 × G9, G9 × G6 were superior then rest of the crosses. Diallel analysis showed that both additive (a) and dominance

(b) components were significant for all of the studied parameters. Non-significant values for both 'c' and 'd' components revealed maternal effect and reciprocal effect respectively. From graphical analysis, overdominance type of gene action was observed for all the traits. High narrow and broad sense heritabilities were estimated for pod length, which shows the presence of additive gene action, whereas, low narrow sense and high broad sense heritability was estimated for the rest of the traits, showing the presence of dominance gene action for these traits. The information obtained from the present study could be used to develop desirable line.

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