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Original Research Article

GENETIC EVALUATION OF *BRASSICA NAPUS* FOR VARIOUS YIELD AND OIL CONTRIBUTING ATTRIBUTES

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Abstract: *Genetic components of variation were estimated for six Brassica napus lines using 6×6 diallel scheme. The current research was conducted in the winter season during 2019-20 in the Department of Plant Breeding and Genetics University of Agriculture Faisalabad. Statistical analysis exhibits great diversity among parental genotypes and F1 hybrids for all the investigated characters. All the characters under study manifested over dominance type of gene pattern excluding the number of primary branches/plants controlled by partial dominance type gene action. The traits like plant height, primary branches/plant, days to 50% flowering, and 1000 grain weight showed the highest dominant gene action exhibited by DGL. Genotype B-56 showed dominant gene action for siliquae per plant days to maturity and grain yield. ZMR-2 and ZM-RN possessed the highest number of dominant genes for the time taken flower completion and oil contents, respectively. Broad sense heritability had a high value for all traits (62%-85%), indicating that these traits can be used for further improvement.*

Keywords: *Brassica napus*, variation, morphological traits, diallel

Introduction

Vegetable oil has multiple uses in industry and serves as one of the essential components of the human diet by enhancing its palatability. Pakistan has been facing a shortage of edible oil since 1960. Currently, the availability of edible oil is 3.291 million tonnes from all sources, while local production is estimated to be 0.374 million tonnes. To overcome the gap between indigenous production and utilization, 2.917 million tons of edible oil are imported, costing about Rs.574.199 billion (Anonymous, 2021). Due to increasing population and per capita consumption, edible oil import has increased 5% annually (Ishaq *et al*., 2016). Only 26% of the demand is met with local production (FBS, 2016**)**. This deplorable cooking oil deficiency situation needs improvement in its production by employing different techniques. Many factors contribute hampering edible oil production, e.g., competition of oil seed crops with major crops like wheat, unavailability of genetically potent varieties (early maturing and short duration) and cultivation of oilseed crops on marginal lands (Bhuiyan, 2012).

Genus *brassica* comprises many species of high value as agricultural and horticultural crops. The oilseed crops from the brassica genus play a driving role in overcoming the production-to-consumption gap. Following palm and soybean, various species of brassica (*B. juncea*, *B. rapa*, *B. napus* and *B. campestris)* are chief vegetable oil sources. Their oil has the potential for use in lubrication oils, polyamide fibers, resins, detergents, emulsifying agents and as a vegetable wax substitute. Brassica species have high quality oil contents (44 - 46%). Their meal is rich in quality protein (38-40%), having almost all the essential amino acids like lysine, methionine and cysteine (Abideen *et al.*, 2013, Ishaq *et al.*, 2016).

Among Brassica species, *Brassica napus* manifest great potential to overcome the oilseed production gap (Zhou, 2001; Momoh *et al.*, 2002). Its oil contents are in the range of 40-50%, depending upon the varietal type and climatic condition. Meal cake obtained after oil extraction is rich in protein content (40%) and utilized to feed animals (Jahreis and Schaefer, 2011). The grain yield in Brassica depends on different agronomic traits, i.e., main branch length, branch number, number of pods/plants, seeds per pod, 1000-grain weight, plant height and days to 50% physiological maturity (Leul and Zhou, 1999). The Genetics of these economically important traits needs to be worked out to develop high yielding varieties. For an appropriate breeding procedure, it is a prerequisite for plant breeders to know the genetic

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basis of variations of concerned traits present in the germplasm. Following biometrical techniques, i.e., line × tester, partial diallel and diallel crosses are utilized as a mating design. Among these, diallel mating design is frequently used to obtain basic information about the mode of gene action. Diallel crosses mean mating selected parents and genotypes in all possible combinations. Depending upon the number of crosses to be made, it is divided into two categories, i.e., full diallel and half diallel. It is a simple, structured and systematized method to check continuous variation among the selected genotypes. In diallel, the basic information of parental lines is measured in an early generation, therefore is a time saving approach for the breeder. In diallel crosses two types of approaches are used for data analysis. The Griffing and Hayman approach. (Griffing *et al.*, 1956). Jinks and Hayman first developed the Hayman approach in 1954. In this approach, dominance and additive genetic variance are estimated based on Vr-Wr graph. Griffing approach is also known as a numerical approach which gives information about genetic components based on GCA and SCA variance.

It provides information regarding the inheritance pattern of various characters that can be used in future breeding programs (Khan and Khan, 2005). Hence, the study was conducted to assess the significant variation among various genotypes for yield attributing traits and oil content in B. napus on a genetic basis.

Materials and Methods

Experimental location and condition:

The experimental work was carried out in the field area of the Department of Plant Breeding and Genetics, University of Agriculture Faisalabad, in the winter season (rabi) 2019-20. Crosses of six parents, Long, ZLT-RBJ, ZMR-2, B-56, ZM-RN and DGL were made in complete diallel design through controlled pollination, and F_1 seeds were harvested. In the next year, parents and their F_{1s} were planted with three replications maintaining a P×P distance of 75cm and R×R distance of 25cm in RCBD to control the variations among treatments. Data for various physiological and morphological parameters of the following traits were recorded, including Days taken to 50% flowering (DFF), Days taken to flower completion (DTF), Days taken to physiological maturity (DTM), Number of Primary branches per plant (NPB), Number of siliquae per plant (NSP), Number of seeds per siliqua (NSS), Plant height (PH), 1000-seed weight (SW), Yield per plant (YP), Oil contents (OC).

Statistical analysis

The data of the traits as mentioned above were analyzed for analysis of variance technique by using (Steel *et al.*, 1997). Significant genotypic traits were genetically analyzed using diallel analysis. F_{1s} and crosses values were arranged in diallel tables and in arrays respectively. The variance (Vr) means of family, including array and covariance (Wr) of these, including non-recurrent parents, were determined from each diallel table using statistics. The data set of different characters were determined by regression coefficient (b) analysis to check the adequacy of additive dominance. Variance components like D, H_1, H_2 and F were determined by using Mather and jinks (1982).

Results and discussion

The ANOVA of all the traits exhibited significant differences among all the genotypes. Moreover, all these traits showed the adequacy of the additive dominance model shown in (Table 2). However, days taken to flower completion showed non-adequacy of the additive dominance model.

Days taken to 50% flowering

The graphical representation (Fig.1) for 50% flower initiation indicated over-dominance gene action. Moreover, non-allelic interaction for this trait is absent. DGL being nearest to the source point indicated a greater number of dominant genes and ZMR-2 being distant from the origin, indicating that it contains recessive allele for days to 50% flowering as shown in the distribution of genotypic value. ZLT-RBJ, ZM-RN and B-56 had more dominant alleles followed by long siliquae. Similar results were presented by Vaghela *et al.* (2011).

Days taken to flower completion

The graphical representation in (Fig.2) for days taken to flower completion indicated over-dominance gene action as the regression line in Vr-Wr graph intercepted the covariance axis below the origin. Estimated regression line showed allelic interaction for this trait as regression line significantly deviated from the unit slope. ZM- RN s the highest number of dominant allele as it falls close to the point of source. The same pattern as ZM-RN followed by B-56, long siliqua, ZM-R2, ZLT_RBJ and DGL, respectively. Rameh (2012) and Mahanta *et al.* (2020) also studied the same type of gene action for days taken to flower completion, showing non-additive behavior for this trait.

Days taken to physiological maturity

The graphical representation in (Fig.3) for days taken to physiological maturity showed over-dominance type of gene action instead of non-allelic gene interaction. Parental population DGL, ZM-RN, B-56, Long siliqua and ZLT-RBJ had higher number of genes with B-56 having a higher number of dominant genes. ZMR-2 is more distant from the origin, having a larger number of recessive alleles. A similar y was conducted by Mahanta et al. (2020), and their results coincided with the present study's results.

Number of primary branches per plant maturity

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Relative growth and vigor of plant is directly associated with the no of primary branches per plant The number of primary branches per plant is important parameter of plant that is directly associated with relative growth, vigor, and plant yield. Moreover, Vr-Wr graph of several primary branches, as illustrated in Fig 4, which exhibits partial dominance gene action number of primary branches. Non-allelic interaction is absent for number of primary branches. The genotype DGL followed by ZMR-2 showed a higher number of dominant genes. While genotypes ZLT-RBJ.B-56 and ZM-RN showed the moderate type of dominant and recessive genes, respectively. Genotype long siliqua distant from the source point, which appeared to have a greater number of recessive genes. Similar results were observed in the studies of Akbar *et al.* (2007) and Ali *et al.* (2010).

Number of siliquae per plant

In the graphical representation of Vr-Wr graph in Fig. 5 shows the dominant type of gene action without epistatic effect. Genotype B-56 carried the highest number of dominant gene and ZMR-2 possessed recessive allele as shown in the array points distribution along with the regression line. Furthermore, the regression line showed the scattering of array points depicted greater number of diversities among parent population. The results of above study were verified by the finding of Ali *et al*. (2014).

Number of seeds per siliqua

Vr-Wr graph in (Fig. 6) expressed over-dominance gene action for this trait and showed non-allelic interaction between these genotypes.ZMR-2 possessed a higher number of dominant genes, while ZLT-RBJ contained a greater number of recessive alleles for number of seeds per siliqua, as verified from the graphical presentation. Genotypes B-56 and DGL carried out a moderate number of dominant and recessive genes. The results of the current study coincide with the similar finding of Sabaghnia *et al.* (2010) and Ali *et al*. (2014).

Plant height (cm)

The height of brassica plant is negatively correlated with the final yield. The height of a plant greater will be the chances of lodging of the plant and, ultimately, a reduction in the yield of plant occurred. Plant height also showed the over-dominance type of gene action shown in the Vr-Wr graph of plant height in (Fig.7). DGL had the highest number of dominant genes while ZM-RN had more recessive alleles for plant height as it falls away from the origin in graphical representation. The pattern of over dominance gene similar with our results was observed by Akbar *et al.* (2008) and Ali *et al.* (2014). Parents ZMR-2, B-56 and long siliqua contain a greater number of dominant alleles, while ZLT-RBJ has a greater number of recessive alleles.

1000-seed weight (g)

This trait is positively correlated with the yield of the plant. The more the 1000-seed weight of a genotype, the higher the yield of that genotype. In Fig. 8 the graphical representation of 1000-seed weight showed over dominance type gene action and absence of non-allelic interaction. DGL fall near the point of origin so it carried a greater number of dominant gene ZM-RN and ZLT-RBJ, respectively. The initiating point carried higher number of recessive alleles with ZMR-2. More recessive alleles are present at distant position from source in long siliqua and B-56 varieties. Our results are in line with the findings of (2010) and Ali *et al.* (2014).

Seed yield per plant

Seed yield per plant is depicted in a graphical presentation in (Fig. 9) showing an over dominance pattern of gene action. Moreover, scattered array point showed significant diversity among the parent population. ZLT-RBJ and DGL have a greater number of genes for seed yield. While B-56 carries highest number of the dominant gene as it is closest to the origin. ZM-RN carries more recessive genes as it is farthest from the origin. These results are coincided and verified by the finding of Akbar *et al*. (2008) and Rameeh (2012).

Oil contents (%)

Graphical explanation in (Fig. 10) exhibits over dominance type of gene action for oil content and absence of epistasis. ZMR-2 carrying highest number of recessive genes while B-56 had a greater number of dominant genes. The regression line exhibited the scattered array line that indicated the presence of diversity among parents. Over dominance type of gene action for oil percentage that showed the statistically similar results to the findings of Iqbal *et al.* (2003) and Sabaghnia *et al.* (2010).

Estimation of genetic components

The value of additive genetic variance D was smaller than the value of dominance variance H_1 and H_2 for all the traits under consideration except no of primary branches per plant which have maximum value for additive genetic effect D as compared with H_1 and H_2 as showed in (Table 3). The magnitude of H_1 was greater as compared to H_2 for all the characters that indicated the unequal distribution of genes which was also calculated by the lower $H_2/4H_1$. Plant height a negative value for F that means it has a maximum number of recessive genes that was greater than the number of dominant genes, as also indicated by the higher value of the ratio $(4DH_1)$ ^ 0.5+F/ $(4DH_1)$ ^0.5-F. All the traits showed positive value for F. The value of the dominance ratio was higher than 1 for all the traits under study. On the other hand, the number of primary branches per plant has an overdominant type of gene action. As a result from the Vr-Wr graph

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showed that the number of primary branches and 1000 grain weight showed a negative relationship for h^2.1000-seed weight and the number of primary branches, have a negative trend for $h^{2,}$ which exhibited that the dominant gene was directional toward the parents with lower values for these characters while the positive value of h^2 for all other characters was showed that the trend of dominant genes was toward the better parent. The traits number of primary branches, days taken to 50% flowering, and days taken to physiological maturity have a minimum value for narrow sense heritability which means having the lower contribution of additive gene action in total variance. Traits a number of primary branches and days taken to 50% flowering showed a negative trend toward narrow sense heritability that exhibiting complete absence of additive variance. All other character showed higher value for broad sense heritability, which is indication of presence of additive variance therefore, these traits can be utilized in a future breeding program. Moreover, the results of the present study conform with the research Rameeh (2012), Singh (2013) and Ali (2104).

Conclusion

The above results indicate that the traits that showed over dominance type of gene action simple selection would be a good strategy for further improvements. In contrast,those traits exhibiting the phenomenon of partial dominance heterosis breeding will be more effective for a future breeding program.

Table 1. Analysis of variance of economically important traits of *Brassica napus*

Source	D.F	DFF	DTF	DTM	NPB	NSP	NSS	PH	YP	SW	OC
Replication	2	7.75	0.73	16.58	1.62	270.79	3.15	227.60	20.16	0.15	0.53
Genotypes	35	37.31**	22.93**	26.73**	1.40*	2332.37**	18.84**	482.19**	30.47**	1.51**	7.94**
Error	70	2.86	2.21	6.71	0.69	477.93	7.63	94.89	7.83	7.94	0.50

Table 2 Adequacy of additive- dominance model to the data

Character	b_0	b_1	Adequacy
DFF	2.97*	1.16	Adequate
DTF	1.96	3.55*	Inadequate
DTM	3.10*	0.34	Adequate
NPB	2.83*	1.17	Adequate
NSP	2.79*	-0.05	Adequate
NSS	2.85*	-0.84	Adequate
PH	3.01*	1.54	Adequate
YP	3.84*	-1.18	Adequate
SW	3.00*	0.17	Adequate

Table 3 Estimation of genetic parameters for different traits in *Brassica napus*

	DFF	DTM	NPB	NSP	NSS	PH	YP	SW	OC
D	15.35 ± 3.84	13.24 ± 3.10	0.67 ± 0.08	541.46 ± 175.42	7.30 ± 1.41	62.96 ± 28.54	10.78 ± 2.16	0.51 ± 0.06	2.58±0.33
H_1	40.88 ± 9.71	38.61 ± 7.86	0.44 ± 0.19	3002.69± 444.22	17.30 ± 3.58	402.14 ± 72.29	28.16 ± 5.45	0.78 ± 0.15	4.99±0.85
H_2	24.49 ± 8.69	21.22 ± 7.04	0.14 ± 0.18	1898.83 ± 397.81	10.03 ± 3.20	352.73 ± 64.74	14.46 ± 4.88	0.64 ± 0.13	3.14±0.76
h^2	15.45 ± 5.85	4.46 ± 4.74	-0.07 ± 0.12	92.90 ± 267.75	0.08 ± 2.15	421.41 ± 43.58	2.01± 3.28	-0.02 ± 0.09	0.07±0.51
F	33.45 ± 9.36	35.82 ± 7.58	0.26 ± 0.19	1215.11 ± 428.55	12.01 ± 3.45	1.15 ± 69.74	17.38 ± 5.26	0.40 ± 0.14	4.13±0.82
$(H_1/D)^{0.5}$	1.63	1.70	0.82	2.35	1.53	2.52	1.62	1.24	1.39
$H_2/4H_1$	0.15	0.14	0.07	0.16	0.15	0.22	0.12	0.21	0.16
$(4DH1)^{0.5}$ + $F/(4DH1)^{0.5}$- F	5.01	8.62	1.63	2.82	3.29	1.01	2.99	1.92	3.72
h^2/H_2	0.63	0.21	-0.57	0.05	0.01	1.19	0.14	-0.02	0.02
h^2_{ns}	-0.14	-0.52	0.57	0.25	0.20	0.32	0.36	0.39	0.13
h^2_{bs}	0.846	0.548	0.629	0.812	0.598	0.82	0.733	0.882	0.85

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E	0.95 ± 1.44	2.24 ± 1.17	0.23 ± 0.03	159.31 ± 66.30	2.54 ± 0.53	31.63 ± 10.79	2.61 ± 0.81	0.038 ± 0.02	0.17±0.13

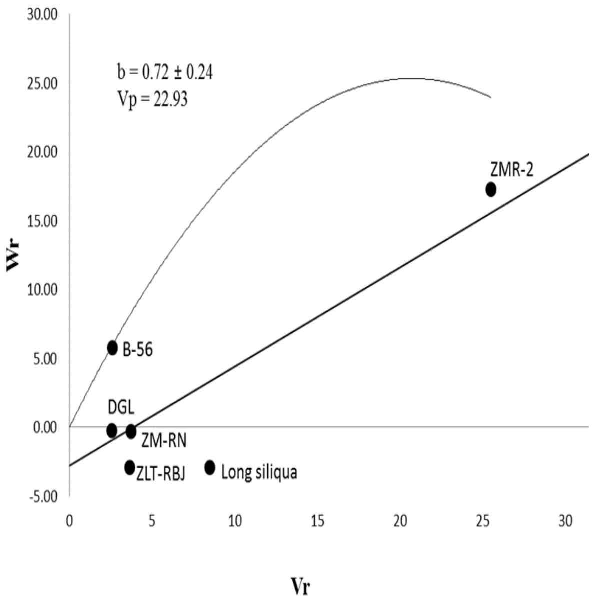

Fig. 1 Graphical representation for days to 50% flowering

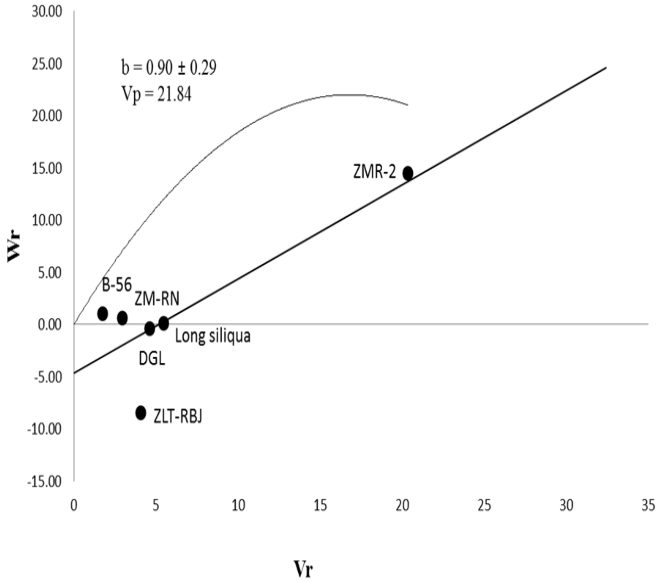

Fig. 3 Graphical representation for days taken to physiological maturity

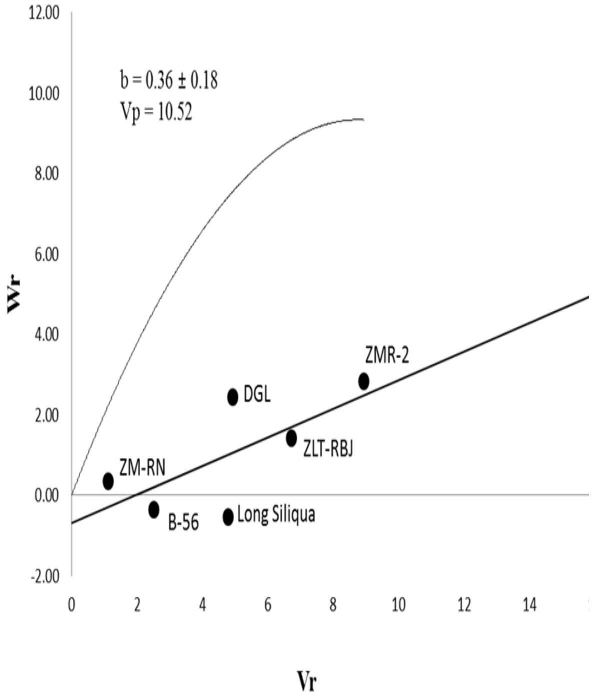

Fig. 2 Graphical representation for days taken to flower completion

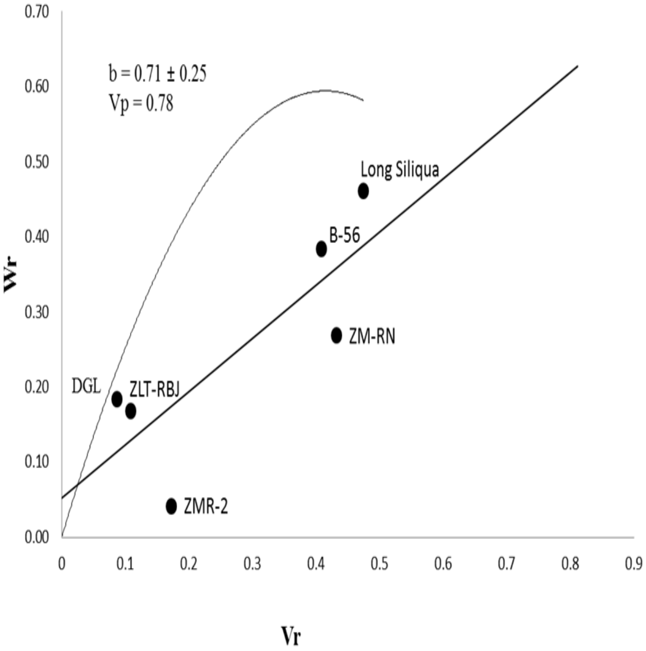

Fig. 4 Graphical representation for number of primary branches per plant

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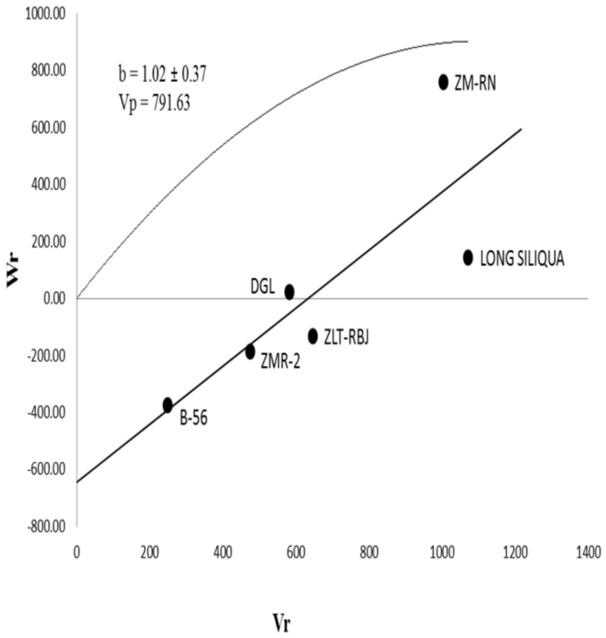

Fig. 5 graphical representation for number of siliquae per plant

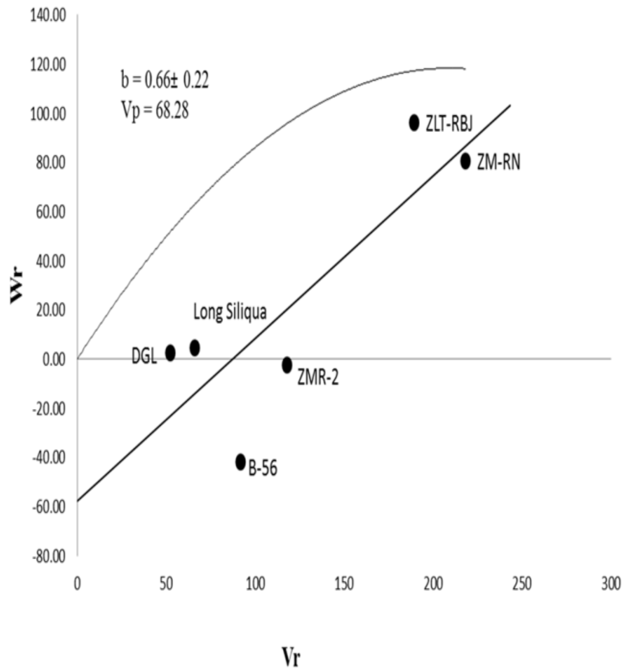

Fig. 7 Graphical representation for plant height

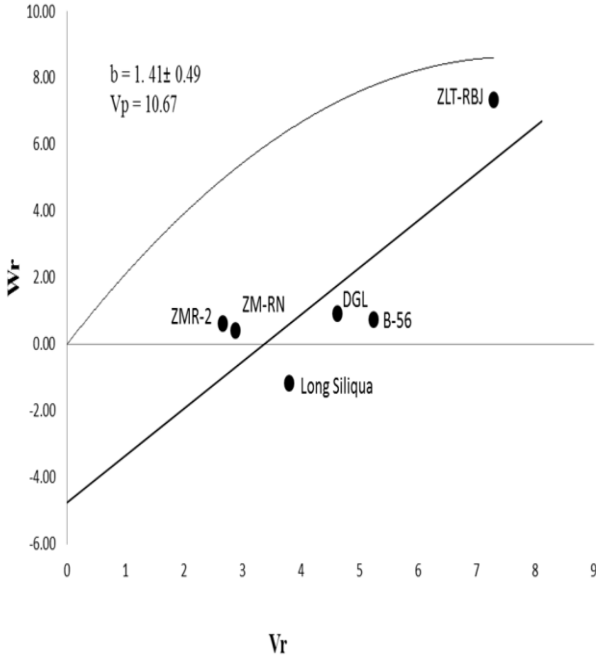

Fig. 6 Graphical representation for number of seeds per siliquae

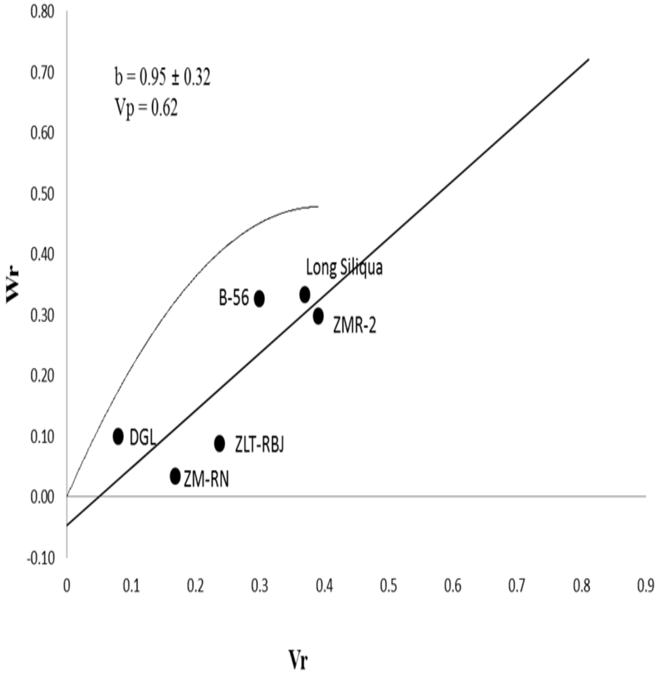

Fig. 8 Graphical representation for 1000-seed weight

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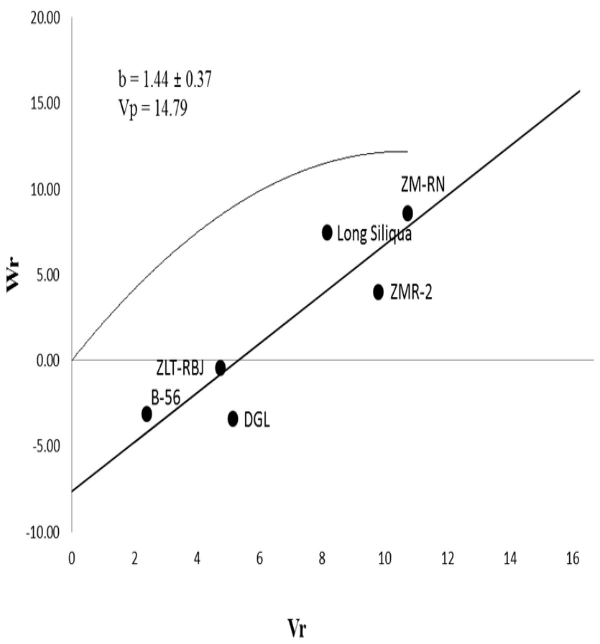

Fig. 9 Graphical representation for seed yield per plant

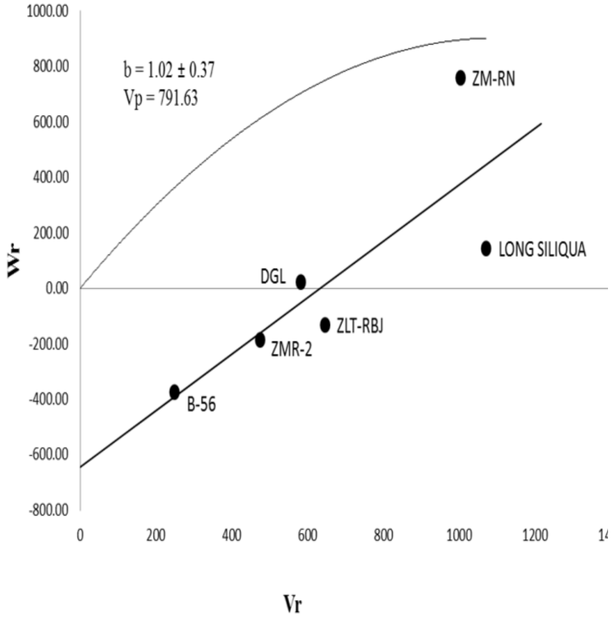

Fig. 10 Graphical representation for oil contents

Conflict of interest

The authors declared absence of conflict of interest.

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