Life Science Journal

Study of Morphological Characters Give an Insight into the Genetic Variation Present in *Brassica napus* L. Germplasm

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Abstract: Rapeseed is an important crop for the whole world among oilseed crops. Development of new cultivars which meet our requirements is a continuous process. Using statistics to find out the possible ways for manipulating the breeding program according to our need is the best accepted way in breeding. So, the present study was conducted to analyze the interrelationship among yield and yield related traits in ten promising *B. napus* L. genotypes from selected from preliminary yield trials at the farm area of Oilseeds Research Institute, Ayub Agricultural Research Institute, Faisalabad during 2016-2017. Sowing was completed in Randomized Complete Block Design with 3 replications. Relevant data were recorded at already specified phenological and developmental stages. Analysis of variance was constructed. Phenotypic and genotypic interrelationship co-efficients (r_p and r_g respectively), path coefficients analysis and heritability analysis were done. Higher heritability was estimated for seed yield. At genotypic level, direct as well as highly significant relation was observed among all studied traits. Seed yield/plot depicted positive and highly significant phenotypic and genotypic association with primary branches/plant, days to flowering and days to physiological maturity. Besides, No. of primary branches/plant had direct association with duration of flowering and maturity, phenotypically. Plant height and number of branches had highest positive direct and highest total indirect effects on overall yield respectively. All these findings can assist in selection of genotypes with high yield, from a diverse germplasm, under normal field conditions.

1. Introduction

Rapeseed is a conventional oilseed crop of Pakistan. It is an important crop of family *Brassicaceae* or *Cruciferae*. Being an amphidiploid species (AACC), it contains two sets of each of two different genomes A and C (Liu *et al.,* 2013). It is thought to be originated from the cross between two brassica species which are *Brassica compestris* and *Brassica oleracea* (Gupta and Partab, 2007). Its diploid (2n) chromosome number is 38 (Prakash and Hinata, 1980). Rapeseed oil (40-46 %) is core ingredient of daily diet. Rapeseed meal is a good source of protein (38-40%) and is a necessary component of animal diet (Rashid, 2013).

Rapeseed ranks second important oilseed crop all over the world after soybean (Anonymous 1, 2018; An *et al.,* 2019), While it is the 2nd essential oilseed crop of Pakistan after cotton (Sarwar, 2014; Khan *et al.,* 2008). Rapeseed contributes 17% to meet domestic need of edible oil. During the year 2018-19, it was grown on 0.643 million acres and gave 0.318 million tonnes seed yield along with 102,000 tonnes of oil (Government of Pakistan, 2018-19).

Economy of Pakistan is based on agriculture with the contribution of 18.5% to the GDP (Government of Pakistan, 2018-19). But, domestic needs of edible oil are far more than this. Import of edible oil from other countries gets a substantial share from import basket and this trend is increasing with every passing year

because of increased population growth (Ahmad *et al.,* 2013a). In the year 2018-19, total edible oil requirement was estimated to be 2.921 million tonnes. The local produce contributed only 17 % while remaining 83 % was imported at the cost of 1.455 billion US dollars (Government of Pakistan, 2018-19). To develop oilseed varieties having high yield must be given a high priority so that we can be self-sufficient in edible oil.

The per unit area production of rapeseed is increased from 922 kg/ha to 1406 kg/ha, yet has wide range of potential which is 3500kg/ha (Agricultural statistics of Pakistan, 2018-19). There are many factors which are involved in the low yield per unit area which include non-availability of essential plant nutrients, dearth of well adapted genotypes, use of marginal lands for cultivation, insect and disease prevalence, competition with the other major Rabi season crops like wheat, chickpea and lentil. (Khan *et al.,* 2006). Therefore, it is very important to adopt strategies for rapeseed crop improvement (Shah *et al.,* 2000).

Seed yield is a complicated trait and is controlled by several interconnected polygenic characters (Luo *et al.,* 2015). There is need to find out the influence of each trait towards final yield (Mary and Gopalan, 2006; Tuncturk and Ciftci, 2007). Correlation studies help in the selection of such traits which are positively correlating with the yield hence increasing the yield through indirect selection (Ivanovska *et al.,* 2007; Basalma, 2008; Aytaç & Kinaci, 2009; Hashemi *et al.,* 2010; Belete, 2011; Ahmad *et al.,* 2013b; Rameeh, 2015; Hoveize, 2016). Selection on the basis of simple correlation coefficients without considering interaction of yield and yield related components is not enough as it may mislead the main breeding purposes. For accurate selection, path coefficient analysis offers the best criteria as it can quantify the overall effects (direct and indirect) of component and interlinked traits contributing towards seed yield (Tuncturk and Ciftci, 2007).

Zhang and Zhou, (2006) found positive correlation of No. of pods/plant, 1000 seed weight and seeds per plant with seed yield. Positive correlation was estimated by Nasim *et al.,* (2013) and Ansar *et al.,* (2014) for height of plant, No. of pods/plant and 100-seed weight. No. of seeds per pod exhibited positive association with pod length and width. Sheikh *et al.,* (1999) concluded a direct interrelationship between yield and yield related traits. Path co-efficient analysis showed that days to 50% flowering and 80% physiological maturity, seeds/silique, seeds/plant and weight of 1000 seed had positive as well as direct contribution towards seed yield. Hasan *et al.,* (2014) concluded that seed/ plant is the trait having highest selection potential to increase seed yield because this character possesses high broad sense heritability,

highly significant positive association and highest direct effects positively with the seed yield.

The present study was done out to find the interrelationship between seed yield, its component traits and the identification of the potential yield related trait which can be used in future breeding programs as a selection criteria.

2. Materials and Methods

The experiment for identification of trait contributing positively towards yield was carried out at Oilseed Research Institute, AARI, Faisalabad, during 2016-17. Experimental material consisted of 10 genotypes from preliminary yield trials. Genotypes were sown in randomized complete block design (RCBD) with three replications for each entry. Each entry was sown in a plot having 3 rows of length 5 m. Sowing was done by using seed drill by maintaining 45 cm row to row and 15 cm plant to plant distance. Routine agronomic operations were applied to let the experimental genotypes grow properly and to the maximum of their potential. Data based on the phenology of plant was recorded at the phenological stages of genotypes for example, days to flowering (DF) and days to maturity (DM). For other traits like plant height (PH) and primary branches per plant (B/P) from each row of plot selection of plants were done randomly and recorded the data whereas, seed yield/plot (SY/P) was recorded of each individual plot. For statistical analysis, ANOVA was performed for each measured character by method developed by Steel and Torrie (1980). Heritability was calculated by method proposed by Falconer (1989). Phenotypic (r_p) and genotypic correlation (r_g) was estimated according to method as suggested by Kwon and Torrie (1964) while analysis of path co-efficients was performed as defined by Dewey and Lu, 1959. Path co-efficient analysis was performed by assuming seed yield as dependent and other characters under study as an independent variable.

Results And Discussion
Analysis of Variance and Mean Values of Genotypes

The presence of variability in any crop population is essential for improvement in breeding program of a crop (Hasan *et al.,* 2006). Highly significant results for genotypic mean squares and extensive range of phenotypic variation were found for all studied traits. It means that these genotypes may be potentially exploited in the rapeseed variety development program. Results described by Aytac and Kinaci, (2009), Sabaghnia *et al.,* (2010) and Rameeh, (2015) were in agreement with that of present experiment. Value of Mean for the days to flower ranging from 63-110. Minimum days to flower taken by RBN-16009 while

check variety Faisal canola took 110 days to flower. Lesser No. of days to flowering are preferable for development of early maturing genotypes (Koornneef, *et al.,* 2002). So, RBN-16009 and RBN-16010 would be preferred for being lesser No. of days to flowering. Early maturity is desired character for the development of an ideotype as it helps crop to escape (Borghi *et al.,* 2019) from serious pest damage caused by aphids and provide enough time for next crop cultivation. In the present research, mean of days to maturity ranged from 155 to 161 in genotypes RBN-16010 to RBN-16001.

Genotype RBN-16010 could be selected in breeding programs for early maturing varieties in *Brassica napus*. Numbers of branches/plant ranged from 6 to 10 in genotypes RBN-16009, RBN-16010 and Faisal canola to RBN-16014. Plant height (PH) ranged from 139 cm to 201 cm in RBN-16009 to RBN-16001. As short stature of plant is the desirable ideotype, so, RBN-16009 would be suitable option for development of short stature Brassica varieties. Mean values of yields were ranged from 2741 kg/ha to 630 kg/ha in genotype RBN-16001 to RBN-16010 respectively.

Table 1: Mean values and mean squares of yield related traits of all genotypes

Genotype	DF	DM	B/P	P/H (cm)	SY/P (kg/ha)
RBN-16001	107	161	8	201	2741
RBN-16004	70	159	8	172	1259
RBN-16007	71	157	7	177	1630
RBN-16008	106	158	9	203	2296
RBN-16009	63	156	6	139	611
RBN-16010	65	155	6	156	630
RBN-16011	106	159	8	192	2444
RBN-16014	106	160	10	189	2074
Faisal Canola	110	157	6	149	1444
Rohi Sarson	109	156	8	185	1241
Mean Squares	1305.37**	11.2**	5.869**	1476.46**	330750**

*=Significant (P<0.05), **=Highly significant (P<0.01)

Heritability, Genotypic and Phenotypic Variance Estimates

Heritability is a statistical tool being utilized in plant breeding programs for many years to estimate the heritable portion of variation in a phenotypic trait within a population. It is considered as the most vital concept in selective breeding. Broad sense heritability was estimated for studied characters. Higher heritability value was observed for seed yield (0.88) as

well as days to flowering (0.991). Maximum broad sense heritability value for days to flowering indicates that selection gain to improve this trait would be higher. Similar findings of higher heritability estimate for these characters were also calculated by Hasan *et al.,* (2014), Yadava *et al.,* (2011), Aytac *et al.,* (2008) and Ali *et al.,* (2002). Maximum phenotypic variance and genotypic variance was observed for SY/P i.e., 105472.2 and 119805.5 respectively (Table 2).

Table 2: Broad sense heritability, genotypic and phenotypic variance of yield related traits

Genetic parameters	DF	DM	B/P	PH	SY/P
Heritability (broad sense)	0.991	0.611	0.531	0.5	0.88
Genotypic variance	433.933	3.081	1.474	369.203	105472.2
Phenotypic variance	437.5	5.037	2.774	738.852	119805.5

Correlation Analysis

For plant breeders, the studies of correlation are of significant interest in evaluating the characters which are either positively or negatively associated with main objectives of a breeding program. The phenotypic and genotypic associations among traits under study are shown in Table 3. All traits under study depicted highly significant as well as positive genotypic correlation. It concludes that all the traits are supposed to be positively correlated and contributing to attain higher yield (Table 3). SY/P and PH were found positively associated (Khayat *et al.,* 2012; Sabaghnia *et al.,* 2010 and Jeromel *et al.,* 2007).

Positive and significant association was found between days to maturity and flowering, at genotypic and phenotypical level (r_g = 0.531** and r_p = 0.39* respectively), confers that this trait can be used for early selection for the development of short duration genotypes. Similar results were found by Tuncturk and Ciftci (2007) and Naderi and Toorchi (2012).

A positive as well as highly significant genotypic and phenotypic interrelationship of plant height towards all other traits was found. This was also witnessed in case of No. of primary branches, days to flowering and maturity with yield. While phenotypically, branches/plant were positively and

significantly linked with days to flowering (r_p=0.462*) and days to maturity (r_p=0.426*), days to flowering with days to maturity (r_p=0.39*). Correlation coefficient depicted the same trend at both genotypic and phenotypic level in correlation analysis. Rameeh (2011) and Naznin *et al.,* (2015) concluded the same results.

Table 3: Genotypic (r_g) and phenotypic (r_p) correlation coefficients for yield contributing traits

		B/P	DF	DM	SY/P
PH	r_g	0.955**	0.695**	0.844**	1**
	r_p	0.574**	0.505**	0.464**	0.661**
B/P	r_g		0.622**	0.721**	0.655**
	r_p		0.462*	0.426*	0.501**
DF	r_g			0.531**	0.725**
	r_p			0.39*	0.683**
DM	r_g				0.964**
	r_p				0.646**
*=Significant (P<0.05), **=Highly significant (P<0.01)					

Path Co-efficient Analysis

The purpose of path co-efficient analysis is to figure out direct and indirect effects of correlation coefficient separately. It depicts whether the association of characters with yield is the consequence of their direct effect or due to their indirect effect through other characters. As presented in Table 4, the plant height showed maximum positive direct effect on yield (7.23) which is in contrary to results given by Sinha *et al.,* (2001) and Khayat *et al.,* (2012). However, branches/plant, days to flowering and maturity indicated negative direct effects towards yield (-5.052,

-0.5 and -1.231) respectively. A positive and direct effect of days to maturity and days to flowering on yield was also presented by Sinha *et al.,* (2001) and Khayat *et al.,* (2012). Negative and direct effect of branches/plant on yield was observed by Basalma (2011).

Plant height contributed negative total indirect effects (-1.039) on yield. While the total indirect effects of branches per plant (5.708), days to flowering (1.226) and physiological maturity (2.197) was positive on yield.

Table 4: Path co-efficient analysis of all the yield contributing traits

	Direct effects	Indirect effects				Total indirect effects	Total effects
		PH	B/P	DF	DM		
PH	7.23		-4.826	-0.347	-1.039	-1.039	1.018
B/P	-5.052	6.907		-0.311	-0.888	5.708	0.656
DF	-0.5	5.025	-3.145		-0.654	1.226	0.726
DM	/*9-1.231	6.105	-3.643	-0.265		2.197	0.966

Conclusions

Isolating the superior genotypes from diverse germplasm is the basic goal of a plant breeder so that the selected lines could be used in future varietal developmental programs. Based on the phenotypic performance, genotypes were selected as it is the long-tested, efficient and the easiest way. Therefore, the traits which played evident role and had considerable correlation with the yield, in this experiment, would be helpful for the *Brassica* breeders to efficiently select superior genotypes. Moreover, highly significant differences among all genotypes for all traits under study give an insight into the existence of genetic variation in the available genotypes. Overall, genotype RBN-16001 gave the maximum yield/plot. Positive and highly significant correlation of all yield related traits indicate that these can be potentially selected and utilized for the variety development program of Brassica.

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3/6/2020