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Genetic variability and regression analysis for yield and quality traits in *Brassica napus*

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ABSTRACT

An experiment was conducted to estimate the genetic variability and regression analysis for yield and quality traits in a set of eight brassica genotypes in a randomized complete block design with three replications at The University of Agriculture Peshawar, during 2011-12 cropping season. Significant genetic variability was recorded among genotypes for plant height, pods main raceme⁻¹, pod length, seed yield plant⁻¹, 1000-seed weight, seeds pod⁻¹, oil content, protein content, glucosinolate content, erucic acid content, oleic acid content and linolenic acid content except for primary branch plant⁻¹ and pods plant⁻¹ which showed non-significant differences. Genotypes, AUP-401, AUP-402, AUP-404 and AUP-407 showed potential performance for glucosinolate content (55.1 $\mu\text{mol g}^{-1}$), seed yield plant⁻¹ (23.93 g), pods plant⁻¹ (268.83), protein contents (21.1 %), erucic acid contents (42.7 %) and oil contents (53.3 %). Seed yield plant⁻¹ was taken as a dependent variable to study the effects of many morphological yield traits on it. Branches plant⁻¹, pods main raceme⁻¹, pods plant⁻¹ and seed pod⁻¹ showed a positive effect on seed yield plant⁻¹, while 1000-seed weight, pod length, and plant height showed a negative effect on seed yield plant⁻¹. Seed yield plant⁻¹ as an independent variable showed a negative effect on oil content. Protein content as an independent variable showed a positive effect on erucic acid content, while oil contents as independent variables show a negative effect on protein contents, respectively. The developed germplasm could be used in the upcoming brassica breeding programs to release high yielding, disease resistance, stress tolerance, and insect resistance varieties, which will eventually upsurge the productivity and decrease the gap between demand and domestic production of the brassica crop.

KEYWORDS: Brassica napus, genetic variability, oil content, protein content, regression analysis.

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INTRODUCTION

Pakistan is a net importer of oilseeds and edible oils. The domestic production of edible oils is only sufficient to meet 20 percent of total demand. According to the Foreign Agricultural Service of United States Department of Agriculture (USDA), Pakistan's vegetable oil imports are forecast at a record 2.45 million metric tons (MMT) in the marketing year 2010-2011, which is ten percent higher than the previous year imports estimated at 2.23 MMT. Introduction to oilseed rape (*Brassica napus* L.) has become one of the most important oil crops and, at present, is the third-largest source of vegetable oil all over the world [1]. Rapeseed is an important oilseed crop. In Pakistan, rapeseed and mustard is the second most important source of oil after cotton.

Conventional rapeseed and mustard varieties impose health concerns due to the presence of erucic acid in oil and glucosinolate in the meal. Canola has the advantage over other

vegetable oils because it contains the lowest content of saturated fatty acid (< 2 % in oil), glucosinolate (< 30 $\mu\text{mol gram}^{-1}$ in the meal) and has a lower level of saturated fats (only 6%) than any other vegetable oil [2]. Canola is an oilseed crop that has gained widespread acceptance worldwide due to the advantages of healthy edible oil and high oil yield. Oil containing only seven percent saturated fatty acids, along with cholesterol lowering monounsaturated and polyunsaturated fatty acids are the main components of canola seed oil [3]. The oil content of rape is an important quantitative trait influenced by environmental conditions [4] [5]. Canola oil is high in oleic acid relative to other vegetable oils and has been competitive in price with other cooking oils. *B. napus* have been known as a rich source of oil with a low content of saturated fatty acids (5-7%) and a high content of polyunsaturated fatty acids with about 7-10% linolenic and 17-21% linoleic acids. It is the reform considered as very healthy edible oil [6]. In this regard, scientist has tried to improve the situation by manipulating genetics of *Brassica* species and their genotypes for oil meal consumption.

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Rapeseed breeders aim to improve seed yield [7]. Seed yield is a complex character that can be controlled by several components having positive or negative effects on traits [8]. Poor water management and inadequate use of fertilizer are major causes of low yield. Larger seed size and higher oil content of seeds are important considerations in breeding for increased yield. Pakistan is chronically deficient in the production of edible oil, and this deficit is being continuously enlarged. The local production of edible oil from oil crops is only sufficient to meet about one-third of the domestic consumption, remaining being met through massive imports. These imports are continuously increasing at an alarming rate of 13% annually. More than 31 billion rupees were spent on the import of edible oil during 2003-2004 [9]. Therefore, plant breeders should concentrate on the genetic study of morpho-yield traits and qualitative traits. Regression analysis is a statistical technique for estimating the relationships among variables. Regression analysis helps one to understand how the typical value of the dependent variable changes when any one of the independent variables is varied, while the other independent variables are held fixed. Keeping in view the importance of *Brassica napus*, efforts were made in the present study to determine the extent of genetic variability, estimate regression analysis of different morpho-yield traits with quality traits and identify the best potential genotypes for future brassica breeding programs.

MATERIALS AND METHODS

The present study was conducted in 2011-2012, at The University of Agriculture-Peshawar, Pakistan to find out the extent of genetic variability, estimate regression analysis for major traits and identify the best superior genotypes for future use in brassica breeding programs. Eight different genotypes (AUP-401, AUP-402, AUP-403, AUP-404, AUP-405, AUP-406, AUP-407, and AUP-408) were evaluated in a randomized complete block (RCB) design with three repeats. Standard agronomic practices were performed uniformly for all genotypes. Data was recorded on the following traits.

Morphological Traits

Plant height, primary branches plant⁻¹, pods main raceme⁻¹, pod length, seed yield plant⁻¹, 1000-seed weight, pods plant⁻¹, and seeds pod⁻¹.

Biochemical Analysis

Quality seed production is one of the major objectives of breeding oilseed crops. In Brassica, the quality of seed depends on the high percentage of oil, protein, oleic acid, and the low percentage of glucosinolate (GSL), linolenic acid, and erucic acid. To determine the chemical contents (Oil content, Protein content, glucosinolate, moisture content, erucic acid, oleic acid, linolenic acid) seed sample from each selected plant was scanned on near infra-red (NIR) spectroscopy at biochemical laboratory nuclear institute for food and agriculture (NIFA) Peshawar.

Statistical Analysis

Analysis of variance

The data were statistically analyzed according to the appropriate method, as suggested for RCB design [10]. Mean separation was carried out following the LSD_(0.05) test.

Estimation of regression

In statistics, regression analysis is a statistical technique for estimating the relationships among variables. In this study, regression is represented graphically in the results, each graph showing the dependent variable on its Y-axis and independent variable on X-axis.

RESULTS AND DISCUSSION

Morphological Traits

Plant height (cm)

Plant height indicates a crop's growth efficiency. Environmental factors also play an essential role in determining plant height. Statistical Analysis showed significant genetic variability for plant height among the studied genotypes (Table-1). Mean values for plant height ranged from 155.67 to 180.08 cm, with an average height of 169.67 cm (Table-2). Genotype AUP-408 were showing the shortest height (155.67 cm) while AUP-401 were showing the longest height (180.08 cm) (Table-2). The finding of [11] [12], who observed that the varietal differences were highly significant for plant height and other morphological traits, further support our results.

No. of Primary branches plant⁻¹

The number of primary plants⁻¹ is the mutual effect of the genotype and environment, which have an important role in the ultimate seed yield of the crops. Mean square values revealed non-significant differences for the number of primary branches plant⁻¹ among the genotypes (Table-1). The number of primary branches plant⁻¹ exhibited a range of 6.83 to 8.5 branches with the mean performance of (7.75 branches) (Table-2). Maximum branches (8.5) were recorded for AUP-401, while minimum branches (6.83) were observed for AUP-406 (Table-2). The contrast result was found by [12] [13] [14], who reported significant genetic variability for the number of primary branches plant⁻¹.

No. of pods main raceme⁻¹

The number of pods on the main raceme is a major contributor to the yield of Brassica and contributes significantly to seed yield. Analysis of variance for pods main raceme⁻¹ showed highly significant differences among the studied genotypes (Table-1). Data for pods main raceme⁻¹ ranged from 44.33 (AUP-408) to 77.17 (AUP-401) with an average performance of 66.53 pods main raceme⁻¹ (Table-2). Our results are in agreement with the earlier findings of [15] [16] [17], who reported significant differences for the number of pods per main raceme⁻¹.

Table-1: Mean squares for various Morpho-yield and quality traits of *Brassica napus* L.

Source of variation	Replication (df = 02)	Genotypes (df = 07)	Error (df = 14)	CV (%)
Plant height	37.42	239.45**	39.88	3.72
Primary branch plant ¹	0.59	1.11 ^{NS}	0.66	10.49
Pods main raceme ¹	157.32	296.91**	61.69	11.81
Pod length	0.20	2.53**	0.13	5.35
Seed yield plant ¹	2.91	27.52**	1.45	6.62
1000-seed weight	0.09	0.48*	0.16	9.99
Pods plant ¹	1364.46	2824.28 ^{NS}	2855.5	24.48
Seeds pod ¹	3.44	12.43**	2.57	7.37
Oil content	0.01	3.77**	0.15	1.07
Protein content	0.08	1.62**	0.04	1.47
Glucosinolate	16.31	428.00**	8.84	5.95
Erucic acid	1.10	141.36**	0.60	2.14
Oleic acid	0.41	52.62**	0.39	1.66
Linolenic acid	0.13	1.39**	0.06	3.89

*, ** = Significant at the 1% and 5% level of probability, respectively

Table 2: Mean values for various morpho-yield traits in *Brassica napus* L.

Genotypes	PH	PBP	PMPR	PL	SYPP	TSW	PPP	SPP
AUP-401	180.08 ^a	8.50 ^a	77.17 ^a	8.17 ^a	18.73 ^{bc}	3.60 ^{cd}	216.00 ^a	25.27 ^a
AUP-402	162.58 ^{bc}	7.75 ^{abc}	66.17 ^a	5.54 ^e	23.93 ^a	3.40 ^d	268.83 ^a	22.57 ^{abc}
AUP-403	174.42 ^a	8.08 ^{abc}	74.67 ^a	6.96 ^{bc}	20.43 ^b	4.40 ^{ab}	230.17 ^a	23.63 ^{ab}
AUP-404	169.75 ^{ab}	8.42 ^{ab}	68.08 ^a	6.48 ^{cd}	17.13 ^{cd}	4.10 ^{ab} ^{cd}	252.33 ^a	20.35 ^{cd}
AUP-405	179.17 ^a	7.00 ^{bc}	70.17 ^a	6.92 ^c	14.07 ^e	3.90 ^b ^{cd}	205.25 ^a	21.38 ^{bcd}
AUP-406	174.33 ^a	6.83 ^c	64.42 ^a	7.59 ^{ab}	17.77 ^c	4.70 ^a	199.50 ^a	20.89 ^{bcd}
AUP-407	161.33 ^{bc}	7.92 ^{abc}	67.25 ^a	5.58 ^e	18.23 ^c	3.90 ^b ^{cd}	199.13 ^a	18.72 ^d
AUP-408	155.67 ^c	7.50 ^{abc}	44.33 ^b	6.29 ^d	15.43 ^d ^e	4.30 ^{abc}	175.30 ^a	21.13 ^{bcd}
Mean	169.67	7.75	66.53	6.69	18.22	4.03	218.32	21.74
LSD(0.05)	11.06	1.423	NS	0.6314	2.109	0.7005	NS	2.802

Mean followed by different letters within a column are significantly different at 5% of probability, NS=non-significant. PH = Plant height, PBP = Primary branches plant¹, PMPR = Pod main raceme¹, PL = Pod length, SYPP = Seed yield plant¹, TSW = 1000-seed weight, PPP = Pod plant¹, SPP = Seed pod¹

Pod length (cm)

Pod length plays an essential role in seed setting and seed yield. Analysis of variance showed highly significant differences for pod length among the studied breeding material (Table-1). Pod length ranged from 5.54 cm (AUP-402) to 8.17 cm (AUP-401) with an average length of 6.69 cm (Table-2). Previous researchers [11] [12] [18], also reported significant genetic variations among brassica genotypes for pod length.

Seed yield plant⁻¹ (g)

Seed yield plant⁻¹ is the cumulative consequence of various components such as the number of pods plant⁻¹, seeds pod⁻¹, and 100-seed weight. Highly significant differences were recorded for seed yield plant⁻¹ (Table-1). Data presented in Table-2 ranged from 14.07 g (AUP-405) to 23.93 g (AU-402). The average seed yield plant⁻¹ of eight brassica napus genotypes was 18.22 g (Table-2). Our findings are in agreement with the earlier results of [12] [19] [20], who also recorded significant genetic variability for seed yield plant⁻¹ among brassica lines.

1000-Seed weight (g)

Weight of seed expresses the degree of seed improvement and is an imperative yield determinant. Seed weight plays an influential role in determining the yield potential of a genotype.

Statistical analysis for 1000-seed weight revealed significant differences among the genotypes (Table-1). The performance of genotypes for 1000-seed weight varied from 3.40 g (AUP-402) to 4.70 g (AUP-406), with an average performance of 4.03 g (Table-2). Previous researcher [21] reported significant differences in 1000-seed weight while [11] recorded non-significant differences. These differences may be due to the difference in the environment as well as the breeding material used in the experiment.

No. of pods Plant⁻¹

Number of pods plant⁻¹ contributes considerably toward the final seed yield. Analysis of variance for the number of pods plant⁻¹ revealed non-significant differences among the studied genotypes (Table-1). The performance of genotypes for the number of pods plant⁻¹ varied from 175.30 (AUP-408) to 268.83 (AUP-402) with the average performance of 218.32 (Table-2). The contrast result was observed by [22], who reported significant variations for number pods plant⁻¹.

Seeds pod⁻¹

Seeds pod⁻¹ is a vital yield contributing trait. Highly significant differences for seeds pod⁻¹ were observed among eight brassica napus lines (Table-1). Data presented in Table-2 related to the number of seeds pod⁻¹ was in the range of 18.72 (AUP-407) to

25.27 (AUP-401) seeds (Table-2). Our results are supported by [23], who studied genetic variability and parameter association studies in Indian mustard.

Biochemical Traits

Oil content (%)

An oilseed crop rich in oil content of high value is the important goal of many research projects. The quality of seed is determined from its oil content. Statistical analysis for oil contents showed highly significant differences ($P \leq 0.01$) among the studied genotypes (Table-1). The performance of genotypes for oil contents varied from 49.8 to 53.3 %, with an average performance of 51.1 % (Table-3). Maximum oil content (53.3 %) was reported for AUP-407, while minimum oil content (49.8 %) was observed for AUP-403 (Table-3). Similarly, significant genetic variability was followed by [14] [20].

Protein content (%)

Results regarding protein content were highly significant, which coincide with the results of [24], who also reported significant genetic variability among brassica lines (Table-1). Data regarding mean performance varied from 18.8 % (AUP-401) to 21.1 % (AUP402). The overall mean for protein content was 19.7 % (Table-3).

Glucosinolate content ($\mu\text{mol g}^{-1}$)

Glucosinolates is the second principal unwanted constituent of Brassica, which has adverse effects on human beings as well as animals. Therefore, preference is given to low contents of glucosinolate (GSL); for this purpose, breeders are trying to develop such varieties possessing low content of glucosinolates. Statistical analysis for glucosinolate showed highly significant differences among the genotypes (Table-1). Regarding mean data for glucosinolate contents, varied from 55.1 $\mu\text{mol g}^{-1}$ (AUP-401) to 86.0 $\mu\text{mol g}^{-1}$ (AUP-406) with the average performance of 70.7 $\mu\text{mol g}^{-1}$ (Table-3). Similar results were also reported by [25] also recorded significant genetic variations for glucosinolate content among different brassica lines.

Table 3: Mean values for various Quality traits in *Brassica napus* L.

Genotypes	OC	PC	GSL	EAC	OAC	LAC
AUP-401	51.1 ^{cd}	18.8 ^e	55.1 ^f	45.8 ^{cd}	58.0 ^a	8.5 ^{bc}
AUP-402	50.8 ^d	21.1 ^a	63.5 ^e	55.2 ^b	51.5 ^c	9.5 ^a
AUP-403	49.8 ^f	20.1 ^b	78.6 ^{bc}	46.4 ^c	55.2 ^b	9.7 ^a
AUP-404	50.6 ^{de}	19.9 ^b	68.9 ^d	42.7 ^e	55.3 ^b	9.5 ^a
AUP-405	51.9 ^b	19.0 ^{de}	82.3 ^{ab}	54.4 ^b	52.0 ^c	8.1 ^c
AUP-406	51.5 ^{bc}	20.0 ^b	86.0 ^a	58.9 ^a	49.2 ^d	8.7 ^b
AUP-407	53.3 ^a	19.2 ^{cd}	76.1 ^c	59.9 ^a	45.7 ^e	8.1 ^c
AUP-408	50.0 ^{ef}	19.5 ^c	55.3 ^f	44.6 ^d	57.1 ^a	8.3 ^{bc}
Mean	51.1	19.7	70.7	51	53	8.8
LSD(0.05)	0.6782	0.3502	5.207	1.356	1.094	0.429

Mean followed by different letters within a column are significantly different at 5% of probability, NS=non-significant. OC = Oil content, PC = Protein content, GSL = Glucosinolate content, EAC = Erucic acid content, OAC = Oleic acid content, LAC = Linolenic acid content

Erucic acid content (%)

Erucic acid is a crystalline mono-saturated omega-9 fatty acid that is present in the form of glycerides in Brassica species [26]. Low erucic acid content is desirable in Brassica varieties due to its harmful effects [14]. Statistical analysis for erucic acid contents showed highly significant differences among the genotypes (Table-1). Erucic acid content varied from 42.7 % (AUP-404) to 59.9 % (AUP-407). Mean erucic acid content was 51 % (Table-3). Our findings are in agreement with the earlier results of [14] [17], who also reported significant genetic variability for erucic acid content.

Oleic acid content (%)

Oleic acid belongs to the class of mono-saturated omega-9 fatty acids. The high oleic acid content in Brassica is desirable for the nutritional purpose [27]. Statistical analysis for oleic acid contents showed highly significant differences among the genotypes. The mean performance of genotypes for oleic acid contents was varied from 45.7 to 58.0 %, with the overall mean of 53.0 % (Table-3). Maximum oleic acid content was recorded for AUP-401, while the minimum was observed for AUP-407. Similar results were found by [28], who also reported highly significant differences for oleic acid contents.

Linolenic acid content (%)

Linolenic acid is a nutritionally essential omega-3 fatty acid. It has potential benefits for health, and thus a high percentage of this fatty acid is advantageous [29]. Statistical analysis revealed significant differences among the genotypes for linolenic acid (Table-1). Mean data for linolenic acid content varied from 8.1 % (AUP-405, AUP-407) to 9.7 % (AUP-403). The mean linolenic acid content was 8.8 % (Table-3). Earlier researcher [17] also reported significant genetic variability among brassica lines for linolenic acid contents.

Regression Analysis

Regression analysis helps one understand how the typical value of the dependent variable changes when any one of the independent variables is varied, while the other independent variables are held fixed. Seed yield plant^{-1} is used as a dependent variable in this experiment. It was effected by various independent variables as, in a unit increase in 1000-seed weight, seed yield plant^{-1} decreased 2.97 units with the coefficient of determination (R^2) = 0.155 (Figure 1), in a unit raise in seeds pod^{-1} , seed yield plant^{-1} resulted 0.54 units increase with $R^2=0.134$ (Figure 2), a unit increase in pod length resulted 0.894 units decrease in seed yield plant^{-1} with $R^2=0.073$ (Figure 3), a unit increase in plant height resulted 0.048 units decrease in seed yield plant^{-1} with $R^2=0.020$ (Figure 4), a unit raise in pods plant^{-1} resulted 0.069 units increase in seed yield plant^{-1} with $R^2=0.497$ (Figure 5), a unit increase in pods main raceme⁻¹ resulted 0.097 units increase in seed yield plant^{-1} with $R^2=0.102$ (Figure 6), a unit increase in branches plant^{-1} resulted 1.75 units increase in seed yield plant^{-1} with $R^2=0.126$ (Figure 7), a unit

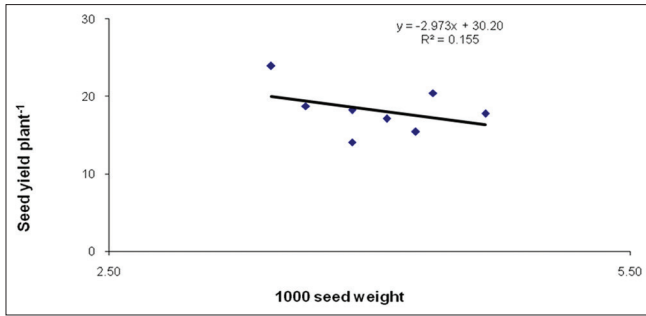


Figure 1: Relationship between 1000-seed weight and seed yield plant⁻¹

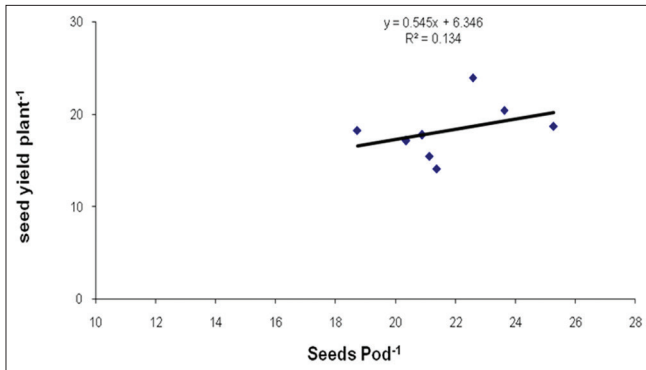


Figure 2.: Relationship between seed pod⁻¹ and seed yield plant⁻¹

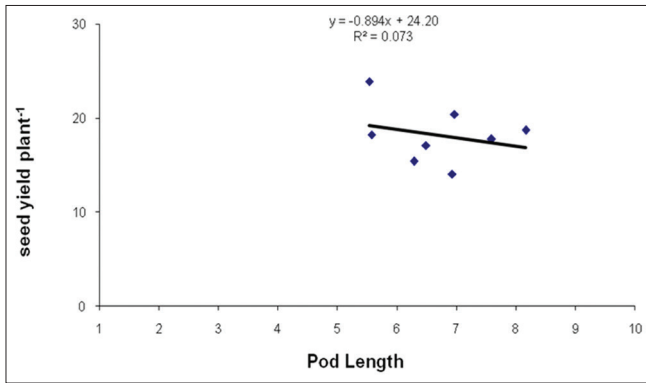


Figure 3.: Relationship between pod length and seed yield plant⁻¹

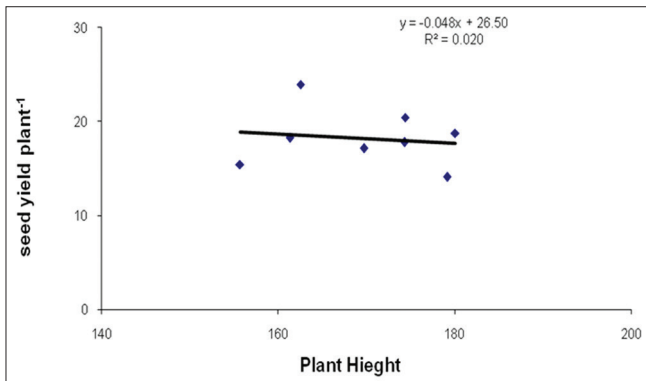


Figure 4: Relationship between plant height and seed yield plant⁻¹

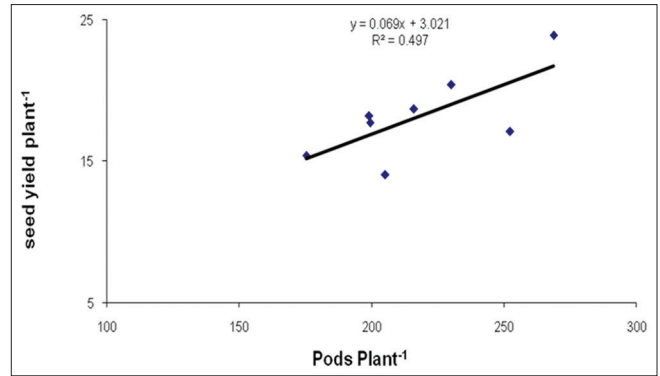


Figure 5: Relationship between pods plant⁻¹ and seed yield plant⁻¹

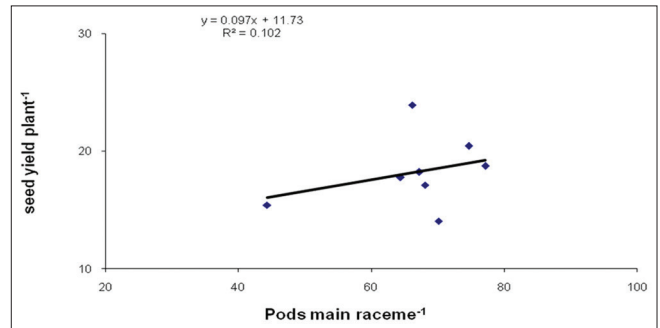


Figure 6: Relationship between pod main raceme⁻¹ and seed yield plant⁻¹

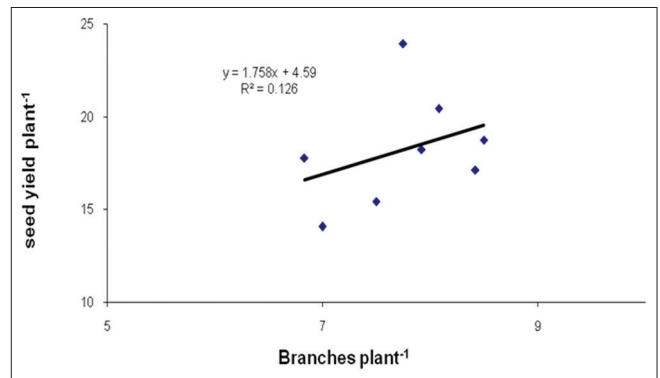


Figure 7: Relationship between primary branches plant⁻¹ and seed yield plant⁻¹

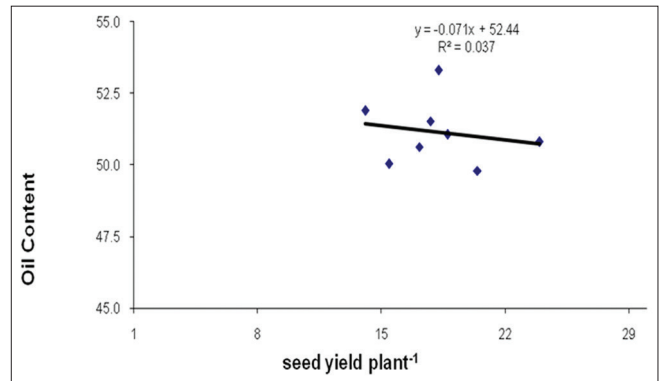


Figure 8: Relationship between seed yield plant⁻¹ and oil content

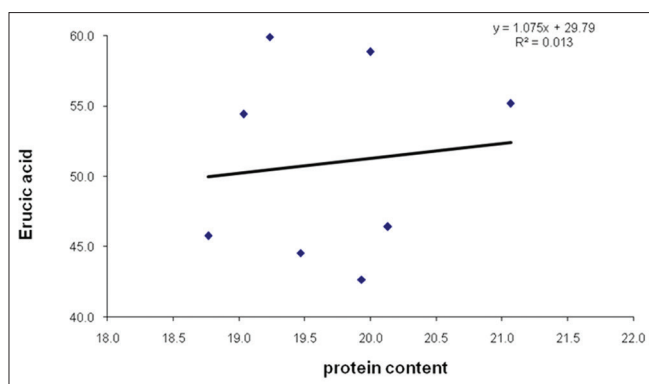


Figure 9: Relationship between protein content and erucic acid content

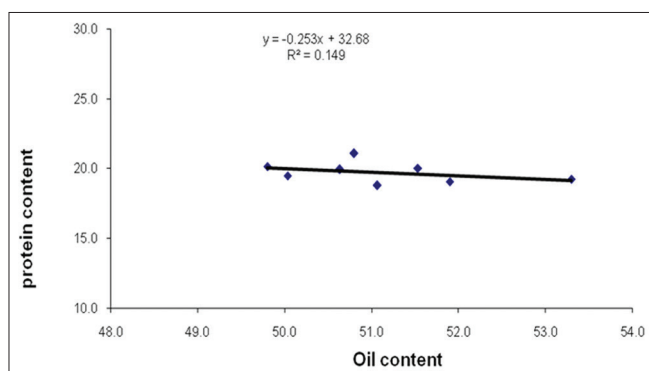


Figure 10: Relationship between oil content and protein content

increase in seed yield plant⁻¹ as independent variable resulted 0.071 units decrease in oil content with $R^2 = 0.037$ (Figure 8), a unit increase in protein content as an independent variable resulted 1.075 units increase in erucic acid content with $R^2 = 0.013$ (Figure 9) and a unit increase in oil content as an independent variable resulted 0.253 units decrease in protein content with $R^2 = 0.149$ (Figure 10).

CONCLUSIONS AND RECOMMENDATIONS

A significant amount of genetic variability was observed among *brassica napus* genotypes for all the major traits studied. Based on results, AUP-401, AUP-402, AUP-404, and AUP-407 are recommended to be utilized in future brassica breeding programs for progressing genotypes with less glucosinolate content, high seed yield plant⁻¹, pods plant⁻¹ and protein contents, less erucic acid and high oil contents. Pods plant⁻¹ affected the seed yield plant⁻¹ positively. The developed germplasm could be used in the upcoming brassica breeding programs to release high yielding, disease resistance, stress tolerance, and insect resistance varieties, which will eventually upsurge the productivity and decrease the gap between demand and domestic production of the brassica crop.

REFERENCES

- Miri HR. Morph-physiological basis of variation in rapeseed (*Brassica napus* L.) yield. *Int. J. Agric. Bio.* 2007.
- Kaushik N. Separation and quantification of quality parameters in rapeseed mustard. In Abstract of third Int. Symp. and short course on separation sciences. 1998; 15: 23-26.
- McDonald B.E. *Canola Oil: Nutritional Properties*. Canola Council Publications. Available online at: <http://www.canolacouncil.org/healthnutritional.aspx/>. 2011.
- Jensen CR, Mogensen VO, Mortensen G, Fieldsend JK, Milford GF, Andersen MN, Thage JH. Seed glucosinolate, oil and protein contents of field-grown rape (*Brassica napus* L.) affected by soil drying and evaporative demand. *Field Crops Res.* 1996; 47(2-3): 93-105.
- Boem FH, Lavado RS, Porcelli CA. Note on the effects of winter and spring waterlogging on growth, chemical composition and yield of rapeseed. *Field Crops Res.* 1996; 47(2-3): 175-179.
- Baux A, Hebeisen T, Pellet D. Effects of minimal temperatures on low-linolenic rapeseed oil fatty-acid composition. *Eur. J. of Agron.* 2008; 29(2-3): 102-107.
- Engqvist GM, Becker HC. Correlation studies for agronomic characters in segregating families of spring oilseed rape (*Brassica napus*). *Hereditas.* 1993; 118(3): 211-216.
- ÖZER H, ORAL E, DOĞRU Ü. Relationships between yield and yield components on currently improved spring rapeseed cultivars. *Turkish J. Agric. and Forestry.* 1999; 23(6): 603-608.
- Razi R. Edible Oil worth Rs. 31 billion imported. *Business News*. pp 08. ``The News``. International Pakistan. 2004.
- Singh RK, Chaudhary BD. *Biometrical methods in quantitative genetic analysis* Kalyani Publishers, New Delhi, India. 1979; Pp. 318.
- Akbar A, Tariq M, Yaqub M, Anwar M, Ali M. Genetic variability, combining ability, and correlation studies in 5 x 5 diallel cross of (*B. napus* L.). *Pak. Asian J. Plant Sci.* 2008; 14: 376-379.
- Ahad F, Raziuddin, Ahmad N, Nauman M, Iqbal T, Khan N, Hameed F, Hussain Q. Genetic analysis for yield traits using f_3 populations in rapeseed (*Brassica napus* L.). *Pak. J. Agri. Res.* 2020; 33(2): 253-263.
- Choudhary BR, Joshi P, Ramarao S. Genetic diversity and combining ability study in a 6 x 6 diallel cross of *B. juncea*. *Plant breed.* 2003; 122: 328-331.
- Khan S, Farhatullah, Khalil IH. Phenotypic correlation analysis of elite $F_{3:4}$ Brassica populations for quantitative and qualitative traits. *ARPN J. Agric. Biol. Sci.* 2008; 3(1): 38-42.
- Khan RS, Khan FA. Evaluation of genetic potential of some Brassica germplasm collections. *Int. J. Agric. Biol.* 2003; 6(4): 630-631.
- Tahir MHN, Bashir S, Bibi A. Genetic potential of canola (*Brassica napus* L.) varieties under water stress conditions. *Caderno de Pesquisas. Bio.* 2006; 18(2): 127-135.
- Ahmad H, Islam M, Khan IA, Ali H, Rahman H, Ullah I. Evaluation of advance rapeseed line hs-98 for yield attributes and biochemical characters. *Pak. J. Bot.* 2013; 40(3): 1099-1101.
- Azadgoleh ME, Zamani M, Esmaeil Y. Agronomical important traits correlation in rapeseed (*Brassica napus* L.) genotypes. *Res. J. Agric. Bio. Sci.* 2009; 5(5): 798-802.
- Khan FU, Raziuddin, Khalil IA, Khalil IH, Ullah I. Heritability and genetic potential of *Brassica napus* genotypes for yield and yield components. *Am-Eurasian J. Agric. Environ. Sci.* 2013; 13(6): 802-806.
- Ghosh SK, Gulati SC. Genetic variability and association of yield components in Indian mustard (*Brassica juncea* L.). *CROP RESEARCH-HISAR.* 2001; 21(3): 345-349.
- Dar ZA, Wani SA, Zaffar G, Habib M, Wani MA, Ashfaq A, Khan M.H Razvi S.M. Variability studies in brown sarson (*Brassica rapa* L.). *Res. J. Agric. Sci.* 2010; 1(3): 273-274.
- Kandil AA, Mahrous NM, El Mohandes SI. Genotypic and phenotypic variability, heritability and enter-relationships of some characters in oilseed rape, *Brassica napus* L. *J. Agric. Sci.* 1994; 25: 155-166.
- Yadava DK, Giri SC, Vignesh M, Vasudev S, Kumar Yadav A, Dass B, Singh R, Singh N, Mohapatra T, Prabhu KV. Genetic variability and trait association studies in Indian mustard (*Brassica juncea* L.). *Indian. J. Agric. Sci.* 2011; 81(8): 712-716.
- Shaukat SR, Fahim UK, Ibni AK. Genetic variation and heritability estimates of quality traits in *Brassica napus* L. *J. Bio. Agric. Healthcare.* 2014; 4(20):1-4.
- Fayyaz L, Farhatullah, Shah S, Iqbal I, Kanwal M, Ali S. Genetic variability studies in Brassica f_2 populations developed through inter and intra-specific hybridization. *Pak. J. Bot.* 2014; (1): 265-269.
- Davis J. Plant-based omega chewable supplement. 2011. <http://www.google.com/patents/US20110044964>.

27. Iqbal S, Farhatullah, Nasim A, Kanwal M, Fayyaz L. Heritability studies for seed quality traits in introgressed segregating populations of Brassica. Pak. J. Bot. 2014; 46(1): 239-243.
28. Alemayehu N, Becker H. Quantitative genetic analysis of total glucosinolate, oil and protein contents in Ethiopian mustard (*Brassica carinata* A. Braun). SINET: Ethiopian Journal of Science. 2005; 28(2): 141-150.
29. Simopoulos AP. Omega-3 fatty acids in health and disease and in growth and development. The Amer. J. Clin. Nutri. 1991; 54(3): 438-463. <https://doi.org/10.1093/ajcn/54.3.438>