### GENETIC VARIABILITY AND GENETIC ADVANCE ANALYSIS FOR SOME MORPHOLOGICAL TRAITS IN BRASSICA NAPUS L.

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#### ABSTRACT

Eleven accessions and a standard variety DGL of *Brassica napus* L. were tested in the Department of Plant Breeding and Genetics, University of Agriculture, Faisalabad to estimate the genetic variability, heritability and genetic advance values. Coefficient of variability exhibited that number of primary branches per plant and oil contents were less variable traits than plant height, number of secondary branches per plant, pods per plant, seeds per pod, pod length, grain yield per plant, protein contents and seed yield per plant. Phenotypic coefficients of variability were although greater than respected genotypic ones but a narrow gap was found indicating little influence of environment in the expression of characters. Higher values of heritability coupled with high genetic advance for protein contents indicate the effectiveness of selection for this trait due to additive component of gene action.

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

#### INTRODUCTION

Pakistan is deficient in the production of edible oils. Sixty eight percent of its total edible oils needs are met through imports at a total cost of Rs. 483.1 million (1). The situation is very alarming for Pakistan's economy because local production of edible oil is not increasing with the increase in consumption rate. Rape and mustard have been a valuable source of edible oil in Indo-Pak sub-continent since ages. Although the area under these crops is continuously decreasing due to non-availability of better-adapted genotypes, yet these are still the second largest contributor to vegetable oil production. The recent studies have shown that improved types have a yield potential of over 2500 kg per hectare which reflects that a substantial increase upto 2-3 times in average yield is possible. Success of any crop improvement depends upon the presence of substantial amount of genetic variability, co-variability, habitability as well as genetic gain in selection.

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Khehra and Singh (4) carried over their research using 29 genotypes of *Brassica napus* L. and reported significant differences for seed yield, number of siliqua, number of secondary branches and plant height. Chay and Thurling (3) compared ten selections from China and found wide range of variations in pod lengths. Paramjit *et al.* (6) studied 29 genotypes of *Brassica napus* L. for nine quantitative traits and reported significant variability for various seed yield related traits. Yadav and Singh (11) tested 25 newly evolved lines of Indian mustard for variability and reported wide genetic variation for primary and secondary branches, dry root weight, number of siliqua on main stem and seed yield. Khulb *et al.* (5) estimated the variability, heritability and genetic advance for yield and its components in Indian mustard and found maximum variability for seed yield and high heritability coupled with high genetic advance in all traits except oil content. Similar findings have also been reported by some other researchers (7, 8).

The present research was conducted to gain information about genetic variability, heritability and genetic advance estimates of yield controlling traits in different accessions of *Brassica napus* L.

#### MATERIALS AND METHODS

This research work was conducted in the Department of Plant Breeding and Genetics, University of Agriculture, Faisalabad during 2002-2003. Eleven accession of Brassica napus L. (Pak. 85924, Pak. 85843, Pak.85956, Con-1, DGL (as a standard variety), Range, Shiralee, Asker, Rainbow, Pak. 85950, Pak. 85956 and Dunkled Canola) and a standard variety DGL were sown in four replications. Layout system was RCBD with plant to plant distance of 30 cm and row to row 60 cm. Row length was kept as 360 cm, containing only seven rows in each plot for each genotype in each replication. Ten guarded plants were randomly selected from five middle rows and data were recorded on plant height, number of primary branches per plant, number of secondary branches per plant, number of pods per plant, number of seeds per pod, pod length, 1000-grain weight, seed yield per plant, seed yield per plot, oil contents and protein contents. The data were subjected to analysis of variance following Steel and Torrie (10). Coefficient of variation for phenotypic and genotypic components was calculated using the method given by Burton (2). Heritability and genetic advance estimates were calculated using the standard methods given by Steel and Torrie (10).

#### **RESULTS AND DISCUSSION**

The analysis of variance for the traits indicates that the genotypic mean squares for all traits were highly significant except for 1000-seed weight which was non-significant (Table 1). This fact reflects that selection for 1000-grain weight is strongly misleading (9). These results are in accordance with earlier findings (6, 11).

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

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

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

DMR test was applied to know the variations between genotypes for all traits. Performance of all genotypes using DMR (Table 2) indicates that variety Pak.85924 attained maximum plant height (227.0 cm) while DGL topped in

## Table 2. Mean performance of genotypes for some morphological traits in *Brasica* napus L.

Genotype	PH	NPBP	NSBP	NPP	NSP	PL	SYP	SYPP	OC	PC
Pak.85924	227.0a	5.05h	10.15cd	258.3f	25.15a	3.58i	4.73k	385.0k	33.88g	23.75b
			е							
Pak.85843	203.7b	6.32f	12.22ab	164.2I	11.13k	5.81d	5.31j	0.701j	36.90c	24.90a
Pak.85856	199.5c	7.28b	9.95cde	220.0k	16.17g	3.64i	4.76k	570.01	30.701	22.50d
Con-1	189.4d	7.25b	11.74b	235.7i	16.10g	4.50h	12.95e	572.4h	34.45f	23.70b
DGL	179.8e	7.40a	9.40e	397.8a	18.00f	6.32c	12.80f	750.6a	38.10b	19.10g
Range	175.4f	5.50g	10.65c	261.9e	21.00d	6.71b	11.99g	560.8j	32.10j	22.65d
Shirlee	173.8f	6.68d	12.20ab	243.0h	23.17c	4.77g	16.53a	702.7c	35.40d	22.30d
Asker	171.9g	6.98c	12.50ab	293.4d	25.15a	7.50a	13.59c	574.7g	31.50k	23.20c
Rainbow	160.3h	6.32f	12.80a	301.0c	20.00e	5.47e	15.60b	592.3f	34.78e	22.35d
Pak.85950	158.2i	6.67d	12.01ab	230.5j	15.50h	5.77d	10.76h	691.0d	40.15a	21.35f
Pak.85956	148.2j	4.71i	9.95cde	249.3g	14.41i	5.92d	6.28i	713.8b	33.40h	19.10g
Dunkled	145.2k	6.47e	9.75de	315.6b	24.21b	5.20f	13.40d	620.3e	32.70i	21.84e
Canola										

PH = Plant height (m), NPBP = no. of primary branches/plant, NSBP = no. of secondary branches/plant, NPP = no. of pods per plant, NSP = no. of seeds/pod, PL = pod length (cm), SYP = seed yield/plant (g), SYPP = Seed yield/plot (g), OC = oil contents (%), PC = protein contents (%)

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primary branches (7.40), pods per plant (397.8) and seed yield per plot (750.6 g). Higher estimates for secondary branches were noted in Rainbow while Asker had maximum seeds per pod (25.15) and pod length (7.50 cm). Higher estimates for seed yield per plant (16.53 g) were exhibited by Shiralee. Pak. 85843 and Pak. 85950 gave maximum protein contents (24.9%) and oil contents (40.15%), respectively.

The estimates of genotypic coefficient of variation (GCV) were higher than phenotypic coefficient of variation (PCV) for all the characters but gap was found narrow (Table 3).

Tuelde	V-	M-	Ma	0.01/	DOV	1120/	~
Traits	vg	ve	vp	GCV	PCV	Н %	GA
						(BS)	(l = 1.755)
Plant height	582.811	1.608	584.419	81.99	82.201	99.7	42.299
No. of primary branches/plant	0.771	0.003	0.774	0.313	0.315	99.7	1.539
No. of secondary	1.3695	0.302	1.6825	3.332	4.117	80.9	1.847
branches/plant							
No. of pods/plant	3392.3385	1.230	3393.5685	173.35	173.41	99.9	102.134
No. of seeds/pod	20.8852	0.118	20.9932	15.76	15.84	99.4	7.992
Pod length	1.3762	0.015	1.3812	6.333	6.356	99.6	2.054
Seed yield/plant (g)	18.569	0.010	18.579	43.28	43.3	99.9	7.557
Seed yield/plot	3.005	0.100	3.1005	3.379	3.847	96.9	2.994
Oil contents (%)	7.77075	0.034	7.80475	5.53	5.556	99.5	2.924
Protein contents (%)	9226.9	0.906	9227.806	379.04	379.05	99.9	168.419

# Table 3.Mean performance of genotypes for some morphological traits in<br/>Brassica napus L.

It indicated a little influence of environment in the expression of characters and selection for improvement of such characters based on phenotype would be rewarding to improve present material of *Brassica napus* L. Highest value of heritability was found for protein contents, pods per plant and seed yield per plant. It suggested that selection based on heritability estimates alone may not be useful until the genetic advance values are given importance. Higher estimates of genetic advance has been found for protein contents followed by pods per plant. It confirmed that heritability is due to additive genes and is fixable in the next generation indicating the efficiency of selection for these traits. Similar results have been reported earlier (4,5,6). Following conclusions are made from the present research work.

- The area under DGL should be increased as it exhibited highest seed yield per plot.
- For maximum oil production, Pak. 85950 should be given importance.
- Selection should be practiced in the present material for varieties having maximum protein contents and plant height to develop high yielding cultivars.

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