

Full Length Research Paper

Genetic evaluation of yield and yield components at advanced generations in rapeseed (*Brassica napus* L.)

Hashemi Ameneh Sadat^{1*}, Ghorban Ali Nematzadeh¹, Nadali Babaeian Jelodar¹ and Omid Ghasemi Chapi²

¹College of Agricultural Sciences, University of Agricultural Sciences and Natural Resources of Sari, P. O. Box 578, Iran.

²Agricultural and Natural Resources Research Center of Mazandran Province, Mazandran, Sari, Iran.

Accepted 26 June, 2010

Three varieties of rapeseed namely Foseto, Option500 and Goliath including F₂ and F₃ generations (crosses among them) were planted in a complete randomized block design for evaluation of genetic variation, heritability, genetic advance and relationships between yield and its components, in experimental field of Rice and Citrus Research Institute, University of Agricultural Science and Natural Resources of Sari, Iran. The results indicated that the maximum phenotypic and genotypic variation related to the number of pod/plant and seed yield, and also their heritability in F₂ and F₃ generations were 94, 83 and 89, 96% including the good genetic advance in F₂ and F₃ generations, 33.81, 40.5 and 45.69, 53.7%, respectively. These genetic values express the role of additive effect of the genes controlling the heritability of the studied traits, so, selection of the agronomic important traits at the early generations will be effectiveness. The correlation between phenotype and genotype showed, the positive and significant relationship among seed yield, number of pod/plant, number of branch/plant, 1000 grain weight and pod length in F₂ and F₃ generations. The path analysis also indicated, the direct effect of the number of pod/plant in F₂ and number of branch/plant in F₃ generation, so these traits can be good criteria for selection at the segregating generations in rapeseed breeding pro-ram.

Key words: Genetic variation, heritability, genetic advance, correlation, path analysis.

INTRODUCTION

Rapeseed is an important species from *Brassica* genus and high value crop for oil industries. It is an important crop in Iran and for more than a decade has become one of the main crops for oil production, so a density breeding program focused on this crop. The study of the genetics and its components for main agronomy characteristics are the goal of the breeding strategy for this crop. So heritability is one of the popular indexes, between the phenotypic and breeding value (Falconer, 1989) and direct effect on selection. Khan et al. (2006a) reported high genetic variability for number of pod/plant, plant height and seed yield among 11 rapeseed varieties, including high heritability and genetic advances (GA) for

these traits too. Nassimi et al. (2006) also reported the same results in a diallel cross among 8 varieties. High heritability for 1000 grain weight, pod length and number of pod/plant in F₁ generation of *Brassica juncea* was reported by Mahmud et al. (2005).

As we know, the seed yield of rapeseed is the results of physiological and morphological effects, during the phonological period and yield components also have the significant role on the final performance of plant, in other words, the direct selection of the seed yield is not possible, so indirect selection can be the main policy for rapeseed breeding program. According to the results that was reported by Bhatt (1973), indirect selection is not sufficient enough for seed yield breeding, and for this purpose, the direct and indirect selection should be done simultaneously. Ahmad et al. (2003) showed the quantitative value of direct and indirect effect through path analysis for yield performance. Several researchers

*Corresponding author. E-mail: a_hashemi2004@yahoo.com.
Tel/Fax: 0981513822715.

studied the correlation between yield and yield components via path analysis as an index for selection of rapeseed improvement. Basalma (2008) reported the significant relationship between yield and oil content, non significant with other yield components. Jeromela et al. (2007) studied 30 rapeseed varieties and demonstrated that the number of pod/plant has maximum correlation with seed yield. Khan et al. (2006b) also reported, the positive significance between seed yield and plant height, number of branch/plant, number of pod/plant, number of seed/pod and pod length. The same results also were reported by Ozer et al. (1999). Engqvist and Becker (1991) evaluated F_3 generation of four crosses during two years, and announced, the significant correlation between yield with plant height and date of maturity in one year, but not significant for seed weight in two years.

We studied genetic variation, heritability, genetic advance and relationships between the yield and its components, to determine the best index of selection among three rapeseed varieties and their offspring in F_2 and F_3 generations in our research program.

MATERIALS AND METHODS

Three rapeseed varieties (Foseto, Option500 and Goliath) including the offspring of their F_2 and F_3 generations were planted for two years at complete randomized block design with three replications at experimental field of Rice and Citrus Research Institute, University of Agricultural Science and Natural Resources of Sari, Iran. Forty single plant of F_2 generation, including their parents, were evaluated in each replication and then for the next generation (F_3), twenty-five single plants accompanied by their parents in each replication were evaluated. All common agronomy practices were done. Then date of maturity, flowering (days), plant height (cm), number of branch/plant, main branch length (cm), number of pod/main branch, number of pod/plant, pod length, number of seed/pod, 1000 seed weight (g) and finally yield (g/m^2) were measured.

The analysis of variance was done according to the M-STAT C software and the mean square was also evaluated on the basis of Panse and Sukhatme (1967) (Table 1).

The components of variance including error variance (σ_e^2), genotypic variance (σ_g^2) and phenotypic variance (σ_p^2), were estimated, according to the following formula:

$$\sigma_e^2 = M_e$$

$$\sigma_g^2 = (M_g - M_e) / r$$

$$\sigma_p^2 = \sigma_g^2 + \sigma_e^2$$

Heritability (h^2) was studied based on Singh and Ceccarelli (1996)

formula (σ_g^2 / σ_p^2). The coefficient of genotypic and phenotypic variation was evaluated according to Burton' formula (Burton, 1952)

as the square root of σ_g^2 and σ_p^2 divided by the mean and converted into percentage, and the genetic advanced was

estimated based on formula of Alard (1960), [$GA = (k)(h^2)(\sqrt{\sigma_p^2})$].

Five percentage selection pressure and 2.06 value for k, was used to obtain the GA. Meanwhile, the phenotypic and genotypic correlation between variable x and y ($r_{(xy)p}$ and $r_{(xy)g}$), were also estimated following Kwon and Torrie (1964):

$$r_{(xy)p} = \frac{Cov_{(x,y)p}}{\sqrt{\sigma_{(x)p}^2 \sigma_{(y)p}^2}}$$

$$r_{(xy)g} = \frac{Cov_{(x,y)g}}{\sqrt{\sigma_{(x)g}^2 \sigma_{(y)g}^2}}$$

Where $Cov_{(x,y)p}$ and $Cov_{(x,y)g}$ are phenotypic and genotypic covariance between variable x and y respectively. Finally the path analysis (P_{ij}) was done based on Dewey and Lu (1956):

$$r_{16} = P_{16} + r_{12}P_{26} + r_{13}P_{36} + r_{14}P_{46} + r_{15}P_{56}$$

$$r_{26} = r_{12}P_{16} + P_{26} + r_{23}P_{36} + r_{24}P_{46} + r_{25}P_{56}$$

$$r_{36} = r_{13}P_{16} + r_{23}P_{26} + P_{36} + r_{34}P_{46} + r_{35}P_{56}$$

$$r_{46} = r_{14}P_{16} + r_{24}P_{26} + r_{34}P_{36} + P_{46} + r_{45}P_{56}$$

$$r_{56} = r_{15}P_{16} + r_{25}P_{26} + r_{35}P_{36} + r_{45}P_{46} + P_{56}$$

Where five independent variables were 1) number of branch/plant, 2) number of pod/plant, 3) pod length, 4) number of seed/pod and 5)1000 seed weight and dependent variable was 6) seed yield.

RESULTS AND DISCUSSION

The results indicated that all traits except date of maturity and number of seed/pod were significant at 1% probability (Table 2). Also the estimation of coefficient of genotypic variation (GCV) showed less than the estimate of coefficient phenotypic variation (PCV). GCV values for number of pod/plant (16.93 and 23.57 in F_2 and F_3 generations, respectively) and seed yield (21.69 and 26.60 in F_2 and F_3 generations, respectively) was high, but for some traits were negligible; it means that selection based on phenotype may be useful for yield improvement. These results are the same as those reported by Khan et al. (2006a). The value of h^2 showed in Table 2 and this index helps the breeder for making decision for continuity of selection. The value of h^2 was high for number of pod/plant (94 and 89%), 1000 seed weight (70 and 97%) and grain yield (83 and 96%) for both generations (F_2 and F_3) respectively, but for plant height, date of maturity and number of seed/pod were lower.

Genetic advance (GA), as percentage of the mean showed high values for number of pod/plant and seed yield (Table 2). These two traits also had high GCV and h^2 and suggested that there is high importance of additive gene action for number of pod/plant and seed yield. So selection of these traits, even in early generations, can be effective. Other traits showed moderate to low values of genetic advance. These results are similar to the findings of Khan et al. (2006a).

The results of genotypic and phenotypic correlation coefficients between studied traits in two generations have been showed in Table 3. Genotypic correlation was

Table 1. Evaluation of mean square.

Source	Degree of freedom	Mean square (MS)	Expected mean square (EMS)
Replication	$r-1$		$\sigma_e^2 + t\sigma_r^2$
Genotype	$g-1$	M_g	$\sigma_e^2 + r\sigma_g^2$
Error	$(r-1)(g-1)$	M_e	σ_e^2

Table 2. Mean square of genotype (MSG), replication (MSR) and error (MSE), range, mean, coefficient of genotypic variation (GCV), coefficient of phenotypic variation (PCV), heritability (h^2) and genetic advance (GA) among the studied traits in rapeseed.

Traits	Generation	MSG	MSR	MSE	Range	Mean±SE	GCV	PCV	h^2	GA
Days to flowering	F ₂	8.98 ^{ns}	5.05 ^{ns}	3.45	123 - 132	127.2 ± 1.85	0.72	0.69	0.65	1.20
	F ₃	24.26 ^{**}	2.18 ^{ns}	2.00	84 - 93	87.7 ± 1.41	3.10	3.49	0.78	5.62
Days to maturity	F ₂	40.35 ^{ns}	2.88 ^{ns}	16.28	196 - 215	205.5 ± 4.03	1.37	2.39	0.33	1.63
	F ₃	1.57 ^{ns}	1.55 ^{ns}	0.53	190.6 - 194	192.3 ± 0.74	0.28	0.49	0.34	0.34
Plant height (cm)	F ₂	98.23 ^{**}	14.04 ^{**}	2.82	124.8 - 144.2	136.5 ± 1.67	4.12	4.30	0.91	8.08
	F ₃	131.70 ^{**}	6.24 ^{ns}	19.94	141.6 - 168.5	154.8 ± 4.46	3.94	4.80	0.65	6.53
Number of branch/plant	F ₂	0.95 ^{**}	0.12 ^{ns}	0.20	3.9 - 6.1	4.8 ± 0.45	10.35	14.06	0.54	15.67
	F ₃	1.76 ^{**}	0.06 ^{ns}	0.33	4.8 - 8.2	6.4 ± 0.57	10.66	13.91	0.58	16.68
Main branch length (cm)	F ₂	25.21 ^{**}	1.95 ^{ns}	5.01	49.8 - 68.9	55.1 ± 2.96	6.40	8.36	0.58	9.99
	F ₃	40.24 ^{**}	1.83 ^{ns}	4.38	49.8 - 64.2	57.5 ± 2.09	6.00	7.09	0.73	10.56
Number of pod/ main branch	F ₂	53.45 ^{**}	2.85 ^{ns}	3.98	40.2 - 54.3	46.0 ± 1.99	8.82	9.83	0.80	16.20
	F ₃	26.07 ^{**}	3.14 ^{ns}	5.88	43.6 - 55.2	49.7 ± 2.42	5.20	7.12	0.53	7.78
Number of pod/plant	F ₂	19581.83 ^{**}	192.72 [*]	40.41	111.9 - 182.1	149.3 ± 6.35	16.93	7.46	0.94	33.81
	F ₃	19653.10 ^{**}	112.59 ^{ns}	743.27	237.2 - 476.9	336.7 ± 27.26	23.57	24.92	0.89	45.69
Pod length (cm)	F ₂	0.57 ^{**}	0.02 ^{ns}	0.03	5.9 - 7.3	6.6 ± 0.17	6.38	6.92	0.84	11.98
	F ₃	0.97 ^{**}	0.01 ^{ns}	0.04	4.9 - 5.9	5.4 ± 0.21	2.61	4.89	0.28	2.82

Table 2. Contd.

Number of seed/pod	F ₂	1.97 ^{ns}	0.28 ^{ns}	1.15	21.2 - 25.8	23.6 ± 1.07	2.19	5.09	0.18	1.88
	F ₃	2.19 ^{ns}	0.77 ^{ns}	1.03	22.1 - 26.5	24.3 ± 1.01	2.53	4.88	0.26	2.61
1000 seed weight (g)	F ₂	0.18 ^{**}	0.06 ^{ns}	0.02	2.4 - 3.4	2.9 ± 0.15	7.93	9.40	0.70	13.65
	F ₃	1.07 ^{**}	0.01 ^{ns}	0.01	2.8 - 4.6	3.5 ± 0.10	16.47	16.71	0.97	27.85
Yield (g/m ²)	F ₂	1.75 ^{**}	0.26 ^{ns}	0.11	2.0 - 4.5	3.4 ± 0.33	21.69	23.62	0.83	40.51
	F ₃	15.18 ^{**}	0.23 ^{ns}	0.20	6.2 - 12.5	8.5 ± 0.45	26.60	27.15	0.96	53.70

* Significant at P < 0.05; **, significant at P < 0.01; ns, not significant.

Table 3. Phenotypic (F) and genotypic (G) correlation coefficients of rapeseed traits in F₂ and F₃ generations.

Traits		Days to flowering	Days to maturity	Plant height (cm)	Number of branch/plant	Main branch length (cm)	Number of pod/ main branch	Number of pod/plant	Pod length (cm)	Number of seed/pod	1000 seed weight (g)
Days to maturity	F ₂	F	0.270 ^{ns}								
		G	-0.194 ^{ns}								
	F ₃	F	-0.376 ^{ns}								
		G	-0.585 [*]								
Plant height (cm)	F ₂	F	-0.209 ^{ns}	0.173 ^{ns}							
		G	0.434 ^{ns}	0.188 ^{ns}							
	F ₃	F	0.432 ^{ns}	-0.118 ^{ns}							
		G	0.614 ^{**}	-0.173 ^{ns}							
Number of branch/plant	F ₂	F	-0.151 ^{ns}	0.276 ^{ns}	0.255 ^{ns}						
		G	-0.350 ^{ns}	0.232 ^{ns}	0.270 ^{ns}						
	F ₃	F	0.192 ^{ns}	-0.537 [*]	-0.100 ^{ns}						
		G	0.359 ^{ns}	-0.090 ^{ns}	0.086 ^{ns}						
Main branch length (cm)	F ₂	F	-0.401 ^{ns}	-0.033 ^{ns}	0.109 ^{ns}	-0.302 ^{ns}					
		G	-0.319 ^{ns}	-0.015 ^{ns}	-0.011 ^{ns}	-0.139 ^{ns}					
	F ₃	F	0.546 [*]	-0.221 ^{ns}	0.594 ^{**}	0.406 ^{ns}					
		G	0.572 [*]	-0.071 ^{ns}	0.701 ^{**}	0.684 ^{**}					

Table 3. Contd.

Number of pod/ main branch	F ₂	F	-0.048 ^{ns}	-0.021 ^{ns}	0.634 ^{**}	0.031 ^{ns}	0.599 ^{**}					
		G	-0.061 ^{ns}	0.060 ^{ns}	0.679 ^{**}	0.268 ^{ns}	0.310 ^{ns}					
	F ₃	F	0.013 ^{ns}	0.065 ^{ns}	0.646 ^{**}	0.007 ^{ns}	0.422 ^{ns}					
		G	-0.041 ^{ns}	0.196 ^{ns}	0.648 ^{**}	0.867 ^{**}	0.621 ^{**}					
Number of pod/plant	F ₂	F	-0.262 ^{ns}	0.326 ^{ns}	0.170 ^{ns}	0.720 ^{**}	0.079 ^{ns}	0.378 ^{ns}				
		G	-0.579 [*]	0.290 ^{ns}	0.148 ^{ns}	0.961 ^{**}	0.027 ^{ns}	0.344 ^{ns}				
	F ₃	F	0.416 ^{ns}	-0.502 [*]	0.314 ^{ns}	0.770 ^{**}	0.735 ^{**}	0.350 ^{ns}				
		G	0.488 [*]	-0.202 ^{ns}	0.403 ^{ns}	0.234 ^{ns}	0.940 ^{**}	0.408 ^{ns}				
Pod length (cm)	F ₂	F	-0.625 ^{**}	-0.082 ^{ns}	-0.621 ^{**}	-0.056 ^{ns}	0.449 ^{ns}	-0.036 ^{ns}	0.336 ^{ns}			
		G	-0.990 ^{**}	0.006 ^{ns}	-0.660 ^{**}	0.171 ^{ns}	0.340 ^{ns}	-0.144 ^{ns}	0.353 ^{ns}			
	F ₃	F	-0.407 ^{ns}	0.111 ^{ns}	0.453 ^{ns}	-0.104 ^{ns}	-0.437 ^{ns}	0.082 ^{ns}	-0.172 ^{ns}			
		G	-0.685 ^{**}	-0.050 ^{ns}	-0.614 ^{**}	0.531 [*]	-0.590 ^{**}	-0.061 ^{ns}	-0.306 ^{ns}			
Number of seed/pod	F ₂	F	-0.141 ^{ns}	-0.281 ^{ns}	-0.200 ^{ns}	-0.305 ^{ns}	-0.413 ^{ns}	0.227 ^{ns}	-0.009 ^{ns}	0.285 ^{ns}		
		G	-0.062 ^{ns}	-0.980 ^{**}	-0.645 ^{**}	-0.228 ^{ns}	-0.033 ^{ns}	-0.001 ^{ns}	0.148 ^{ns}	0.334 ^{ns}		
	F ₃	F	0.625 ^{**}	0.065 ^{ns}	0.638 ^{**}	-0.035 ^{ns}	0.486 [*]	0.596 ^{**}	0.341 ^{ns}	-0.039 ^{ns}		
		G	0.665 ^{**}	-0.528 [*]	0.841 ^{**}	0.531 [*]	0.842 ^{**}	0.461 ^{ns}	0.649 ^{**}	-0.747 ^{**}		
1000 seed weight (g)	F ₂	F	-0.473 [*]	0.196 ^{ns}	-0.020 ^{ns}	0.078 ^{ns}	0.551 [*]	0.390 ^{ns}	0.403 ^{ns}	0.521 [*]	0.111 ^{ns}	
		G	-0.631 ^{**}	0.386 ^{ns}	-0.009 ^{ns}	0.094 ^{ns}	0.613 ^{**}	0.572 [*]	0.483 [*]	0.726 ^{**}	-0.003 ^{ns}	
	F ₃	F	-0.582 [*]	0.180 ^{ns}	-0.772 ^{**}	-0.126 ^{ns}	-0.717 ^{**}	-0.373 ^{ns}	-0.552 [*]	0.472 [*]	-0.588 [*]	
		G	0.631 ^{**}	0.471 [*]	-0.859 ^{**}	-0.400 ^{ns}	-0.764 ^{**}	-0.502 [*]	-0.611 ^{**}	0.644 ^{**}	-0.845 ^{**}	
Yield (g/m ²)	F ₂	F	-0.400 ^{ns}	0.260 ^{ns}	0.029 ^{ns}	0.505 [*]	0.331 ^{ns}	0.435 ^{ns}	0.910 ^{**}	0.537 [*]	0.268 ^{ns}	0.668 ^{**}
		G	-0.701 ^{**}	0.178 ^{ns}	-0.040 ^{ns}	0.786 ^{**}	0.194 ^{ns}	0.399 ^{ns}	0.924 ^{**}	0.597 ^{**}	0.130 ^{ns}	0.696 ^{**}
	F ₃	F	0.304 ^{ns}	-0.289 ^{ns}	0.046 ^{ns}	0.841 ^{**}	0.506 [*]	0.264 ^{ns}	0.833 ^{**}	0.140 ^{ns}	0.284 ^{ns}	-0.241 ^{ns}
		G	0.304 ^{ns}	-0.243 ^{ns}	0.079 ^{ns}	0.981 ^{**}	0.595 ^{**}	0.263 ^{ns}	0.901 ^{**}	0.280 ^{ns}	0.460 ^{ns}	-0.252 ^{ns}

*, significant at P < 0.05; **, significant at P < 0.01; ns, not significant.

estimated to eliminate environmental variance. The results of correlation in F₂ generation, indicated that there was positive and significant relationship between seed yield and number of pod/plant, number of branch/plant, 1000 seed

weight and pod length (at 1% probability). These results were similar to phenotypic correlation. So it can be concluded that the environmental variance and covariance are very low and selection of these traits can be effective. The genotypic

correlation in F₃ generation showed that there was positive significance (at 1% probability) between seed yield and number of pod/plant, number of branch/plant and main branch length. Based on the results of the correlation in F₂ and F₃ generations,

Table 4. Path analysis of studied traits in rapeseed in F₂ and F₃ generations.

Traits	Generation	Direct effect	Indirect effects					
			Number of branch/plant	Number of pod/plant	Pod length (cm)	Number of seed/pod	1000 seed weight (g)	Correlation with yield
Number of branch/plant	F ₂	-0.063	-	0.821	-0.001	-0.053	0.030	0.768
	F ₃	0.597	-	0.056	0.127	0.114	-0.046	0.981
Number of pod/plant	F ₂	0.855	-0.060	-	0.003	-0.034	0.300	0.924
	F ₃	0.243	0.517	-	-0.073	0.139	-0.070	0.940
Pod length (cm)	F ₂	0.011	-0.010	0.301	-	0.077	0.233	0.597
	F ₃	0.240	0.317	-0.074	-	-0.160	0.074	0.280
Number of seed/pod	F ₂	0.233	0.018	0.126	0.003	-	0.000	0.130
	F ₃	0.215	0.317	0.157	-0.179	-	-0.098	0.460
1000 seed weight (g)	F ₂	0.321	-0.005	0.415	0.007	0.000	-	0.696
	F ₃	0.116	-0.238	-0.148	0.154	-0.181	-	-0.252

it may be concluded that the number of pod/plant and number of branch/plant are very important for rapeseed breeding program. These results are the same as those reported by Jeromela et al. (2007) and Ozer et al. (1999). Meanwhile, the number of seed/pod and 1000 seed weight in F₃ generation showed negative significance and it was the same as the findings reported by Basalma (2008).

The correlation between the traits may be due to linkage or pleiotropy (Adams, 1967) or environment (Aastveit and Aastveit, 1993). Some correlation coefficients in F₂ generation were different from those of F₃ generation (Table 3). So it is suggested that these differences may be due to the genetic differences between two generations. The same results were also reported by Engqvist and Becker (1991). Most genotypic and phenotypic correlations were different. These differences were due to environmental variance or genetic error variance, so the appearance of traits in rapeseed, are strongly influenced by environment. Ozer et al. (1999) obtained different results from similar genotypes in two consecutive years. They argued that this difference can be partly attributed to the variation in precipitation during the growing season in the study years.

The simple correlation coefficient cannot give the clear information from relationship between traits, so it could be divided into series of direct and indirect effects. Path analysis provides a measure of relative importance of each independent variable to prediction of changes in the dependent one. In F₂ generation, maximum direct effects on yield were observed in number of pod/plant followed by 1000 seed weight and number of seed/pod (Table 4). The same results were reported by Ozer et al. (1999) and Ali et al. (2003). In F₃ generation, maximum direct effects

on yield were observed in number of branch/plant. Our results confirm the finding of Basalma (2008). So, aforesaid traits are the best criteria for yield improvement in rapeseed. Also the analysis of path coefficient showed that the direct effect of the number of branch/plant, pod length and 1000 seed weight in F₂ and F₃ generations were not significant, but correlation between these traits and yield was significant. So, larger indirect effects (including number of pod/plant and number of branch/plant) are the best criteria for selecting desired cultivars in plant breeding program.

In conclusion it may be said that GCV, heritability and GA for number of seed/pod and yield were high and they are used for improvement of these traits in rapeseed breeding program. Meanwhile, simultaneous evaluation of correlation and path coefficient as well as the close relationship between number of pod/plant and number of branch/plant indicated that these traits can be suitable for direct selection index in yield improvement.

ACKNOWLEDGEMENT

We appreciate the Director and Staff of Rice and Citrus Research Institute for financial and technical support of this experiment.

REFERENCES

- Aastveit AH, Aastveit K (1993). Effects of genotype-environment interactions on genetic correlations. *Theor. Appl. Genet.*, 6: 1007-1013.
- Adams MW (1967). Basis of component compensation in crop plants with special reference to the field bean (*Faseolus vulgaris*). *Crop Sci.*,

- 7: 505-510.
- Ahmad HM, Khan BM, Khan S, Kissana NS, Laghari S (2003). Path coefficient analysis in bread wheat. *Asian J. plant. Sci.*, 2: 491-494.
- Allard RW (1960). Principles of plant breeding. Wiley, New York.
- Ali N, Javidfar F, Jafarieh YE, Mirza MI (2003). Relationship among yield components and selection criteria for yield improvement in winter rapeseed (*Brassica napus* L.). *Pakistan J. Bot.*, 35: 167-174.
- Basalma D (2008). The correlation and path analysis of yield and yield components of different winter rapeseed (*Brassica napus* ssp. *oleifera* L.) cultivars. *Res. J. Agri. Biol. Sci.*, 4: 120-125.
- Bhatt GM (1973). Significance of path coefficient analysis in determining the nature of character association. *Euphytica*, 2: 338-343.
- Burton GW (1952). Quantitative inheritance in grasses. *Proc. 6th Int. Grassland Congr. National Publishing Co., Washington D.C.* I: pp. 277-283.
- Dewey JR, Lu KH (1956). A correlation and path coefficient analysis and components of crested wheat seed production. *J. Agron.*, 51: 515-518.
- Engqvist GM, Becker HC (1991). Heterosis and epistasis in rapeseed estimated from generation means. *Euphytica*, 58: 31-35.
- Falconer DS (1989). Introduction to quantitative genetics. 3rd Edn. Long Man Scientific and Technical, UK. p. 163.
- Jeromela A, Marinkovic R, Mijic A, Jankulovska M, Zdunic Z (2007). Interrelationship between oil yield and other quantitative traits in rapeseed (*Brassica napus* L.). *J. Central Europ. Agri.* 8: 165-170.
- Khan FA, Ali S, Shakeel A, Saeed A (2006a). Genetic variability and genetic advance analysis for some morphological traits in *Brassica napus* L. *J. Agri. Res.* 44: 83-87.
- Khan FA, Ali S, Shakeel A, Saeed A (2006a). Correlation analysis of some quantitative characters in *Brassica napus* L. *J. Agri. Res.* 44:7-14.
- Kwon SH, Torrie JH (1964). Heritability and interrelationship among traits of two soybean populations. *Crop. Sci.*, 4: 196-198.
- Mahmud T, Rahman MH, Stringam GR, Yeh F, Good A (2005). Molecular markers for yield components in *Brassica juncea* do these assist in breeding for high seed yield. *Euphytica* 144: 157-167.
- Nassimi AW, Raziuddin NA (2006). Heterotic studies for yield associated traits in *Brassica napus* L. using 8x8 diallel crosses. *Pakistan J. Biol. Sci.* 9: 2132-2136.
- Ozer H, Oral E, Dogru U (1999). Relationships between yield and yield component on currently improved spring rapeseed cultivars. *Turkish J. Agri. Fores.*, 23: 603-607.
- Panse VG, Sukhatme PV (1967). Statistical methods for agricultural workers. Indian Council of Agricultural Research, New Delhi, p.381.
- Singh M, Ceccarelli S (1996). Estimation of heritability of crop traits from variety trial data. Technical Manual International Center for Agricultural Research in the Dry Areas, Aleppo, Syria. p. 21.