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GENETIC VARIABILITYAND CORRELATION STUDIES FOR MORPHO-PHYSIOLOGICAL TRAITS IN *BRASSICA NAPUS* L.

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Abstract

Genetic variability, heritability, genetic advance and correlation were determined in ten *Brassica napus* L. genotypes for morpho-physiological traits at The University of Agriculture, Peshawar, Pakistan. Significant differences among genotypes for most of the characters indicated presence of sufficient genetic variability for effective selection. High heritability and high genetic advance were observed for flowering initiation, 50% flowering and flowering completion, plant height, seeds pod^{-1} and 100-seed weight. Significant positive correlations were observed for plant height with main raceme length (r=0.48**), pods main raceme^{-1} (r=0.67**) and 100-seed weight (r=0.47**). Seeds pod^{-1} was positively correlated with pod length (r=0.51**) and pod width (r=0.46**). Similar associations were observed for pod length with pod width (r=0.44*) and 100-seed weight (r=0.59**). Plant height, seeds pod^{-1}, pod length and 100-seed weight can be used as selection criteria.

Introduction

Oilseed *Brassica* species (*B. napus*, *B. campestris* and *B. juncea*) ranks the third most important source of edible oil in world (Zhang & Zhou, 2006). The Brassica oil crops are the world's third most important source of edible oil. Due to a continually increasing demand for rapeseed oil for food and non-food uses, the production of hybrid cultivars with higher seed and oil yields has become increasingly important in recent years (Ahmad *et al.,* 2011). In Pakistan, it ranks second after cotton seed (Khan *et al.,* 2008), contributing about 21% of domestic edible oil production (Abbas *et al.,* 2008). Rapeseed oil is used as food, as well as for industrial purposes including biodiesel production (Sabaghnia *et al.,* 2010). Pakistan is deficient in the production of edible oils. Around 77% of total edible oils needs are met through imports at a cost of $1,054.7 million. Import bill of Pakistan is continuously the second largest after petroleum and constitutes the single largest expenditure on any of the imported food items (Ahmad *et al.,* 2013). The total availability of edible oil in 2009-10 was 2.9 million tons. Local production of edible oil stood at 662 thousand tons during 2009-10, which is 23% of the total availability in the country (Anon., 2010-11). A number of efforts have been undertaken to improve the rapeseed - canola cultivars for quality, production and new genotypes and varieties have been evolved and tested in different parts of Pakistan (Mahmood *et al*., 2011; Ahmad *et al.,* 2012).

Non-availability of better adapted genotypes is a reason for decreasing acreage of these crops (Khan *et al.,* 2006a). Oilseed *Brassica,* being well entrenched in the cropping system of Pakistan, can potentially reduce consumption and production gap (Syed *et al.,* 1994) and reduce burden on exchequer. Diversity of plant genetic resources is imperative for crop improvement (Jatoi *et al.,* 2012) and information on these reserves can contribute to the pace of improvement (Zada *et al.,* 2013). Genetic variability, heritability as well as genetic gain in selection contribute to success of any crop improvement program (Khan *et al.,* 2006a).

Correlation analysis is essential to see interrelationships between pairs of traits. In the genetic context, there is little likelihood of separate control for any pair of characters (Aytaç & Kinaci, 2009). Estimates of genetic variability, heritability, genetic advance and trait correlations (Ali *et al.,* 2003; Khan & Khan, 2003; Akbar *et al.,* 2003 & 2007; Aytaç & Kinaci, 2009; Sadat *et al.,* 2010) will help to devise efficient selection criteria in the present study.

Material and Methods

Ten *B. napus* L. genotypes viz. 223, 266, 2745, 2762, 2756, 2736, 2735, 254, 255 and Zafar were grown during 2009-10 at The University of Agriculture Peshawar, Pakistan to determine genetic variability, heritability, genetic advance and correlation between various traits. The experiment was laid out in a randomized complete block (RCB) design with three replications. Row length was 5m, while row to row and plant to plant spacing was kept 60 cm and 30 cm respectively. Recommended cultural practices were applied during the crop season. At maturity five plants were randomly selected from each plot replication^{-1}**.** Data were recorded for days to flowering (initiation, half and completion), plant height, primary branches plant^{-1}, pods main raceme^{-1}, main raceme length, pod length, pod width, seeds pod^{-1} and 100-seed weight. Analysis of variance was carried out according to Gomez and Gomez (1984) using MSTAT-C computer software. The components of variance including genotypic variance (σ_g^2) and phenotypic variance (σ_p^2) and error variance (σ_e^2) were estimated according to the following formula (Panse & Sukhatme, 1967):

$$\sigma_e^2 = M_e$$

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

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

Standard error of the mean difference for any pair of means was computed according to Gomez & Gomez (1984).

$$\text{Standard error / S.E} = \sqrt{2s^2/r}$$

where **r** is the number of replications that is common to both treatments in the pair and s^2 is the error mean square in the analysis of variance.

Heritability was calculated according to Singh & Ceccarelli (1996).

$$h^2 = \sigma_g^2 / \sigma_p^2$$

According to Stansfield (1986), heritability estimates were grouped into high (>50%), moderate (20-50%) and low (<20%).

The coefficient of genotypic (GCV) and phenotypic (PCV) variations were calculated according to Burton (1952).

$$GCV = \sqrt{\sigma_g^2}/\bar{X} \times 100$$

$$PCV = \sqrt{\sigma_P^2}/\bar{X} \times 100$$

Genetic advance was also estimated according to Allard (1960).

$$GA = (K)\,(h^2)\,(\sqrt{\sigma_p 2})$$

where **'k'** is selection differential and at 5% the K value was 2.06.

$$GA\% = GA / \text{Mean value} \times 100$$

Results and Discussion

Study of genetic behavior such as genetic variability, heritability, genetic advance and correlation etc. of the germplasm is a key step for initiation of any breeding program (Mehdi & Khan, 1994).

Genetic variability: Highly significant differences ($p \leq 0.01$) were found for 100-seed weight, plant height, seed pod^{-1}, pod length, pod width, days to flowering initiation, days to half flowering, days to flowering completion whereas differences were non-significant for primary branches per plant^{-1}, pods main raceme^{-1} and main raceme length (Table 2) as also reported earlier (Samad & Khaleque, 2000; Ali *et al.,* 2003; Akbar *et al.,* 2003 & 2007; Khan *et al.,* 2008; Aytaç & Kınacı, 2009; Inayt *et al.,* 2009; Dar *et al.,* 2010; Sadat *et al.,* 2010; Emrani *et al.,* 2012).

Heritability and genetic advance: Heritability is the measure of value of selection of a particular character and an index of transmissibility of genes controlling the character (Mehdi & Khan, 1994). In estimating the selection effects, heritability accompanied with genetic advance is rather useful than heritability alone (Johnson & Hanson, 2003; Aytaç & Kinaci, 2009). These are also indicative of the mode of gene action operated in trait expression (Mahmood *et al.,* 2003; Akbar *et al.,* 2003 & 2007; Aytaç & Kinaci, 2009). Additive genes are said to control a trait having high heritability and high genetic advance which highlights the usefulness of plant selection based on phenotypic performance (Akbar *et al.,* 2003 & 2007; Aytaç & Kinaci, 2009; Sadat *et al.,* 2010) whereas high heritability but low genetic advance, is indicative of non-additive (dominant/epistatic) control (Akbar *et al.,* 2003).

Days to flowering initiation: Data for days to flowering initiation ranged from 52 to107 days. In genotype 2735 initiation of flowers was late whereas in the genotype 2745 was early of all (Table 1). Mean days recorded for flower initiation were 81.10 days (Table 2). The genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability broad sense (h^2 BS) and genetic advance as percentage of mean (G.A) estimates were 23.31, 23.39, 0.99 and 47.69 respectively (Table 2). Emrani *et al.,* 2012 strengthen our results who reported high heritability.

Days to half flowering: The data for Days to half flowering ranged from 47 to120 days. The maximum value was recorded for genotype 1500 whereas minimum value was recorded for 2720 (Table 1) with overall mean 83.50 days (Table 2). Data perusal revealed 25.73 (GCV), 25.78 (PCV), 0.99 (h^2 BS) and 53.10 as G.A (Table 2). Results are in conformity with (Mahto & Haider, 2002; Dar *et al.,* 2010) who reported high heritability and moderate to high genetic advance.

Days to flowering completion: Data ranged days to flowering completion from 84 (for genotype 2745) to 127 (for genotype 2735) days (Table 1) with a mean of 107.80 days (Table 2). The genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability broad sense (h^2BS) and genetic advance as percentage of mean (G.A) estimates were 12.48, 12.68, 0.97 and 25.34 respectively (Table 2). Khan *et al.,* (2008) and Sadat *et al.,* (2010) reported similar results. They reported high heritability for days to flowering completion.

Main raceme length: Mean performance ranged from 56.70 to 84.65 cm in which the lowest length was observed for genotype 255 and highest recorded for 2756 (Table 1) with an overall mean of 68.718 (Table 2). The genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability broad sense (h^2 BS) and genetic advance as a percentage of mean (G.A) were found to be 9.87, 18.62, 0.28 and 10.74 respectively (Table 2). Zhang & Zhou (2006) reported the same.

Plant height: Plants of genotype 2736 were the shortest (140.7) whereas of genotype 2745 were the tallest (220.8 cm) (Table 1). Mean value was found to be 179.517 cm (Table 2). Computations revealed 15.92 (GCV), 17.91 (PCV), 0.79 (h2 BS) and 29.14 (G.A as % of mean) (Table 2). Similar results were reported by (Tariq *et al.,* 2003; Khan *et al.,* 2006a; Dar *et al.,* 2010; Emrani *et al.,* 2012; Shehzad & Farhatullah, 2012).

Primary branches plant^{-1}: The data exhibited a range of 5 to 11 branches. The minimum number was recorded jointly for the genotypes 2736 and Zafar whereas it was highest for genotype 223 (Table 1). Mean value for number of primary branches plant^{-1} was 6.867 branches (Table 2). The genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability broad sense (h2 BS) and genetic advance as percentage of mean (G.A) estimates were 12.86, 40.99, 0.10 and 8.44 respectively (Table 2). Findings of Mahmood *et al.,* (2003) are in line. Results are in partial similarity with Dar *et al.,* (2010) but in contrast to the findings of (Ghosh & Gulati 2001; Tariq *et al.,* 2003; Khan *et al.,* 2008).

Table 1 . Mean performance for days to flowering (initiation, half flowering and completion), plant height, primary branches plant^{-1}, pods main raceme^{-1} , main raceme length, pod length, pod width, seed pod^{-1} and 100-seed weight in *B. napus* L.

Genotypes	Days to flowering initiation	Days to half flowering	Days to flowering completion	Plant height (cm)	Primary branches plant^{-1}	Pods main raceme^{-1}	Main raceme length (cm)	Pod length (cm)	Pod width (cm)	Seed pod^{-1}	100-seed weight (g)
223	80 d	105 bc	110 de	187.8 b	11	54	69.60	5.680 fg	0.4733 bc	13 d	0.3667 b-e
266	54 f	68 f	86 g	220.2 a	8	74	67.52	8.710 a	0.5367 a	20 abc	0.4800 a
2745	52 f	65 f	84 g	220.8 a	6	75	76.92	5.920 efg	0.5267 ab	17 cd	0.4233 abc
2762	97 b	104 bc	112cde	159.8 cd	6	53	59.15	5.453 g	0.4467 c	17 cd	0.3333 de
2756	96 b	105 bc	114bcd	213.5 a	7	81	84.65	7.830 b	0.4900 abc	21 abc	0.4100 a-d
2736	70 e	102 cd	117 b	140.7 d	5	47	57.75	6.133 efg	0.5433 a	23 ab	0.3500 cde
2735	107 a	119 a	127 a	160.8 cd	7	66	65.22	6.807 cde	0.5100 ab	18 bc	0.3567 b-e
254	96 b	107 b	116 bc	150.8 d	7	62	75.30	7.663 bc	0.5033 abc	19 bc	0.4400 ab
255	88 c	99 d	109 e	179.8 bc	8	51	56.70	7.440 bcd	0.5433 a	25 a	0.4733 a
Zafar	71 e	84 e	103 f	160.8 cd	5	63	74.38	6.587 def	0.5067 ab	21 abc	0.3100 e
LSD	3.0	3.0	4.0	25.2	-	-	-	0.858	0.0543	4.55	0.07671

Mean separation by DMR test at 5% probability level.

Table 2 . Analysis of variance Replication mean square (RMS), genotype mean square (GMS), error mean square (EMS), grand mean (Mean) and , coefficient of variation (CV) Error variance (Ve), genotypic variance (Vg), and phenotypic variance (Vp), genotypic (GCV) and phenotypic coefficient of variation (PCV), heritability broad sense (h^2 bS) and genetic advance as percentage of various traits in *B. napus* L.

Traits	RMS	GMS	CV	Mean	S.E (±)	V_e	V_g	V_p	GCV	PCV	h^2BS	GA
Days to flowering initiation	1.90	1074.30**	1.98	81.10	1.31	2.57	357.24	359.81	23.31	23.39	0.99	47.69
Days to half flowering	3.10	936.53**	1.90	95.80	1.49	3.32	311.07	314.39	18.41	18.51	0.99	37.75
Days to flowering completion	0.00	549.20**	2.23	107.80	1.96	5.78	181.14	186.92	12.48	12.68	0.97	25.34
Plant height	46.63	2667.08**	8.19	179.52	12.01	216.35	816.91	1033.26	15.92	17.91	0.79	29.14
Primary branches plant^{-1}	5.633	9.50^{ns}	38.95	6.87	2.18	7.15	0.78	7.93	12.86	40.99	0.10	8.44
Pods main raceme^{-1}	151.60	395.02^{ns}	20.99	62.60	10.73	172.60	74.14	246.74	13.75	25.09	0.30	15.51
Main raceme length	76.37	255.74^{ns}	15.80	68.72	8.86	117.82	45.97	163.79	9.87	18.62	0.28	10.74
Pod length (cm)	1.28	3.40**	7.32	6.82	0.41	0.25	1.05	1.30	15.02	16.72	0.81	27.86
Pod width	0.002	0.003**	4.85	0.51	0.026	0.001	0.0007	0.0017	5.18	8.08	0.41	6.86
Seed pod^{-1}	0.03	37.63**	13.65	19.43	2.16	7.03	10.20	17.23	16.44	21.36	0.59	25.99
100-seed weight	0.00	0.01**	10.85	0.394	0.037	0.002	0.003	0.005	14.04	18.13	0.60	22.30

** Significant at 1% probability level, * Significant at 5% probability level.

Pods main raceme^{-1}: Data for PMR among the genotypes ranged from 47 to 81 pods in which the maximum number of pods were produced by genotype 2756 and minimum number of pods were recorded for the genotype 2736 (Table 1) with overall mean of 62.60 pods per raceme (Table 2). The genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability broad sense (h^2 BS) and genetic advance as percentage of mean (G.A) estimates were 13.75, 25.09, 0.30 and 15.51 respectively (Table 2). Khan *et al.,* (2008) and Sadat *et al.,* (2010) reported high heritability with the later reporting it coupled with high genetic advance.

Seeds pod^{-1}: The data exhibited a range of 13 to 25 seeds pod^{-1}. Maximum seeds per sillique^{-1} were produced by the genotype 255 and minimum were observed for the genotype 223 (Table 1). Mean value was 19.433 seeds pod^{-1} (Table 2). Data perusal revealed 16.44 (GCV), 21.36 (PCV), 0.59 (h2 BS) and 25.99 (G.A as % of mean) (Table 2). Larik & Rajput (2000); Khan *et al.,* (2006a) and Emrani *et al.,* (2012) reported the similar results whereas Sadat *et al.,* (2010) reported opposite to the current study.

Pod length: Data varied from 5.453 (2762) to 8.710 cm (genotype 266) (Table 1). The mean was recorded to be 6.822 cm (Table 2). Post ANOVA computations revealed 15.02 (GCV), 16.72 (PCV), 0.81 (h^2BS) and 27.86 (G.A as % of mean) (Table 2). Results in $F_{3:4}$ *Brassica* populations (Khan *et al.,* 2008a), rapeseed (Sadat *et al.,* 2010) are in conformity. Shehzad & Farhatullah (2012) also reported high heritability in $F_{2:3}$ *Brassica* populations.

Pod width: The data ranged from 0.4467 to 0.5433 cm. Broadest pods were observed for genotypes 255 and 2736 whereas they were thinest for genotype 2762 (Table 1). The mean value was recorded to be 0.508 cm (Table 2). Data perusal revealed 5.18 (GCV), 8.08 (PCV), 0.41 (h^2 BS) and 6.86 (G.A as % of mean) (Table 2).

100-seed weight: Data for 100-seed weight among the genotypes varied from 0.3100 to 0.4800 g in which the grain weight was lighteset for genotype Zafar and heaviest for genotype 266 (Table 1). The grand mean was found to be 0.394 g (Table 2). Genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability broad sense (h2 BS) and genetic advance as percentage of mean (G.A) estimates were 14.04, 18.13, 0.60 and 22.30 respectively (Table 2). Similar findings were reported in *B. napus* L. (Zhang & Zhou, 2006), mustard (Akbar *et al*., 2007) winter rapeseed (Ali *et al.,* 2003; Aytaç & Kınacı, 2009) brown *sarson* (Dar *et al.,* 2010) and in some F_2; F_3 *Brassica* populations (Shehzad & Farhatullah, 2012).

For most of the traits there was a narrow gap between values computed for GCV and PCV, is indicative of lesser share of environment in trait expression.

Trait correlations: Trait correlations were computed, for the less likelihood of separate control of a pair of traits. Plant height was positively and highly significantly ($p\leq0.01$) correlated with main raceme length (r=0.48**), pods main raceme^{-1}(r=0.67**), 100-seed weight (r=0.47**), negative and highly significantly correlated with days to half flowering (-0.58**), days to flowering completion (-0.67**) whereas negative and significantly ($p\leq0.05$) correlated with days to flowering initiation (-0.43*) (Table 3). Similar associations for plant height with pods per main raceme (Basalma, 2008; Azadgoleh *et al.,* 2009), plant height with main raceme length (Sadat *et al.,* 2010) and plant height with 100 seed weight (Azadgoleh *et al.,* 2009) were reported earlier.

Main raceme length was found to be positive and highly significantly ($p\leq0.01$) correlated with pods main raceme^{-1}(0.73**). Seed pod^{-1} was positively and highly significantly ($p\leq0.01$) correlated with pod length (0.51**) and pod width (0.46**) (Table 3). Current results are supported by (Khan *et al.,* 2006b).

Pod length was positive highly significantly ($p\leq0.01$) and significantly ($p\leq0.05$) correlated with 100-seed weight (0.59**) and pod width (0.37*) respectively. Pod width was revealed to have negative significant correlation with days to flowering inititaion (-0.40*) whereas positive significant correlations with100-seed weight (0.37*) (Table 3).

Correlations between days to flowering initiation and days to half flowering, days to flowering completion were positive and highly significant ($p\leq0.01$) days to half flowering was positively and highly significantly ($p\leq0.01$) correlated with days to flowering completion (0.96**) (Table 3). Negative significant correlation for days to flowering initiation with plant height had negative non-significant correlation for the said trait with pods main raceme^{-1} is in contrast to the findings of Shinwari *et al.,* (2013). Non-significant correlation for seed pod^{-1} with 100-seed weight (Tuncturk & Çiftci, 2007), primary branches plant^{-1} with plant height, seed pod^{-1}, pod length (Khan *et al.,* 2006b) and pods main raceme^{-1} with pod length (Aytaç & Kınacı, 2009) are in conformity. Non-significant correlation for seed pod^{-1} with plant height is in contrast to Emrani *et al.,* (2012) which may be attributed to the genetic background and agro-ecological conditions under which the genotypes were evaluated.

Pleiotropy or linkage relations among genes controlling the traits are some of the reasons of genetic trait correlations. Directions and rates of short term evolution are effected by genetic trait correlations (Falconer, 1989; Roff, 1997; Lynch & Walsh, 1998). Much of dissimilarity phenotypic and genetic correlation estimates seems to be due to imprecise estimates of genetic correlations. In many situations, phenotypic correlations are likely to be fair estimates of their genetic counterparts (Cheverud, 1988). Genetic correlations between morphological traits are more often positive than correlation between other traits (Roff, 1996 & 1997). Competition between processes for a resource may result in negative correlations (Atchley, 1987).

In conclusion, plant height, seeds pod^{-1}, pod length and 100-seed weight were found to be efficient characters as selection criteria. Mass selection is useful to improve a character having high heritability along with genetic gain (Mahto & Haider, 2002; Akbar *et al.,* 2003 & 2007) whereas that with moderate to high heritability and low genetic advance may be improved by selection based on family (Mahto & Haider, 2002).

Table 3 . Phenotypic correlation coefficients among characters calculated from the studied *B. napus* L. genotypes.

	Days to flowering initiation	Days to half flowering	Days to flowering completion	Plant height	Primary branches plant^{-1}	Pods main raceme^{-1}	Main raceme length	Pod length	Pod width	Seed pod^{-1}	100-seed weight
Days to flowering initiation		0.91**	0.86**	-0.43*	0.09ns	-0.13ns	-0.05ns	-0.02ns	-0.40*	-0.02ns	-0.20ns
Days to half flowering			0.96**	-0.58**	0.15ns	-0.31ns	-0.15ns	-0.16ns	-0.34ns	-0.03ns	-0.30ns
Days to flowering completion				-0.67**	0.03ns	-0.32ns	-0.17ns	-0.12ns	-0.22ns	0.10ns	-0.33ns
Plant height					0.04ns	0.67**	0.48**	0.28ns	0.06ns	-0.15ns	0.47**
Primary branches plant^{-1}						-0.23ns	-0.06ns	-0.04ns	-0.13ns	-0.35ns	0.15ns
Pods main raceme^{-1}							0.73**	0.26ns	-0.12ns	-0.14ns	0.15ns
Main raceme length								0.03ns	-0.31ns	-0.20ns	0.02ns
Pod length									0.44*	0.51**	0.59**
P od width										0.46**	0.37*
Seed pod^{-1}											0.30ns
100-seed weight											

** Significant at 1% probability level, * Significant at 5% probability level.

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