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GENETIC VARIABILITY AMONG ADVANCED LINES OF BRASSICA

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Abstract

Genetic variability for morphological and biochemical traits among six advanced lines ($F_{10:11}$) of *brassica* was studied at The University of Agriculture Peshawar during crop season of 2012-13. These lines were developed through interspecific hybridization. Significant differences at ($p \leq 0.01$) for plant height, main, pods main raceme^{-1}, pod length, seed yield plant^{-1} and protein content at ($p \leq 0.05$) for 100-seed weight, oil content were recorded. The advanced line, AUP-05 produced the maximum seed yield plant^{-1} (19.73 g), protein content (24.56%), 100-seed weight (0.64 g). Advanced line AUP-04 had the highest erucic acid (50.31%), linolenic acid (10.60%) and was late maturing (179.33). Advanced line AUP-06 produced the high oil content (48.82%). Advanced line AUP-03 produced comparatively longer main raceme (69.32 cm). Environmental variance was smaller than genotypic variance for majority of the traits. Genotypic and phenotypic coefficients of variation ranged from 2.45 to 25.67% and 2.50 to 27.68%, respectively. Heritability was high for majority of the traits. The maximum heritability was recorded for plant height (0.61), main raceme length (0.81), pods main raceme^{-1} (0.74), seed yield plant^{-1} (0.86) and protein content (0.77). Moderate heritability was observed for oil (0.58) contents. Heritability for 100-seed weight (0.30) was the lowest. These lines may be released as new improved varieties for specific parameters.

Key words: *Brassica*, Genetic variability, Heritability

Introduction

The genus Brassica is one of the most economically important genera in the family Brassicaceae (Rakow, 2004). This genus comprises a diverse group of species including major vegetables and oilseed crops (Rich; 1991, Christopher *et al*., 2005). Brassicaceae consists of 338 genera and 3709 species (Warwick *et al*., 2006). The species of genus Brassica has two major groups commonly known as rapeseed and mustard. Rapeseed-mustard (*B. napus, B. rapa and B. juncea*) are grown worldwide as a source of edible oil (Downey & Rakow, 1987). In Pakistan, *Brassica campestris "rapa"),* Raya *(B. juncea)* and Taramira (*Eruca sativa*) are grown as oilseed crop for centuries (Turi *et al*., 2012). The oil import bill of Pakistan is the second largest after petroleum (Ahmad *et al*., 2013), so it is imperative to develop improved varieties of oilseed Brassica (Khatri *et al*., 2005) and bring more area under cultivation of these.

Pakistan has developed the agriculture sector, but the chronic shortage of edible oil persist unabated for the past many years. Local lines of rapeseed are old and poor yielded. In spite of economic importance of oilseed crops, no major breakthrough has been made for its improvement. The yield unit^{-1} area in Pakistan is low as compared to most of the developed countries, so providing farmers with new improved varieties is the only option for increasing yield. Simple selection in this self-pollinated crop has not been fruitful. Thus the choice of diverse parents for hybridization must be based upon the combining ability of the diverse parental lines (Farhatullah *et al*., 2006).

Genetic variability is a measure of the tendency of individual genotypes in a population to vary from one another. Variability is different from genetic diversity, which is the amount of variation seen in a particular population. The variability of a trait describes how much that trait tends to vary in response to environmental and genetic influences. Genetic variability in a population is important for biodiversity because without variability, it becomes difficult for a population to adapt to environmental changes and therefore makes it more prone to extinction.

The measurement of genetic variation and mode of inheritance of quantitative and qualitative traits are of prime importance in planning the programme efficiently and effectively (Shah *et al*., 2015). Heritability of any trait depends upon genetic properties of breeding material and environmental conditions in which experiments are carried out (Falconer & Mackay, 1996). A character which has higher range of genetic variability, high heritability and high genetic advance would be an effective tool to improve seed yield (Aytaç & Kinaci, 2009). Morphological traits have been used to assess the genetic variation and relationships among populations of different oilseed species, for example, Brassica (Rabbani *et al*., 1998 & 1999; Kop *et al*., 2003), soybean (Iqbal *et al*., 2008) etc. However, the variation patterns in these traits are considered to be the result of both genetic and environmental attributes (Rohlf *et al*., 1990). In addition quality traits like oil, protein and glucosinolate contents as well as fatty-acid can be modified by classical breeding (Nasim & Farhatullah. 2013; Sidra *et al*., 2014) and gene technological approaches (Mahwish *et al*., 2014). Genetic improvement of seed quality can make oilseed rape a source for high quality edible oil for human consumption and high quality protein meal for feeding animals, non-edible industrial products, such as detergents, lubricants, cosmetics, hydraulic oils, biodiesel and bio energy (Ofori & Becker, 2008; Kimber & McGregor, 1995).

For the synthesis of genetically superior rapeseed, variety/hybrids possessing harmonious combination of desirable parameters and increased adaptability to a wide range of climatic conditions is prerequisite. The estimation of the value of heterosis and heterobeltiosis for understanding the genetic control of these parameters in different cross combinations under the prevailing conditions is very important (Adnan *et al*., 2014). Success of any crop improvement program depends upon the presence of substantial amount of genetic variability and heritability (Sidra *et al*., 2014; Laila *et al*., 2014; Adnan *et al*., 2013; Khan *et al*., 2008, 2006) because the ultimate goal is to develop hybrid cultivars that can potentially use the total amount of heterosis available.

Therefore, in the present studies was conducted with the objective to quantify the contribution of various high yielding parental lines in the production of hybrid cultivars, having high seed yield with improved oil quality. The selected hybrids may be included in national oilseed breeding programs of Pakistan.

Materials and Methods

Genetic variability for morphological and quality traits was studied in six advanced lines (Table 1) of Brassica during 2012-13 at The University of Agriculture, Peshawar Khyber Pakhtunkhwa.

History of breeding material: The parental lines (A-20-28, Maluko, Dunkled, UCD-40/1, 1203, 2163, 2065 and 8948-2) were grown in 2001 and interspecific crosses were made in 2002. The F_1 seed were sown on Oct, 2002 and F_2 seeds were harvested in 2003.Then F_2 seeds were sown in 2003-04. Selected from $F_{2:3}$ families (Shehzad & Farhatullah, 2012) to till $F_{9:10}$ generation were advanced.

Field layout: The experiment was conducted using randomized complete block design with three replications. Sowing was done on 18th October, 2012. Each replication consisted of six plots and each plot contained five rows. Row to row distance was 60 cm with row length of 5 meter. Plant to plant distance of 30 cm was maintained by thinning. Normal cultural practices were carried out as recommended for brassica. At maturity, five plants in each row and each plot (total of 25 plants) in each replication were selected. Data was recorded on some morphological and two quality parameters.

Morphological traits: Data on plant height (cm) was recorded through meter rod by measuring the distance from the soil to the tip of the plant, at a stage when crop reached physiological maturity. Number of pods from base to tip of the main raceme terminating on inflorescence were counted. Average pod length (cm) was recorded by measuring the distance from base to tip of selected pods. Seed yield plant^{-1} was recorded by weighing seed of individual selected plant, while 100-seed per entry per replication were also weighed. Both data were recorded in grams.

For oil quality analysis, seed samples were scanned on Near Infrared Reflectance Spectroscopy (Font *et al*., 2006; Hom *et al*., 2006) at Nuclear Institute for Food and Agriculture (NIFA), Tarnab, Peshawar, to determine Oil content (%) and Protein content (%) in seed samples:

Statistical analysis: Data obtained was statistically analysed according to the appropriate method recommended for randomized complete block design (Steel & Tori, 1980). Mean separation was carried out following LSD (0.05) test (Steel & Tori, 1980).

Genetic variability: Genotypic and phenotypic variances, genotypic (GCV), phenotypic coefficients of variance (PCV) and heritability (broad sense) were computed according to Burton & Devane (1953), Johnson *et al.* (1955) and Singh & Chaudhary (1985):

$$\text{Genetic variance (Vg)} = \frac{\text{Genotypes mean squares (GMS)} - \text{Error mean squares (EMS)}}{\text{Number of replications (r)}}$$

Environmental variance (Ve) = Error mean squares (EMS)

Phenotypic variance (Vp) = Vg + Ve

Heritability broad sense (H2) on plots mean basis was calculated as:

$$H^2 = \frac{Vg}{Vp}$$

$$\text{Genotypic coefficient of variation} = \sqrt{\text{Vg}}/\text{GM} \times 100$$

$$\text{Phenotypic coefficient of variation} = \sqrt{\text{V}_\text{P}}/\text{GM} \times 100$$

Where:

V_g= Genotypic variance

V_P= Phenotypic variance

GM= Grand mean of the trait

H^2= Broad sense heritability for a trait.

Table 1. List of advanced lines along with their parentage used in the experiment.

Advanced lines	Parentage	
AUP-01	A-20-28 × 2163	*(B. napus × B. campestris*)
AUP-02	Maluko × 2163	(*B. napus × B. campestris*)
AUP-03	A-20-28 × 1203	(*B. napus × B. campestris*)
AUP-04	Maluko × 2065	(*B. napus × B. campestris)*
AUP-05	Dunkled × 1203	(*B. napus × B. campestris)*
AUP-06	UCD-40/1 × 8948-2	(*B. juncea × B. Campestris*

Results and Discussion

Morpho-yield traits: Plant height is an important characteristic of brassica genotypes due to many reasons. First, it is related to flowering time because as more time passes before flowering, more height is obtained through vegetative growth of the primary stem. The examined data for plant height revealed highly significant differences ($p \leq 0.01$) among brassica advanced lines (Table 2). In advanced lines the shortest plants were observed in genotype AUP-02 (152.05 cm), whereas the tallest for AUP-06 (189.12 cm) with an overall mean of 170.46 cm (Table 3). Our results are in line with the earlier findings of Ali *et al*. (2002) who also reported significant differences for plant height.

Environmental variance (122.26) was smaller than genotypic variance (189.53) for plant height. Genotypic coefficient of variability was smaller (8.08%) than phenotypic coefficient of variability (10.36%). For plant height, high broad sense heritability estimate (0.61) was recorded (Table 4). Our results showed high heritability for plant height, which are in close agreement with the finding of Nasim *et al*. (2013), Singh *et al*. (2012), Dar *et al*. (2010), Zhang & Zhou (2006) and Tariq *et al*. (2003) who had also observed high heritability for plant height in *Brassica napus*.

Pods main raceme^{-1} revealed highly significant differences in studied genotypes showing that there is sufficient variability to have an effective selection (Table 2). Data regarding advanced lines for pods main raceme^{-1} ranged from 35.52 AUP-02 to 66.52 AUP-05. The overall mean values for the genotypes was 56.13 (Table 3) The obtained results are in line with those of Aytac & Kinaci (2009), Nazeer *et al*. (2003) and Tahir *et al*. (2006), who also reported significant differences among the brassica genotypes for pods main raceme^{-1}, seed yield and yield components.

Genotypic variance (120.53) was higher than environmental variance (43.11) for pods main raceme^{-1} and phenotypic coefficient of variability (22.79%) was higher than genotypic coefficient of variability (19.56%). The resultant heritability for pods main raceme^{-1} was (0.74) which indicates that the trait is comparatively more under genetic control (Table 4). These results for high broad sense heritability are similar with the findings of Singh & Singh (2012) and Mahmood *et al*. (2003) who also reported high heritability for pods main raceme^{-1}.

Pod length is an important yield contributing trait having direct association with seeds pod^{-1} and ultimately to final seed yield. Pod length in advanced lines ranged from 4.59 cm for genotype AUP-03 to 7.13 cm for genotype AUP-06. Average pod length in advanced lines was 5.94 cm (Table 3).

Pod length data exhibited highly significant differences ($p \leq 0.01$) among the brassica advanced lines showing the presence of sufficient variability to have an effective selection (Table 2). Our current findings are in agreement with those of Aytac & Kinaci *et al*. (2009), Azadgoleh *et al*. (2009) and Tahir *et al*. (2006) who also reported significant variation for pod length.

Environmental variance for pod length (0.07) was smaller than genotypic variance (1.08). Genotypic (GCV) and phenotypic coefficients of variability (PCV) values for the said trait were 17.49 and 18.05%. Estimated heritability for pod length was high (0.94) which shows that selection for this trait shall be effective (Table 4). Our results are in close conformity with the previous observations of Bozokalfa *et al*. (2010) and Zhang & Zhou (2006) who also reported high broad sense heritability for pod length.

Statistical analysis for 100-seed weight showed significant differences ($p \leq 0.05$) among the brassica advanced lines (Table 2). Significant differences among the evaluated brassica advanced lines showing the presence of genetic variation among the genotypes to have an effective selection. Among the advanced lines, minimum 100-seed weight (0.46g) were recorded for genotype AUP-01 whereas maximum (0.64g) for advanced line AUP-05. Among the genotypes the mean value for 100-seed weight was 0.53g (Table 3). Our findings are in agreement with those of Nazeer *et al*. (2003), Azadgoleh *et al*. (2009) and Tahir *et al*. (2006) who also reported significant variation for 100-seed weight.

Environmental variance was similar to genotypic variance for 100-seed weight. Genotypic coefficient of variability (11.34%) was smaller than phenotypic coefficient of variability (15.43%). The resultant heritability for 100-seed weight was 0.30 (Table 4). Heritability for 100-seed weight is low. Our results are contrast with Nasim *et al*. (2013), Zhang & Zhou (2006) and Ali *et al*. (2003) who also observed high heritability for 100-seed weight.

Seed yield plant^{-1} varied highly significantly ($p \leq 0.01$) among the studied brassica advanced lines (Table 2), indicating the presence of sufficient genetic variability for effective selection. Our results are supported by Tahir *et al*. (2006) and Ghosh & Gulati (2001) who also reported significant variation for seed yield of different genotypes. Among the advanced lines minimum seed yield plant^{-1} (10.14g) was recorded for genotype AUP-03 whereas maximum (19.73g) for advanced line AUP-05. Among the genotypes, the mean value for seed yield plant^{-1} was 14.67g (Table 3).

Environmental variance (2.30) was smaller than genotypic variance (14.17) for seed yield plant^{-1} and genotypic coefficient of variability (25.66%) was smaller than phenotypic coefficient of variability (27.67%). Seed yield plant^{-1} revealed high broad sense heritability (0.86), indicating more genetic control and less environmental influence on this trait (Table 4). Our findings are supported by Singh and Singh (2012), Tahira *et al*. (2006), Aytac & Kinaci (2009) and Ali *et al.* (2003) who also observed high heritability for seed yield plant^{-1}.

Biochemical traits: Chemical analysis is one of important feature of this study because quality seed production is as important attribute of a cultivar. In brassica, quality refers to high percentage of oil, protein, oleic acid and low percentage of glucosinolates (GSL), linolenic acid and erucic acid. Here we report two quality parameters i.e. Oil and protein contents.

Table 2. Mean square values of different morphological and biochemical traits of brassica advanced lines.

Traits	Replication df=2	Genotypes df = 5	Error df = 10	CV %
Plant height (cm)	162.588	690.846**	122.257	6.49
Pods main raceme^{-1}	47.846	404.692**	43.106	11.70
Pod length(cm)	0.040	3.305**	0.070	4.45
100-seed weight (g)	0.001	0.014*	0.003	10.47
Seed yield plant^{-1} (g)	2.265	44.821**	2.304	10.35
Oil content (%)	0.352	5.928*	1.165	2.27
Protein content (%)	0.823	14.887**	1.063	4.50

Table 3. Mean performance of morpho-yield and biochemical traits of brassica advanced lines.

Genotypes	PH	PMR	PL	SYP	HSW	OIL	PRO
AUP-01	164.36	50.60	4.59	0.46	12.22	45.62	24.55
AUP-02	152.05	35.52	4.79	0.47	12.86	47.56	24.30
AUP-03	177.47	65.27	6.05	0.49	10.14	48.73	20.41
AUP-04	156.14	57.39	6.25	0.56	14.05	48.76	23.90
AUP-05	183.59	66.25	6.84	0.64	19.73	46.25	24.56
AUP-06	189.12	61.74	7.13	0.54	19.02	48.83	19.71
LSD $_{(0.05)}$	20.11	11.94	0.48	0.10	2.76	1.96	1.88

PH: Plant height, PMR: Pods main raceme^{-1}, PL: Pod length, HSW: 100-Seed weight, SYP: Seed Yield plant^{-1}, Oil: Oil content, PRO: Protein content

Table 4. Environmental, genotypic and phenotypic variances, GCV and PCV with heritability for various Morpho-yield and Biochemical traits of Brassica Advanced lines.

Traits	EMS	VG	VP	GCV	PCV	H^2(bs)
Plant height (cm)	122.26	189.53	311.79	8.08	10.36	0.61
Pods main raceme^{-1}	43.11	120.53	163.63	19.56	22.79	0.74
Pod length (cm)	0.07	1.08	1.15	17.49	18.05	0.94
100-seed weight (g)	0.003	0.003	0.01	11.34	15.43	0.30
Seed yield plant^{-1}	2.30	14.17	16.48	25.66	27.67	0.86
Oil content (%)	1.16	1.58	2.74	2.63	3.47	0.58
Protein content (%)	1.06	4.61	5.97	9.36	10.65	0.77

Vg = Genotypic variance, EMS = Ve = Environmental variance, Vp = Phenotypic variance

Oil content (%): The analysis of variance for oil content showed highly significant differences ($p \leq 0.01$) for genotypes (Table 2). These results are similar with the findings of Tuncturk & Ciftci (2007). They also obtained significant results for oil content in brassica genotypes. The oil content ranged from 45.62% for genotype AUP-01 to 48.83% for genotype AUP-06 among advanced lines. Average oil content was 47.62% in advanced lines (Table 3).

Environmental variance (1.16) was smaller than genotypic variance (1.58) for oil content and genotypic (GCV) and phenotypic coefficients of variability (PCV) values for the said trait were 2.63 and 3.47%. Moderate broad sense heritability (0.58) value was recorded for oil content, respectively (Table 4). Moderate heritability broad sense for oil percent are supported by Aytac & Kinaci (2009).

Protein content (%): Analysis of variance showed highly significant differences ($p \leq 0.01$) among the brassica genotypes (Table 2). Our findings are similar with the results of Aytac & Kinaci (2009) who noted high significant differences for protein content in *Brassica napus* and *Brassica juncea*. In the present study, the protein content ranged from 19.71% for genotype AUP-06 to 24.56% for genotype AUP-05 among the advanced lines. The overall average protein content was 22.93% in advanced lines (Table 3).

Environmental variance (1.06) was smaller than genotypic variance (4.61) for protein content and genotypic (GCV) and phenotypic coefficients of variability (PCV) values for the said trait were 9.36 and 10.65%. However, for said trait, the broad sense heritability value was high (0.77), respectively (Table 4). High broad sense heritability was reported for protein content. Similarly high heritability for protein content was also observed by Aytac & Kinaci (2009) in rapeseed while Khan *et al.* (2008) found low heritability for protein content in brassica.

Conclusions and recommendations

On the basis of results obtained from this experiment it can be concluded that;

1. Most of the advanced lines varied significantly for all the studied parameters.
2. AUP-05 and AUP-06 were the best advanced line, as they excelled in majority of traits.
3. High broad sense heritability estimates were recorded for plant height, pods main raceme^{-1}, pod length, seed yield plant^{-1}, protein content.
4. Seed yield plant^{-1} had positive significant correlation with plant height, pod length, 100-seeds weight.

From the above conclusions it is recommended that: Advanced lines AUP-05 and AUP-06 may be considered as the best lines for seed pod^{-1}, 100-seed weight, seed yield plant^{-1}, oil and protein contents.

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