CORRELATION ANALYSIS OF SOME QUANTITATIVE CHARACTERS IN *BRASSICA NAPUS* L.

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ABSTRACT

Correlation for some quantitative traits relating to yield and quality were studied in the Department of Plant Breeding and Genetics, University of Agriculture, Faisalabad during 2002-2003. Eleven accessions of *Brassica napus* L. alongwith DGL as a standard variety, were studied. The results indicated that a wide range of genetic variation existed among all the characters under study except 1000-grain weight. Correlation analysis revealed that seed yield per plant was positively and significantly correlated with number of primary branches (0.4015), siliqua per plant (0.505), seeds per siliqua (0.79648), siliqua length (0.37037) and seed yield per plot (0.40931). However, it was negatively and non-significantly associated with number of secondary branches (-0.36663) and protein contents (-0.1372) at genotypic level. It was also found that indirect selection for number of seeds per siliqua would be effective in improving the seed yield per plant in present breeding material.

KEYWORDS: *Brassica napus;* cultivars; agronomic characters; Pakistan.

INTRODUCTION

Pakistan is deficient of edible oil production and only 32 percent of total demand is met through local production (2). This wide gap between production and consumption is a serious threat to the economy of Pakistan. This gap will continue to increase in next ten years mainly due to high population growth rate. Rapes and mustards occupy a leading position among edible oilseed crops of the country. At present it seems difficult to increase the area under rapeseed and mustard due to competition with important rabi crops like wheat and legumes. However, yield potential of these crops can be increased with better adaptable and high yielding cultivars provided proper incentives are extended to the farmers. Area can also be increased by intercropping with wheat, legume and fodder crops. Adoption of canola types may be a hope for increasing the area due to better quality oil. Also, it is more convenient to introduce Brassica among the growers as

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compared to non-conventional edible oil crops like sunflower, safflower and soybean. Dhillon *et al.* (3) observed that plant height had stone association with seed yield and secondary branches per plant were also important contributor to seed yield. Chowdhury *et al*. (4) found that seed yield per plant was positively associated with number of siliquae per plant, siliqua length and protein content. Singh and Singh (12) studied the correlation between seed yield and other characters and found that seed yield was positively correlated with 1000-seed weight and number of seeds per siliqua. Kandil *et al.* (5) found that number of siliquae per plant possessed strongest association with seed yield per plant in *Brassica napus.* Lakshmamma *et al*. (7) found that high yielding cultivars had greater siliquae number and silquae weight per plant in their seed trial. Anil *et al*. (1) found that seed yield was positively correlated with number of seeds per siliqua, number of siliquae per plant and plant height. In general, they found that traits of *Brassica juncea* L. were less correlated with seed yield than those of *Brassica napus* L. cultivars.

The present study was conducted to generate the information to understand the association of different traits with seed yield in different accessions of *Brassica napus* L.

MATERIALS AND METHODS

This study was conducted in the Department of Plant Breeding and Genetics, University of Agriculture, Faisalabad, Pakistan during 2002-2003. Eleven accessions viz Asker, Dunkled Canola, Shiralee, Range, Rainbow, DGL (standard), Pak.85856, Con-1, Pak.85924 and Pak. 85843 alongwith a standard variety of *Brassica napus* L. were studied. Layout system was RCBD in four replications keeping plant to plant distance of 30 cm and row to row distance of 60 cm. Length of each row was 360 cm with seven rowed plots of each accession in each replication. Ten guarded plants from five middle rows were randomly selected for recording data from each replication. Standard agronomic practices were followed for growing normal crop of Brassica. Data were recorded for plant height, number of primary branches per plant, number of secondary branches per plant, number of siliquae per plant, number of seeds per siliqua, siliqua length, 1000-grain weight, seed yield per plant, oil contents, protein contents and seed yield per plot.

Data were subjected to analysis of variance following Steel and Torrie (13). All possible correlations were computed following the statistical technique prescribed by Kwon and Torrie (6) as given below:-

$$r_p = Mij \quad Mi.i.Mj.j. \quad \text{--------------------} \; (i)$$

where, r_p = Phenotypic correlation coefficient
Mij = Mean product of genotypes for ith and jth trait.
Mii = Genotype mean squares for ith trait
Mjj = Gentotype mean squares for jth trait

$$r_g = Covi.j. \quad Var.gi.Var.g.j. \quad \text{----------------} \; (ii)$$

where, r_g = Genotypic correlation coefficient
Cov i.j. = Genotypic covariance of ith and jth trait
Var g.i. = Genotype variance of ith trait
Var.g.j. = Gentotype variance of jth trait

Genotypic correlation coefficients were tested against the double value of standard error (SE) genotypic correlation.

$$\text{S.E. of } r_g = 1-r^2_g \quad 2 \bullet \quad (S.E.h^2) \,.\, (SEH^2Y)/\,(h^2_x).(h^2_y) \quad \text{----------------} \; (iii)$$

where, r_g = Genotypic correlation coefficient between X and Y traits
h^2_x = Heritability of X trait
h^2_y = Heritability of Y trait
SE h^2_x and SE h^2_y = Standard error for heritability associated with X and Y traits.

A correlation was considered significant statistically if the absolute value exceeded twice of the respective standard error. Statistical significance of phenotypic correlation was determined by t-test as described by Steel and Torrie (13).

t (cal.) = rp 1-r2p n-2 --------------- (iv)

where, r_g = Phenotypic correlation coefficient
n = No. of observations

RESULTS AND DISCUSSION

The data (Table 1) on mean squares for the analysis of variance for different morphological traits exhibited that differences among all accessions and a standard variety DGL for all morphological traits were highly significant except 1000-grain weight for which the accessions were statistically non-significant. Genotypic correlation coefficients (Table 2) were higher than their respective phenotypic correlation coefficients ($r_g > r_p$) for all the traits except 1000-grain weight, having non-significant mean square value. It indicated adverse environmental influences on the traits studied. Plant height was positively and significantly correlated with protein contents and positively but non-significantly correlated with number of primary branches. This trait showed negative and significant correlation with number of siliquae per plant, seeds per siliqua, siliqua length, seed yield per plant and seed yield per plot.

Table 1. Mean squares from the analysis of variance for morphological traits in *Brassica napus* L.

S.No.	Traits	Error mean square	Genotype mean square	Block mean square
1.	Plant height (cm)	1.608NS	2332.855**	0.621NS
2.	Primary branches/plant	0.003NS	3.087**	0.011NS
3.	Secondary branches/plant	0.302NS	5.80**	0.646NS
4.	Siliqua/plant	1.230NS	13570.584*	0.707NS
5.	Seeds/siliqua	0.118NS	83.659**	0.037NS
6.	Siliqua length	0.015NS	5.520**	0.002NS
7.	1000-seed weight (g)	0.013NS	2.024NS	0.013NS
8.	Seed yield/plant (g)	0.010NS	74.286**	0.006NS
9.	Yield/plot (kg)	0.100NS	12.120**	0.146NS
10.	Oil contents (%)	0.034NS	31.117**	0.105NS
11.	Protein contents (%)	0.906NS	36908.506	0.113NS

*Significant at 0.05 probability level, **Significant at 0.01 probability level, NS=Non-significant.

Table 2. Genotypic (rg) and phenotypic (rg) correlation coefficients for some morphological characters.

Traits		Plant height (cm)	Primary branches/ plant	Secondary branches/ plant	Siliqae/ plant	Seeds/ siliqua	Siliqua lengh (cm)	Seed yield/ plant (g)	Protein contents (%)	Oil contents (%)	Seed yield /plot (g)
Plant height(cm)	r(g)	1	0.0179NS	-0.02NS	-0.3371*	-0.5369*	-0.5018*	-0.5425*	0.597*	-0.664NS	-0.6924*
	r(p)	1	0.017NS	-0.0192NS	-0.337*	-0.5363**	-0.5009**	-0.5442**	0.59416**	-0.661NS	-0.6924**
Primary branches	r(g)		1	0.2711NS	0.20686NS	0.2942NS	0.0096NS	0.4015*	0.07859NS	0.17757NS	0.28649*
	r(p)		1	0.2621NS	0.20669NS	0.9240NS	0.00921NS	0.40129**	0.07791NS	0.17715NS	0.2846NS
Secondary branches	r(g)			1	0.4407*	0.13837NS	0.17971NS	0.36663NS	0.55184*	0.17884	0.0872NS
	r(p)			1	0.4279*	0.13396NS	0.17671NS	0.36652*	0.53968**	0.17287NS	0.0848NS
Siliquae/plant	r(g)				1	0.50433*	0.31876*	0.505*	-0.5957*	0.03151NS	0.33479*
	r(p)				1	0.5038**	0.31829*	0.50497**	-0.593**	0.03151NS	0.33477*
Seeds/siliqua	r(g)					1	0.39661*	0.79648*	-0.112NS	-0.3637*	0.23854*
	r(p)					1	0.39601**	0.79287**	-0.1119NS	-0.3632*	0.23832NS
Siliqua length (cm)	r(g)						1	0.37017*	-0.2527NS	0.1186NS	0.96401*
	r(p)						1	0.36976*	-0.2521NS	0.11189NS	0.39401*
Seed yield/plant (g)	r(g)							1	-0.1372NS	0.12094NS	0.40931*
	r(p)							1	-0.1365NS	0.12089NS	0.40927**
Protein contents(%)	r(g)								1	-0.2176NS	-0.7738*
	r(p)								1	-0.2164NS	-0.7705**
Oil contents (%)	r(g)									1	0.442*
	r(p)									1	0.4417**

However, it was negative and non-signifciantly correlated with secondary branches and oil contents at genotypic level. Number of primary branches had positive and significant association with seed yield per plant and seed yield per plot while positive and non-significant genotypic association with all remaining traits at genotypic level. Similar findings have been reported by Chowdhury *et al*. (4). Similarly, positive and significant correlation of number of secondary branches was exhibited by number of siliquae per plant and protein contents at genotypic level as reported by Swain (14).

Number of siliquae per plant exhibited a positive and significant genotypic association with number of seeds per siliqua, siliqua length, seed yield per plant and seed yield per plot at genotypic level. This finding is also supported by Singh and Singh (12). The data (Table 2) also revealed that seeds per siliqua had highly significant and positive correlation with siliqua length, seed yield per plant and seed yield per plot but significantly negative with oil contents at genotypic level. The present results are in line with the findings of Saini and Sharma (9). Number of siliquae and siliqua length had a positive and significant correlation with seed yield per plant and seed yield per plot at genotypic level as reported by Chowdhury *et al*. (4) while working on different species of mustard.

Singh *et al*. (10) also found that seed yield per plant had a significant positive correlation with seed yield per plot at genotypic level. Correlation between protein contents and seed yield per plot was found to be negative and significant at genotypic level while oil contents was negatively and significantly correlated at genotypic level. However, oil contents was positively and significantly associated with seed yield per plot at genotypic level. These results did not agree to the findings of Singh and Singh (11) showing a negative association between oil contents and seed yield per plant. Correlation of these results would be mainly due to different environmental conditions for crop development or due to different cultivars/genotypes used.

It is concluded that indirect selection for number of seeds per siliqua followed by siliquae per plant, primary branches and siliqua length would prove as a more effective breeding strategy in the germplasm under study.

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