INTERNATIONAL JOURNAL OF ENVIRONMENT

Volume-4, Issue-2, March-May 2015 ISSN 2091-2854

Received:24 December 2014 *Revised:3 February 2015* *Accepted:5 May 2015*

GENETIC POTENTIAL AND HERITABILITY ESTIMATES OF YIELD AND YIELD ASSOCIATED TRAITS IN Rape Seed *Brassica napus* L

Sadia Shaukat, Raziuddin, Fahim Ullah Khan*, Ibni Amin Khalil

Department of Plant Breeding and Genetics, The University of Agriculture, Peshawar

*Corresponding author: fahimbiotech@yahoo.com

Abstract

To investigate genetic variability and heritability, eight *Brassica napus* genotypes were evaluated at New Developmental Research Farm, Faculty of Agriculture. Peshawar University, during 2010-11. Analysis of variance revealed significant differences ($P \leq 0.01$) among *Brassica napus* genotypes for all the studied characters. Mean values showed that maximum primary branches plant^{-1} (15) was observed for genotype PGRI-8, plant height (220.66 cm) for genotype CH-6 and PGRI-8, pods main raceme^{-1} (96.33) for genotype CH-1, pods plant^{-1} (994) for genotype PGRI- 8, pod length (8.3 cm) for genotype PGRI- 7, seeds pod^{-1} (27) for genotype CH-1, 1000-seed weight (3.97 g) for genotype CH-2, and seed yield plant^{-1} (91.1 g) for genotype PGRI-8. In t terms of heritability values, high broad sense heritability estimates were observed for primary branches plant^{-1} (0.83), plant height (0.78), pods main raceme^{-1} (0.65), seeds pod^{-1} (0.61), 1000-seed weight (0.61), while moderate heritability values were recorded for pod length (0.57), pods plant^{-1} (0.55), and seed yield plant^{-1} (0.50). In conclusion, the significant differences among *Brassica napus* genotypes showed that there is sufficient variability for effective selection. The trend of heritability (moderate to high) in the present study indicates that there is more genetic control and selection should lead to quick improvement. Furthermore genotype PGRI-8 surpassed all other genotypes in yield and yield component and could be used in future breeding programs.

Keywords: Brassica napus, Genetic variability, Heritability, Yield and yield components

Introduction

Rapeseed is considered the third largest source of vegetable oil in the world (after soybean and palm) and the second world source of protein, although it reached only a fifth of the soybean production. Rape seed-mustard seed is rich in oil and protein and contains 40-46% oil and 18-22% protein. Raw rape seed oil contains 50% erucic acid. Wild seeds also contain high levels of glycosides (mustard oil glycosides), chemical compounds that significantly lowered the nutritional value of rape seed press cakes for animal feed. In addition the oil content of rape seed seed meal contains about 40% protein with well balanced amino acid (Miller *et al.*, 1962) but lower amino acid content would be desired.

Success of any crop improvement depends upon the presence of substantial amount of genetic variability, heritability, as well as genetic gain in selection (Khan et al., 2007). The potential of a crop to favorably respond to breeding/selection and bioengineering programs depends upon nature and magnitude of genetic variability (Akhtar *et al.*, 2007). Heritability is an index of transmissibility of traits and as such partitions the total variance into genetic and environmental components (Falconer and Mackay 1996; Marwede *et al.,* 2004). Heritability of any trait depends upon genetics properties of breeding material and environmental conditions in which experiments are carried out (Falconer and Mackay, 1996). A character which has higher range of genetic variability, heritability and genetic advance would be an effective tool to improve seed yield (Aytac and Kinaci, 2009). Parameters having high heritability and genetic advance are considered under control of additive genes, which highlights the usefulness of selection based on phenotypic performance (Ghosh and Gulati, 2001).

Efforts are underway to develop better oilseed *Brassica napus* genotypes. Such breeding efforts need critical evaluation of existing genetic variability, heritability, genetic advance as studied earlier (Khan *et al.,* 1992; Chaudhary *et al.,* 1999; Kakroo *et al.,* 2000; Mahmood *et al.,* 2003).
Keeping in view the importance of *Brassica napus* as oil seed crop, an experiment was conducted to determine the extent of genetic variability and broad sense heritability for yield and yield components among some *Brassica napus* genotypes.

Materials and methods

The present research work was conducted at New Developmental Research Farm, Faculty of Agriculture, Peshawar University, Pakistan, during 2010-11 season. Eight *Brassica napus* L. genotypes i.e., CH-1, CH-2, CH-3, CH-4, CH-5, CH-6, PGRI-7 and PGRI-8 were sown on 20th October, 2010 in RCB design with three replications. Row to row and plant to plant distances were kept as 60 and 20 cm, respectively. Standard agronomic practices were employed throughout the growing season. Data were recorded on randomly selected 10 plant in each plots on primary branches plant^{-1},plant height (cm), pods main raceme^{-1}, pods plant^{-1}, pod length (cm), seeds pod^{-1}, 1000-seed weight (g) and seed yield plant^{-1} (g).

Statistical analysis

Analysis of variance

The data recorded on each parameter were subjected to analysis of variance (ANOVA) techniques appropriate for RCBD using Statix ver 8.1 software programme. The mean differences among *Brassica napus* genotypes for yield and yield components were determined by using least significant differences (LSD) test at 5% level of probability.

Heritability $_{\text{(B.S)}}$

The heritability estimates provide information on transmission of trait (s) from parents to offspring. Such estimates facilitate the evaluation of genetic and environmental effects, aiding in selection. Estimate of heritability can also be used to predict genetic advance under selection, so that plant breeder can anticipate the improvement of selection.

The genotypic, phenotypic, and environmental variances and heritability were calculated by the following formula:

$$Genotypic\,Variance\ (\delta^2{}_g)\ =\ \frac{GMS - EMS}{r}$$

$$Phenotypic\,Variance\ (\delta^2{}_p)\ =\ \delta^2{}_g + \delta^2{}_e$$

$$Environmental\ Variance\ (\delta^2{}_e)\ =\ EMS$$

$$h^2_{(BS)} = \frac{\delta^2_g}{\delta^2_p}$$

δ^2_g = Genotypic variance for a trait.

δ^2_p = Phenotypic variance for a trait.

$h^2_{(BS)}$ = Broad sense heritability for a trait.

Results and discussion

Primary branches plant^{-1}

Analysis of variance showed highly significant differences ($P \le 0.01$) among *Brassica napus* genotypes for primary branches plant^{-1}. The coefficient of variation for primary branches was 13.04 % (Table 1). Raj and Singh (1998) and Khan and Khan (2003) also reported significant difference among rape seed genotypes for primary branches plant^{-1}. Data regarding primary branches plant^{-1} ranged from 7 to 15 with the mean value of 9. Minimum primary branches plant^{-1}(7) were recorded for genotype CH-2, CH-5 and CH-6 followed by genotype CH-3 and CH- 4 (8), whereas maximum primary branches plant^{-1}(15) were recorded for genotype CH-8 followed by genotype PGRI-7 (10) and genotype CH-1 (9) (Table 2). Genetic and environmental variances for primary branches plant^{-1} were 6.26 and 1.33, respectively. High broad sense heritability 0.83 was recorded for primary branches plant^{-1} (Tab 4). Khulbe *et al.*, (2000), Raj and Singh (1998), Marinkovic *et al.*, (2003), Mahmood *et al.*, (2003) and Khan *et al.*, (2008) also observed high heritability for primary branches plant^{-1}.

Plant height (cm)

Analysis of variance showed highly significant differences ($P \le 0.01$) among all the genotypes for plant height. The coefficient of variation for plant height was 2.67 % (Table 1). Ali *et al.*, (2002), Khan and khan (2003), Tahir *et al.*, (2006) and Khan *et al.*, (2008) also reported significant difference among rape seed genotypes for plant height. Data regarding plant height ranged from 188.00 to 220.66 cm with the mean value of 209.00 cm. Minimum plant height (188.00 cm) were recorded for genotype CH-2 followed by genotype CH-3 (201 cm) and genotype CH-1 (204 cm), whereas, maximum plant height (220.66 cm) were recorded for genotype CH-6, PGRI-8 followed by genotype CH-4 (215 cm) and genotype CH-5 and PGRI-7 (213 cm) (Table 2). Genetic and environmental variances for plant height were 110.43 and 31.23 respectively. High broad sense heritability 0.78 was recorded for plant height (Tab 4). Zhang and Zhou (2006), Khulbe *et al.*, (2000), Raj and Singh (1998), Mahmood *et al.*, (2003) also observed high heritability for plant height.

Table 1. Mean squares for yield and yield components traits of 8 *Brassica napus* genotypes during 2010-11

Traits	Replications (df=2)	Genotypes (df=7)	Error (df=14)	CV (%)
Primary branches plant^{-1}	0.042	20.095**	1.327	13.04
Plant height (cm)	102.375	362.518**	31.232	2.67
Pods main raceme^{-1}	85.542	380.851**	57.637	9.93
Pods plant^{-1}	3002.042	95099.905**	20466.851	21.39
Pod length (cm)	0.485	1.839**	0.372	8.62
Seeds pod^{-1}	0.542	18.089**	3.161	7.58
1000-seed weight (g)	0.063	0.196**	0.034	4.99
Seed yield plant^{-1} (g)	59.412	791.356**	198.508	24.02

***, **: denote the significance, at 0.05 and 0.01 level of probability, respectively.**

Pods main raceme^{-1}

Analysis of variance showed highly significant differences (P≤0.01) among all the genotypes for pods main raceme^{-1}. The coefficient of variation for pods main raceme^{-1} was 9.93 % (Table 1). Tahir *et al.*, (2006) also reported significant difference among rape seed genotypes for pods main raceme^{-1}. Data regarding pods main raceme^{-1} ranged from 58 to 96 with the mean value of 76. Minimum pods main raceme^{-1} (58) were recorded for genotype PGRI-7 followed by genotype PGRI-8 (66) and genotype CH-2 (74), whereas maximum pods main raceme^{-1} (96) were recorded for genotype CH-1 followed by genotype CH-4 (81) and CH-6 (80) (Table 2). Genetic and environmental variances for pods main raceme^{-1} 107.74 were 57.64 and respectively. High broad sense heritability 0.65 was recorded for pods main raceme^{-1} (Tab 4). Khulbe *et al.*, (2000) and Raj and Singh (1998) also observed high heritability for Pods main raceme^{-1}.

Table 2.Mean performance for yield and yield components traits of 8 *Brassica napus* genotypes during 2010-11

Genotypes	Primary branches plant^{-1}	Plant height (cm)	Pods main raceme^{-1}	Pods plant^{-1}
CH-1	9	204	96	894
CH-2	7	188	74	487
CH-3	8	201	77	646
CH-4	8	215	81	616
CH-5	7	213	79	560
CH-6	7	220	80	584
PGRI-7	10	213	58	569
PGRI-8	15	220	66	994
Mean	9	209	76	668
LSD$_{0.05}$	2.02	9.8	13.3	250.5

Table 3.Mean performance for yield and yield components traits of 8 *Brassica napus* genotypes during 2010-11

Genotypes	Pod length (cm)	Seeds pod^{-1}	1000-seed weight (g)	Seed yield plant^{-1} (g)
CH-1	6.5	27	3.15	76.5
CH-2	7.8	26	3.97	50.4
CH-3	6.2	21	3.65	48.8
CH-4	7.4	20	3.90	48.7
CH-5	7.6	23	3.77	48.8
CH-6	6.5	22	3.89	57.2
PGRI-7	8.3	24	3.71	47.9
PGRI-8	6.4	25	3.67	91.1
Mean	7.0	23	3.71	58.6
LSD$_{0.05}$	1.06	3.11	0.32	24.68

Table 4: Variance components and heritability $_{(BS)}$ for yield and yield components traits of 8 *Brassica napus* genotypes during 2010-11

Traits	Vg	Ve	Vp	$h^2_{(BS)}$
Primary branches plant^{-1}	6.26	1.33	7.58	0.83
Plant height (cm)	110.43	31.23	141.66	0.78
Pods main raceme^{-1}	107.74	57.64	165.38	0.65
Pods plant^{-1}	24877.68	20466.85	45344.54	0.55
Pod length (cm)	0.49	0.37	0.86	0.57
Seeds pod^{-1}	4.98	3.16	8.14	0.61
1000-seed weight (g)	0.05	0.03	0.09	0.61
Seed yield plant^{-1}	197.62	198.51	396.12	0.50

Vg = Genetic variance, Ve = Environmental variance, Vp = Phenotypic variances
$h^2_{(BS)}$ = Heritability (broad sense)

Pods plant^{-1}

Analysis of variance showed highly significant differences ($P \leq 0.01$) among all the genotypes for pods plant^{-1}. The coefficient of variation for pods plant^{-1} was 21.39 % (Table 1). Ali *et al.,* (2002), Mahmood *et al.,* (2003), Sadat *et al.,* (2010), Khan and Khan (2003) also reported significant difference among rape seed genotypes for pods plant^{-1}. Data regarding pods plant^{-1} ranged from 487 to 994 with the mean value of 668. Minimum pods plant^{-1}(487) were recorded for genotype CH-2, followed by genotype CH- 5(560) and genotype PGRI- 7(569), whereas, maximum pods plant^{-1} (994) were recorded for genotype PGRI- 8, followed by genotype CH-1 (894) and CH-3 (646) (Table 2).. Genetic and environmental variances for pods plant^{-1} were 24877.68 and 20466.85 respectively. Moderate broad sense heritability 0.55 was recorded for pods plant^{-1} (Tab 4). Zhang and Zhou (2006) and Uddin *et al.,* (1995) also observed moderate heritability for pods plant^{-1}.

Pod length (cm)

Analysis of variance showed highly significant differences ($P \leq 0.01$) among all the genotypes for pod length. The coefficient of variation for pod length was 8.62 % (Table 1).

Tahir *et al.,* 2006, Aytac and Kinaci (2009), also reported significant difference among rape seed genotypes for pod length. Data regarding for pod length ranged from 6.2 to 8.3 cm with the mean value of 7.0 cm. Minimum Pod length (6.2 cm) were recorded for genotype CH-3 followed by genotype PGRI- 8 (6.4 cm) and genotype CH- 1, CH-6 (6.5 cm), whereas maximum pod length (8.3 cm) were recorded for genotype PGRI- 7, followed by genotype CH-2 (7.8 cm) and CH- 5(7.6 cm) (Table 3). Genetic and environmental variances for pod length 0.49 were 0.37 and respectively. Moderate broad sense heritability 0.57 was recorded for pod length (Tab 4). Uddin *et al.,* (1995) also observed moderate heritability for pod length.

Seeds pod^{-1}

Analysis of variance showed highly significant differences ($P \leq 0.01$) among all the genotypes for seeds pod^{-1}. The coefficient of variation for seeds pod^{-1} was 7.58 % (Table 1). Khan and Khan (2005) also reported significant difference among rape seed genotypes for seeds pod^{-1}. Data regarding seed pod^{-1} ranged from 20 to 27 with the mean value of 23. Minimum seeds pod^{-1} (20) were recorded for genotype CH-4, followed by genotype CH- 3 (21) and genotype CH-6 (22), whereas, maximum seeds pod^{-1} were recorded for genotype CH-1 (27), followed by genotype CH-2 (26) and PGRI-8 (25) (Table 3). Genetic and environmental variances for seeds pod^{-1} were 4.98 and 3.16, respectively. High broad sense heritability 0.61 was recorded for seeds pod^{-1} (Tab 4). Zhang and Zhou (2006) also observed high heritability for seed pod^{-1}.

1000-seed weight (g)

Analysis of variance showed highly significant differences ($P \leq 0.01$) among all the genotypes for 1000-seed weight. The coefficient of variation for 1000-seed weight was 4.99 % (Table 1). Khan and Khan (2005) also reported significant difference among rape seed genotypes for 1000-seed weight. Data regarding 1000-seed weight ranged from 3.15 to 3.97 g with the mean value of 3.71 g. Minimum 1000-seed weight (3.15 g) were recorded for genotype CH-1, followed by genotype CH-3 (3.65g) and genotype PGRI-8 (3.67g), whereas, maximum 1000-seed weight were recorded for genotype CH-2 (3.97g),followed by genotype CH-4 (3.90g) and CH-6 (3.89g) (Table 3). Genetic and environmental variances for 1000-seed weight were 0.05 and 0.03 respectively. High broad sense heritability 0.61 was recorded for 1000-seed weight (Tab 4). Zhang and Zhou (2006), Singh *et al.,* (2002) also observed high heritability for 1000-seed weight.

Seed yield plant^{-1}(g)

Analysis of variance showed highly significant differences ($P \leq 0.01$) among all genotypes for seed yield plant^{-1}. The coefficient of variation for seed yield plant^{-1} was 24.02 % (Table 1). Ali *et al.,* (2002), Aytac and Kinaci., (2009), Ali *et al*., (2003) also reported significant difference among rape seed genotypes for seed yield plant^{-1}. Data regarding seed yield plant^{-1} ranged from 47.9 to 91.1 g with the mean value of 58.6 g. Minimum seed yield plant^{-1} 47.9 g were recorded for genotype PGRI-7, followed by genotype CH-4(48.7 g) and genotype CH-3,CH-5 (48.8 g) whereas, maximum seed yield plant^{-1} were recorded for genotype PGRI-8 (91.1 g), followed by genotype CH-1 (76.5 g) and CH-6 (57.2 g) (Table 3). Genetic and environmental variances for seed yield plant^{-1} were 197.62 and 198.51 respectively. Moderate broad sense heritability 0.50 was recorded for seed yield plant^{-1} (Table 4). Ali *et al.,* (2003) and Uddin *et al.,* (1995) also observed moderate heritability for seed yield plant^{-1}.

References

Akhtar, M. S., Oki, Y. T., Adachi and Khan, M.H.R., 2007. Analyses of the genetic parameters (Variability, Heritability, Genetic Advance, Relationship of Yield and Yield Contributing Characters) for some plant traits among *Brassica* cultivars under phosphorous starved environmental cues. J. of the Faculty of Env. Sci. and Tech., Okayama University. 12 (1): 91-98.

Ali, N., Far, F.J., Elmira, J.Y. and Mirza, M.Y., 2003. Relationship among yield components and selection criteria for yield improvement in winter rapeseed (*Brassica napus*). Pak. J. Bot., 35(2): 167-174.

Ali, N., Javedfar, F. and Attary, A.A., 2002. Genetic variability, correlation and path analysis of yield and its components in winter rapeseed (*Brassica napus* L.). Pak J. Bot. 34(2): 145-150.

Aytac, Z. and Kinaci, G., 2009. Genetic variability and association studies of some quantitative characters in winter rapeseed (*Brassica napus* L.). African J. Biotech. 8(15): 3547-3554.

Chaudhary, A. D., Barua, P. K. and Duara, P. K., 1999. Siliqua traits for determining seed yield in Indian rapeseed. J. Agric. Sci. Soc. North East India., 12(1): 60-63.

Falconer, D. S. and Mackay, T. F. C., 1996. Introduction to Quantitative Genetics (4th Ed.) Longman, Essex, UK.

Ghosh, S. K. and Gulati, S. C., 2001. Genetic variability and association of yield components in Indian mustard. Crop Res. 21(3): 345-349.

Kakroo, S. K., Jindla, L. N. and Satija, D. R., 2000. Genetic determination of seed yield through its components in Indian mustard (*B. juncea* L.) Crop Improvement, 27(3): 247-249.

Khan, A. F. and Khan, R.S.A., 2005. Inheritance pattern of qualitative characters in *Brassica napus*. Int. J. Agric. Biol. 7(3): 420-423.

Khan, A. H., Mahmood, T. and Shah, S. A., 1992. Path coefficient analysis of morphological traits with seed yield in Raya. Pak. J. Agric. Res. 13 (4): 334-337.

Khan, F.A., Ali, S. A., Shakeel, A. Saeed and Abbas, G., 2006. Genetic variability and genetic advance analysis for some morphological traits in *Brassica napus* L. J. Agric. Res., (44) 2: 83-88.

Khan, S. R. A. and Khan, F. A., 2003. Evaluation of genetic potential of some Brassica germplasm collections. Int. J. Agri. Bio. 5:630-631.

Khan, S., Farhatullah, I., Khalil, H., Munir, I., Khan, M. Y. and Ali, N., 2008. Genetic variability for morphological traits in F3:4 brassica populations. Sarhad J. Agric. 24(2): 223-231.

Khulbe, R. K., Pant, D. P. and Saxena, N., 2000. Variability, heritability and genetic advance in Indian mustard [*Brassica juncea* (L.) Czern and Coss]. Crop Res. 20: 551-552.

Mahmood, T., Ali, M., Iqbal, S. and Anwar, M., 2003. Genetic variability and heritability estimates in summer mustard (*Brassica juncea* L.). Asian. J. PI. Sci. 2(1): 77-79.

Marinkovic, R., Jeromela, A. M. and Vasic, D., 2003. Genetic variability components of some quantitative traits of winter oilseed rape (*Brassica napus* L.). Genetika, 35(3): 199-205.

Marwede, V., Schierholt, A., Mollers, C. and Becker, H. C., 2004. Genotype x environment interactions and heritability of tocopherol contents in canola. Crop Science, 44: 728-731.

Miller, R. W., Megrew, C. H., Wolf, I. A. and Jones, Q., 1962. Amino acids composition of seed meals from 41 species of crucifers. J. Agric. Fd. Chem. 10: 426-430.

Raj, L. and Singh, V. P., 1998. Variability studies in rapeseed and mustard. Ann. Agric. Res. 19 (1): 87-88.

Sadat, H, A., Nematzadeh, G. A., Jelodar, N. B. and Chapi, O. G., 2010. Genetic evaluation of yield and yield components at advanced generations in rapeseed (*Brassica napus* L.). Afr. J. Agric. Res. 5(15): 1958-1964.

Singh, M., Swarnkar, G. B., Prasad, L. and Rai, G., 2002. Genetic variability, heritability and genetic advance for quality traits in Indian mustard (*Brassica juncea* L. Czern and Coss). Plant Arch. 2(1): 27-31.

Tahir, M. H. N., Bashir, S. and Bibi, A., 2006. Genetic potential of conola (*Brassica napus*) varieties under water stress conditions. Caderno de Pesquisa Sér. Bio., Santa Cruz do Sul, 18(2): 127-135.

Uddin, M. J., Chowdhury, M. A. and Mia, M. F. U., 1995. Genetic variability, character association and path analysis in Indian mustard (*Brassica juncea* L.). Ann. Bangladesh Agric. 5(1): 51-54.

Zhang, G., and Zhou, W., 2006. Genetic analyses of agronomic and seed quality traits of synthetic oilseed *Brassica napus* produced from inter specific hybridization of *Brassica campestris* and *Brassica olearacea*. J. Genet. 85(1): 45-51.