Genetic Variability and Correlation Studies in Brassica Napus L. Genotypes

Syed Noor UI Abideen¹, Faisal Nadeem², and Syed Ainul Abideen³

¹Institute of Biotechnology and Genetic Engineering, The University of Agriculture, Peshawar, Pakistan

²Department of Plant Breeding and Genetics, The University of Agriculture, Peshawar, Pakistan

³Department of Medical Cell Biology, University of Bergen, Bergen, Norway

Copyright © 2013 ISSR Journals. This is an open access article distributed under the *Creative Commons Attribution License*, which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited.

Abstract: This research work was carried out at The University of Agriculture, Peshawar during crop season year 2011-12. The objectives were to study the genetic variability and correlation among different traits in *Brassica napus* L. Data were recorded on agronomic and quality traits. The breeding material comprised 8 genotypes of *Brassica napus* L. These genotypes were evaluated in replicated trial in a randomized complete block design (RCBD) with three replications. Results revealed highly significant differences among the genotypes for most of the traits. Non-significant differences were, however, observed among the genotypes for primary branches plant⁻¹ and pods plant⁻¹. Genotype 1 was found superior for most of the traits i.e maximum oleic acid content etc. Correlation analysis presented highly significant positive phenotypic correlation of plant height with pods main raceme-1 and pod length seed yield exhibited significant positive phenotypic correlation of oleic acid content was also observed. From the results it can be concluded that Genotype 2 can be used for developing superior genotypes for seed yield, seed pod⁻¹ and protein content while Genotype 7 can be used for yielding high oil content. The significant and positive correlation of seed yield plant⁻¹ with pods plant⁻¹ and protein content was important in making indirect selection for seed yield.

Keywords: *Brassica napus* L, genotypes, linolenic acid content, Correlation, Variability.

1 INTRODUCTION

Brassica napus L is an important oil seed crop which belongs to family Brassicaceae. *Brassica* is a genus within the Brassicaceae (Cruciferae), commonly known as the mustard family. This family contains 375 genera and 3200 species includes crops, ornamental plants, and many weeds. The members of the genus are collectively known as cruciferous vegetables, cabbages, or mustards etc. Common types of brassica used for food include cabbage, cauliflower, broccoli, brussel sprouts, and some types of seeds [1]. The genus is remarkable for containing more important agricultural and horticultural crops than any other genus. Most are annual or biennial, but some are small shrubs. Due to their agricultural importance, Brassica plants have been the subject of much scientific interest. Three important species (*Brassica carinata, Brassica juncea, Brassica napu*) are derived by combining the chromosomes from three diploid species (*Brassica oleracea, Brassica nigra and Brassica rapa*), as described by the Triangle of U theory [2].

Brassica vegetables are full of indole-3-carbinol, a compound which enhances DNA repair in cells and tissues and appears to block the growth regarding cancer tissues [3][4]. Both *Brassica napus* and *Brassica juncea* have remained one of the major sources of oil in the subcontinent for centuries. *Brassica napus* is sparingly grown for young leaves used as pot herb; more generally grown as forage for livestock feed, and as source of rapeseed oil. Rape oil used in food industry, as an illuminant and lubricant, and for soap manufacture. Residual rapeseed cake, though low in food value, used as livestock feed. Rapeseed oil has potential market in detergent lubrication oils, emulsifying agents, polyamide fibers, and resins, and as a vegetable wax substitute. Rapeseed and mustard are rich source of oil and contains 44% to 46% good quality oil. In addition, its meal has 38-40% protein that has a complete profile of amino acids including lysine, methionine and cystine. The toxic content in *Brassica napus* are erucic acid and glucosinolate [5].

In Pakistan the rape and mustard crop was grown on an area of about 216.5 thousands hectares with a seed production of 191.9 thousand tons with the average yield of 886 kg ha⁻¹ while in Khyber Pakhtunkhwa rape and mustard crop was grown on an area of about 17.1 thousands hectares with a seed production of 7.9 thousand tons with a grain yield of 450 kg ha⁻¹ [6].

The major emphasis of the breeders is to enhance grain yield and oil contents along with maturity duration of a variety to meet up the needs of end user. The emphasis of the present study was to evaluate different genotypes with regards to oil content, glucosinulate content and yield attributing traits which can gave returns to the farmers. China is the top rapeseed producer followed by Canada and India [7].

Seed yield is a complex character determined by several characters having positive or negative effects on this trait. It is important to examine the contribution of each of the trait in order to give more attention to those having the greatest influence on seed yield. Therefore, information on the association of traits with seed yield is of great importance to define selection criteria for rape breeding in terms of yield. Generally, correlation coefficients show relationships among independent characteristics and the degree of linear relation between these characteristics [8].

1.1 OBJECTIVES

Keeping in view the importance of *Brassica napus* as vegetable oil, an experiment was conducted with the following objectives:

- 1) To study the variability among different genotypes of *Brassica napus* L.
- 2) To study the correlation among different traits.

2 MATERIALS AND METHODS

This experiment was conducted to study Genetic variability and correlation for agronomic and quality traits in *Brassica napus* L. genotypes at Malakandher research farm, The University of Agriculture, Peshawar during 2011-12. Eight genotypes like (G-1, G-2, G-3, G-4, G-5, G-6, G-7 and G-8) were evaluated in a randomized complete block design with three replications. Each genotype was planted in four meter long row with row-row distance of 50cm and plant-plant distance was 20cm. Crop was irrigated according to the recommended requirements. At maturity level data were recorded on four randomly selected plants per genotype in each replication.

Data were recorded on the following parameters.

2.1 PLANT HEIGHT (CM)

Plant height was measured on four randomly selected plants in each replication from the ground level to the tip of the plant with the help of a measuring rod.

2.2 PRIMARY BRANCHES PLANT⁻¹

Total numbers of primary branches originating from the main stem were counted from the base and data was recorded on them.

2.3 PODS MAIN RACEME⁻¹

Total numbers of pods from the base to the tip of the main raceme were counted on selected plants in each replication.

2.4 PODS PLANT⁻¹

Total numbers of pods present on selected plants were counted in each replication and data was recorded on them.

2.5 POD LENGTH (CM)

Pod length was recorded in centimeters on randomly selected three pods plant⁻¹ by measuring the distance from the base to the tip of the individual pod and then their average was calculated.

2.6 SEED POD⁻¹

Seeds pod⁻¹were recorded by counting seeds from 3 randomly selected pods on main raceme from selected plants in each replication and then their average value was calculated.

2.7 1000- SEED WEIGHT (G)

100-Seed weight was recorded in grams by weighing a sample of 100 seeds plant⁻¹ through an electrical balance and then multiplied by 10 to get 1000-seed weight.

2.8 SEED YIELD PLANT⁻¹ (G)

Seed yield plant⁻¹ was recorded in grams by threshing and weighing grains from all selected plants by means of electrical balance.

2.9 BIOCHEMICAL ANALYSIS

Quality of seed in *Brassica* depends on high percentage of oil, protein and oleic acid while low quantity of glucosinolate (GSL), linolenic acid and erucic acid is desirable.

Biochemical analysis of the studied *Brassica* genotypes was conducted in such a way that seed sample from each selected plant was scanned on Near Infra-Red (NIR) spectroscopy at biochemical laboratory, crop breeding section of Nuclear Institute for Food and Agriculture (NIFA) Peshawar. Following Biochemical parameters were calculated in the present study;

- 1. Oil content (%)
- 2. Protein content (%)
- 3. Oleic acid (%)
- 4. Moisture content (%)
- 5. Glucosinolate (μ mole g⁻¹)
- 6. Linolenic acid (%)
- 7. Erucic acid (%)

2.10 STATISTICAL ANALYSIS

The data recorded for different agronomic and quality traits was statistically analyzed as follows.

2.11 ANALYSIS OF VARIANCE

Analysis of variance was conducted using MS Excel software. LSD $_{(0.05)}$ values were computed for different parameters using MSTAT-C software for means comparison.

2.12 CORRELATION ANALYSIS

Pearson correlation coefficient (phenotypic correlation) was computed using the IBM SPSS Statistics 20.

3 RESULTS AND DISCUSSION

3.1 ANALYSIS OF VARIANCE

3.1.1 PLANT HEIGHT

Highly significant differences (P< 0.01) among *Brassica napus* L. genotypes for plant height were indicated by analysis of variance. Plant height ranged from 156 to 180 cm with the mean value of 170 cm. Shortest plant height (156cm) was observed for genotype G-8, while longest plant height(180cm) was observed for genotype G-1 (Table 2). Our highly significant results were in close resemblance with the earlier results of [9] for plant height among *brassica* genotypes.

3.1.2 PRIMARY BRANCHES PLANT⁻¹

For primary branches plant⁻¹ non-significant differences (P>0.05) among *Brassica napus* L. genotypes were revealed by analysis of variance. Primary branches plant⁻¹ ranged from 7 to 9 with the mean value of 8. Minimum number of primary branches plant⁻¹ about 7 were produced by genotype G-6, while maximum 9 by genotype G-1 (Table 2). [10] results were in contrast to our results for primary branches plant⁻¹, as he observed significant differences for primary branches plant⁻¹.

3.1.3 PODS MAIN RACEME⁻¹

Highly significant differences (P<0.01) among *Brassica napus* L. genotypes for pods main raceme⁻¹were revealed by analysis of variance. Pods main raceme⁻¹ranged from 44 to 77 with the mean value of 67. Minimum number of pods main raceme⁻¹ about 44 were produced by genotype G-8, while maximum 77 by genotype G-1 (Table 2). Significant differences were also obtained by [10] for pods main raceme⁻¹, while working on *Brassica napus* L. genotypes.

3.1.4 POD LENGTH

Analysis of variance presented highly significant differences (P<0.01) among *Brassica napus* L. genotypes for pod length. Pod length ranged from 6 to 8 cm with the mean value of 7 cm. Genotype G-2 produced shortest pods i-e 6cm while longest pods were observed on genotype G-1 which was 8 cm (Table 2). Our highly significant results for pod length were also supported by the findings of [10].

3.1.5 SEED YIELD PLANT⁻¹

Analysis of variance for Seed Yield plant^{-1} revealed highly significant differences (P<0.01) among *Brassica napus* L. genotypes. Seed yield plant^{-1} ranged from 14 to 24g with the mean value of 18g. Minimum seed yield plant^{-1} was 14g produced by genotype G-5, while maximum 24g by genotype G-2 (Table 2). Similar significant differences were also perceived by [11] for seed yield plant^{-1} .

3.1.6 1000 SEEDS WEIGHT

Highly significant differences (P<0.01) for 1000 seeds weight among *Brassica napus* L. genotypes were indicated by analysis of variance.1000 seeds weight ranged from 3.0 to 5.0g with the mean value of 4.0g.Genotype G-2 showed minimum 1000 seeds weight of 3.0g, while maximum 5.0g was obtained for G-6 (Table 2). Our highly significant results for 1000 seeds weight were also supported by the earlier results of [10].

3.1.7 PODS PLANT⁻¹

For pods plant⁻¹ non-significant differences (P>0.05) among *Brassica napus* L. genotypes were displayed by analysis of variance. Pods plant⁻¹ ranged from 175 to 269 with mean value of 218.Genotype G-8 showed minimum number of pods plant⁻¹(175), while genotype G-2 showed maximum number of pods plant⁻¹(269) (Table 2), [12] results were in contrast to our results, who recorded significant differences for pods plant⁻¹ among *Brassica napus* L. genotypes.

3.1.8 SEEDS POD⁻¹

Highly significant differences (P \leq 0.01) among *Brassica napus* L.genotypes were revealed by analysis of variance for seeds pod⁻¹. Number of seeds pod⁻¹ ranged from 19 to 25 with mean value of 22. Minimum number of seeds pod⁻¹ i-e 19 was observed on genotype G-7, while maximum of 25 were observed on genotype G-1 (Table 2). Similar significant differences were also obtained by [10] for seeds pod⁻¹ among *Brassica napus* L. genotypes.

3.1.9 OIL CONTENT

Analysis of variance displayed highly significant differences (P<0.01) among *Brassica napus* L. genotypes for oil content. Oil content ranged from 49.8 to 53.3% with mean value of 51.1%. Minimum oil content 49.8% was recorded for genotype G-3 and maximum of 53.3 % for genotype G-7 Table 3, [13] also observed significant differences for oil content among *brassica* genotypes.

3.1.10 PROTEIN CONTENT

For protein content highly significant differences (P<0.01) among *Brassica napus* L. genotypes were presented by analysis of variance. Protein content ranged from 18.8 to 21.1% with the mean value of 19.7%. Genotypes G-1 showed minimum protein content of 18.8%, while maximum 21.1% was recorded for genotype G-2 (Table 3). Our results were in close resemblance with the earlier results of [13] who also observed significant differences for protein content among brassica genotypes.

3.1.11 GLUCOSINOLATE CONTENT

For glucosinolate content highly significant differences (P<0.01) among *Brassica napus* L. genotypes were revealed by analysis of variance. Glucosinulate content ranged from 55.1to 86.0 μ moleg⁻¹ with the mean value of 70.7 μ moleg⁻¹. Minimum glucosinolate content was 55.1 μ moleg⁻¹ obtained from genotypes G-1, while maximum 86.0 μ moleg⁻¹ from genotype G-6 (Table 3). [14] also perceived similar highly significant differences for glucosinolate content, while working on brassica genotypes.

3.1.12 MOISTURE CONTENT

Highly significant differences (P<0.01) among *Brassica napus* L. genotypes for moisture content were revealed by analysis of variance. Moisture content ranged from 4.9 to 6.2% with the mean value of 5.2%. Genotype G-3 showed 4.9% of minimum moisture content while maximum moisture content was 6.2% was observed for genotype G-2 (Table 3). Similar significant differences were also obtained by [10] for moisture content among *brassica napus* L.genotypes.

3.1.13 ERUCIC ACID CONTENT

For Erucic acid content highly significant differences (P<0.01) among *Brassica napus* L. genotypes were revealed by analysis of variance. Erucic acid content ranged from 42.7 to 59.9% with the mean value of 51.0%.Genotype G-4 showed the minimum erucic acid content of 42.9% and maximum 59.9% for the genotype G-7 (Table 3). Our highly significant results were in close resemblance with the earlier results of [14] for erucic acid content among brassica genotypes.

3.1.14 OLEIC ACID CONTENT

Highly significant differences (P<0.01) were observed for Oleic acid content among *Brassica napus* L. genotypes. Oleic acid content ranged from 45.7 to 58.0% with mean value of 53.0%. Minimum Oleic acid content (45.7%) was observed for genotype G-7, while maximum (58.0%) was obtained for genotype G-1 (Table 3). [14] also detected significant differences for oleic acid content, while working on brassica genotypes.

3.1.15 LINOLENIC ACID CONTENT

Analysis of variance recorded highly significant differences (P<0.01) among *Brassica napus* L. genotypes for Linolenic acid content. Linolenic acid content ranged from 8.1 to 9.7% with mean value of 8.8%. Genotype G-7 produced the minimum

Linolenic acid content (8.1%) and maximum (9.7%) was produced by genotype G-3 (Table 3). Similar significant results were also found by [14] for linolenic acid content among brassica genotypes.

3.2 CORRELATION ANALYSIS

Positive significant phenotypic correlation of plant height with pods main raceme⁻¹ (r=0.77) and pod length (r=0.71) was recorded. Similarly significant positive phenotypic correlation of seed yield with pods plant⁻¹(r=0.71), protein content(r=0.73) and moisture content(r=0.73) was also observed. Positive significant correlation of plant height with pods main raceme⁻¹ and pod length was also supported by the findings of [13].

Significant positive phenotypic correlation(r=0.81) existed between pods plant⁻¹ and linolenic acid. Likewise positively significant correlation of oil with erucic acid(r=0.77) and significant negative correlation with oleic acid(r=-0.80) was also recorded. [15] also observed significant positive correlation between pods plant⁻¹ and seed yield .It was also recorded that protein content was positively correlated with linolenic acid(r=0.77), while significant negative correlation existed between erucic acid and oleic acid(r=-0.93).Positive significant correlation between seed yield and protein content was also recorded by [13].

Non-significant positive phenotypic correlation of oleic acid with seed $pod^{-1}(r=0.68)$ and negative phenotypic correlation with glucosinolate also existed (Table 4).

Traits	Replications	Genotype	Error	CV%
Plant height	37.42	239.45**	39.88	3.72
Primary branches plant ⁻¹	0.58	1.11 ^{NS}	0.66	10.48
Pods main raceme ⁻¹	157.32	296.91**	61.69	11.80
Pod length	0.19	2.53**	0.13	5.34
Seed yield plant ⁻¹	2.91	27.52**	1.45	6.62
1000 Seed weight	0.18	1.08**	0.14	10.41
Pods plant ⁻¹	1364.45	2824.28 ^{NS}	2855.50	24.47
Seeds pod ⁻¹	3.44	12.43**	2.57	7.36
Oil content	0.01	3.77**	0.15	1.07
Proteins content	0.08	1.62**	0.04	1.47
Glucosinolate content	16.31	428.00**	8.84	5.95
Moisture content	0.01	0.55**	0.02	3.88
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

Table 1. Mean Squares for agronomic parameters in Brassica napus L

** Highly significant (P_< 0.01)

Ns. Non- significant (P> 0.05)

Table 2.	Mean values for	r agronomic traits in	Brassica napus L.
----------	-----------------	-----------------------	-------------------

Genotypes	Plt ht (cm)	PB/Plt	Pod/MR	Pod L (cm)	Sd Yld (g)	1000 SW (g)	Pod/Plt	Sd/Pod
G-1	180.08a	8.5a	77.17a	8.17a	18.73bc	3.30bc	216.00a	25.27a
G-2	162.58bc	7.75abc	66.17a	5.54e	23.93a	3.03c	268.83a	22.57abc
G-3	174.42a	8.08abc	74.67a	6.96bc	20.43b	3.90b	230.17a	23.63ab
G-4	169.75ab	8.42ab	68.08a	6.48cd	17.13cd	3.60bc	252.33a	20.35cd
G-5	179.17a	7bc	70.17a	6.92c	14.07e	3.23c	205.25a	21.38bcd
G-6	174.33a	6.83c	64.42a	7.59ab	17.77c	4.97a	199.5a	20.89bcd
G-7	161.33bc	7.92abc	67.25a	5.58e	18.23c	3.43bc	199.13a	18.72d
G-8	155.67c	7.5abc	44.33b	6.29d	15.43de	3.60bc	175.3a	21.13bcd
Lsd(5%)	11.06	1.423	13.75	0.6314	2.109	0.66	93.58	2.802

Genotypes	Oil(%)	Protein(%)	GSL	Moisture	Erucic acid	Oleic acid	Linolenic acid
G-1	51.1cd	18.8e	55.1f	5.2b	45.8cd	58.0a	8.5bc
G-2	50.8d	21.1a	63.5e	6.2a	55.2b	51.5c	9.5a
G-3	49.8f	20.1b	78.6bc	4.9c	46.4c	55.2b	9.7a
G-4	50.6de	19.9b	68.9d	4.9c	42.7e	55.3b	9.5a
G-5	51.9b	19.0de	82.3ab	5.1bc	54.4b	52.0c	8.1c
G-6	51.5bc	20.0b	86.0a	5.1bc	58.9a	49.2d	8.7b
G-7	53.3a	19.2cd	76.1c	5.0c	59.9a	45.7e	8.1c
G-8	50.0ef	19.5c	55.3f	4.9c	44.6d	57.1a	8.3bc
Lsd(5%)	0.6782	0.3502	5.207	0.248	1.356	1.094	0.429

Table 3. Mean values for seed and oil quality traits in Brassica napus L.

Table 4. Correlation coefficients for various agronomic and quality traits

	PB	Pods	Pod	Sdyld	1000	Pods	Sd/P0d	OIL	Protein	GSL	Moisture	Erucic	Oleic	Linolenic
	Plant ⁻¹	/MR	length	Plant ⁻¹	Sd.wt	Plant ⁻¹		content	content	content	content	acid	acid	acid
Plant height	0	0.77	0.81	-0.14	0.18	0.12	0.52	0.03	-0.34	0.37	-0.11	-0.05	0.19	0.05
PB plant ⁻¹	-	0.39	-0.01	0.36	-0.44	0.45	0.35	-0.22	-0.06	-0.55	-0.01	-0.6	0.45	0.41
Pods/MR		-	0.39	0.32	-0.12	0.49	0.44	0.21	- <mark>0.11</mark>	0.31	0.14	0.08	-0.06	0.28
Pod length			-	-0.27	0.42	-0.24	0.6	-0.19	-0.45	0.06	-0.28	-0.26	0.45	-0.1
Sdyld plant ⁻¹				-	-0.14	0.71	0.37	-0.19	0.73	-0.16	0.73*	0.14	-0.1	0.67
1000Sd.wt					7	-0.33	-0.17	-0.07	0.11	0.53	-0.41	0.2	-0.2	0.07
Pods plant ⁻¹						-	0.26	-0.25	0.67	-0.07	0.6	-0.14	0.07	0.81**
Sd/P0d							-	-0.54	0.01	-0.4	0.31	-0.44	0.68	0.32
Oil content								-	-0.4	0.39	0	0.77	-0.80	-0.63
Protein content									2	0.06	0.59	0.11	-0.13	0.77*
GSL content										-	-0.27	0.59	-0.65	0
Moisture content											-	0.31	-0.13	0.27
Erucic acid												-	-0.93**	-0.36
Oleic acid													-	0.26

4 CONCLUSIONS AND RECOMMANDATIONS

- Highly significant differences among genotypes for most of the important traits showed the presence of diversity among these genotypes.
- Genotype G-2 produced maximum seed yield plant⁻¹, seeds pod⁻¹ and protein content, genotype G-7 yielded maximum oil content and number of pods on main raceme while minimum erucic acid and glucosinolate contents were observed for the genotypes G-4 and G-1 respectively.
- Significant and positive correlation of seed yield was observed with pods plant⁻¹ and protein content while negative correlation of erucic acid was observed with pods plant⁻¹ and seeds pod⁻¹. Thus indirect selection for these traits can be practiced

From the above conclusions it was recommended that:

- Genotype G-2 can be used for general cultivation under Peshawar conditions.
- Pods plant and protein content must be focused mainly while indirectly selecting for high yielding genotypes.
- Genotypes G-1, G-2, G-4 and G-7 could be evaluated further to be used in future breeding programmes.

ACKNOWLEDGMENT

Starting with millions of thanks to ALLAH, the Omnipotent and the Omniscient, who is so kind to mankind and who enabled me for successfully completing this internship research and report. And all the respect for his last and HOLY PROPHET (peace be upon him) for enlightens with the essence of faith in ALLAH and guiding the mankind to right path. Special thanks to my brother Syed Ainul Abideen and my friend Faisal Nadeem for their kind help in my experiment's data collection and paper completion. I am extremely thankful to my class fellows for their sincere and kind help throughout my research work.

Last but not the least; I express my deepest appreciation and recognition to my parents, brothers and sister, who supported me morally and financially throughout my educational carrier.

SYED NOOR UL ABIDEEN

REFERENCES

- [1] Brassica [Online] Available: http://en.wikipedia.org/wiki/Brassica (March 2013)
- [2] Nagaharu U. "Genome analysis in Brassica with special reference to the experimental formation of B. napus and peculiar mode of fertilization." *Japanese Journal of Botany* 7: 389 452 (1935).
- [3] "Broccoli chemical's cancer check". BBC News. 7 February 2006. Retrieved 5 September 2010.
- [4] "How Dietary Supplement May Block Cancer Cells". Science Daily. 30 June 2010. Retrieved 5 September 2010.
- [5] Dr. Abdul Rashid, "Rapeseed," Pakistan Agricultural Reseach Council.
- [Online] Available: http://www.parc.gov.pk/1subdivisions/narccsi/csi/rapeseed.html (March 2013)
 [6] FBS 2011-12, agriculture statistics of Pakistan, federal bureau of statistics, Islamabad Pakistan
- [7] FAOSTAT 2009, Food and agricultural organization of United Nations.
- [8] Korkut, Z.K. İ. Başer and S. Bilir. 1993. The studies path coefficient and correlation of drum wheat's. Symposium of Drum Wheat and Its Products, Ankara, 183-87.
- [9] Ali, N., F. Javidfar, and A.A. Attary. 2002. Genetic variability, correlation and path analysis of yield and its components in winter rapeseed (*Brassica napus L.*). *Pak. J. Bot.*, 34(2): 145-150
- [10] Zebarjadi, A., M. Kakaei, and A. Mostafaie. 2011. Genetic variability of some traits in Rapeseed (*Brassica napus* L.) under drought stress and non-stress conditions. Biharean Biologist. 5(2): 127-131.
- [11] EsmaeeliAzadgoleh, M.A., M.Zamani, Esmaeil, and Yasari. 2009. Aagronomical Important Traits Correation in Rapeseed (*Brassica napus* L.) genotypes. *J. Agric. Biol. Sci.* 5(5): 798-802.
- [12] Ali, N., F. Javidfar, J.Y. Elmira, and M.Y. Mirza. 2003. Relationship among yield components and selection criteria for yield improvement in winter rapeseed (*Brassica napus L*.). Pak. J. Bot. 35 (2): 167-174.
- [13] Aytac, Z. and G. Kinaci. 2009. Genetic variability and association studies of some quantitative characters in winter rapeseed (*Brassica napus L.*). Afri. J. Biotech. 8(15): 3547-3554.
- [14] Khan, S., Farhatullah, and I. H. Khalil. 2008. Phenotypic correlation analysis of elite F_{3:4} *Brassica* populations for quantitative and qualitative traits. ARPN *J. Agric. Biol. Sci.* 3(1): 38-42.
- [15] Tuncturk.M., and V.Ciftci. 2007. Relationships between yield and some yield components in rapeseed (*brassica napus* ssp. *oleifera* I.) cultivars by using correlation and path analysis. *Pak. J. Bot.* 39(1): 81-84.