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Genetic Variation and Heritability Estimates of Quality Traits in *Brassica napus* L.

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Abstract

To quantify genotypic variability and heritability among 8 *Brassica napus* genotypes were evaluated at New Developmental Research Farm, The University of Agriculture Peshawar during 2010-11. Analysis of variance revealed significant differences ($P \leq 0.01$) among *Brassica napus* genotypes for all the character studied except for oil content. Mean values showed that maximum for oil content (52.0 %) for genotype CH-4, protein content (22.6 %) for genotype PGRI-7, glucosinolate content (85.4 umolg^{-1}) for genotype CH-4 and erucic acid content (59.2 %) for genotype CH-3. One the other hand, minimum mean values for genotype PGRI-7, oil content (47.3 %) for genotype CH-1, protein content (18.4 %) for genotype CH-2, glucosinolate content (49.0 umolg^{-1}) for genotype CH-2, erucic acid content (35.0 %) for genotype CH-2. In addition, high broad sense heritability estimates were observed for erucic acid content (0.90), glucosinolate content (0.53), protein content (0.45) and oil content (0.16). In conclusion, significant differences among *Brassica napus* genotypes indicated sufficient variability among the tested material to have an 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 CH-2 surpassed other genotype in quality traits and could be used in future breeding program.

Keywords: Brassica napus, variability, heritability, quality traits, oil content

INTRODUCTION

Brassica is a genus of plants in the mustard family (Brassicaceae). The members of the genus may be collectively known either as cabbages, or as mustards. This genus is remarkable for containing more important agricultural and horticultural crops than any other genus. Most are annuals or biennials, but some are small shrubs. Due to their agricultural importance, *Brassica* plants have been the subject of much scientific interest. Six particularly important species (*Brassica carinata*, *B. juncea*, *B. oleracea*, *B. napus*, *B. nigra* and *B. rapa*) are derived by combining the chromosomes from three earlier species i.e. *B. rapa* (AA-2n=2x= 20), *B. nigra* (BB-2n=2x=16) and *B. olaracea* (CC-2n=2x=18) as described by the Triangle of U theory.

Rapeseed was 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. Rapeseed-mustard seed is rich in oil and protein and contains 40-46% oil and 18-22% protein. Natural rapeseed oil contains 50% erucic acid. Wild type seeds also contain high levels of glucosinolates (mustard oil glucosindes), chemical compounds that significantly lowered the nutritional value of rape seed press cakes for animal feed. In addition the oil content of *Brassica* seed meal contains about 40% protein with well balanced amino acid (Miller *et al.,* 1962) but lower than 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., 2006). 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). Keeping in view the importance of Brassica napus as oilseed crop, the experiment was designed to study genetic variation and estimate broad sense heritability for quality traits among *Brassica napus* genotypes.

MATERIALS AND METHODS

The present research work was conducted at New Developmental Research Farm, The University of Agriculture Peshawar, Pakistan during the year 2010-11. 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 in RCB design with three replications. Row to row and plant to plant distance was kept as 60 and 20 cm respectively. Standard agronomic practices were employed throughout the growing season. Biochemical analysis was done at Nuclear Institute for Food and Agriculture (NIFA) Peshawar using Nuclear Infra Red Spectroscopy (NIRS) technique for the following traits.

1. Oil content (%)
2. Protein content (%)
3. Glucosinolate content (umolg^{-1})

4. Erucic acid content (%)

STATISTICAL ANALYSIS

Analysis of variance

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

Heritability $_{(B.S)}$

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

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

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

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

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

$\delta^2{}_g$ = Genotypic variance for a trait.

$\delta^2{}_p$ = Phenotypic variance for a trait.

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

RESULTS AND DISCUSSIONS

Oil content (%)

Analysis of variance showed non significant differences among all the genotypes for oil content. The coefficient of variation for oil content was 4.51 % (Table 1). Data regarding oil content ranged from 47.3 to 52.0 with the mean value of 50.2. Minimum oil content 47.3% were recorded for genotype CH-1, followed by genotype PGRI-7(48.2 %) and genotype CH- 2(50.3 %), whereas, maximum oil content were recorded for genotype CH-4 (52.0 %) followed by genotype CH-3 (51.5 %) and CH-5,CH-6 (51.1 %) (Table 2). Genetic and environmental variances for oil content were 1.01 and 5.13 respectively (Table 3). Low broad sense heritability 0.16 was recorded for oil content. Khulbe *et al.,* (2000) also observed low heritability for oil content.

Protein content (%)

Analysis of variance showed significant differences ($P \leq 0.05$) among all the genotypes for protein content (Table 1). The coefficient of variation for protein content was 5.71 % (Table 1). Aytac and Kinaci (2009) also reported significant difference among Brassica genotypes for protein content. Data regarding protein content ranged from 18.4 to 22.6 with the mean value of 20.5. Minimum protein content (18.4 %) were recorded for genotype CH-2, followed by genotype PGRI-8 (20.0 %) and genotype CH- 3,CH-5 (20.1 %), whereas, maximum protein content were recorded for genotype PGRI-7 (22.6 %) followed by genotype CH-6 (21.5 %) and CH-1 (21.3 %) (Table 2). Genetic and environmental variances for protein content were 1.14 and 1.38 respectively. Moderate broad sense heritability 0.45 was recorded for protein content (Table 3). The present findings are in contrast with the earlier finding of Raj and Singh (1998), Khulbe *et al.,* (2000), Ali *et al.,* (2002), Singh *et al.,* (2002), Khan and Khan (2003), Mahmood *et al.,* (2003), Marinkovic *et al.,* (2003), Tahir *et al.,* (2006), Zhang and Zhou (2006), Khan *et al.,* (2008), Zehra and Kinaci (2009), Sadat *et al.,* (2010), Khan et al (2005) and Ali *et al.,* (2003).

Glucosinolate content (umolg^{-1})

Analysis of variance showed highly significant differences ($P \leq 0.01$) among all the genotypes for glucosinolate content. The coefficient of variation for glucosinolate content was 13.50 % (Table 1). Aytac and Kinaci (2009) also reported significant difference among Brassica genotypes for glucosinolate content. Data regarding glucosinolate content ranged from 49.0 to 85.4 with the mean value of 74.7. Minimum glucosinolate content (49.0 umolg^{-1}) were recorded for genotype CH-2, followed by genotype PGRI-7, PGRI-8 (72.8 umolg^{-1}) and genotype CH-6 (74.7 umolg^{-1}), whereas, maximum glucosinolate content were recorded for genotype CH-4 (85.4 umolg^{-1}), followed by genotype CH-5 (85.0 umolg^{-1}) and CH-3 (81.7 umolg^{-1}) (Table4). Genetic and environmental variances for glucosinolate content were 110.54 and 99.59 respectively. Moderate broad sense heritability 0.53 was recorded for glucosinolate content (Table 3). The present findings are in contrast with the earlier finding of Raj and Singh (1998), Khulbe *et al.,* (2000), Ali *et al.,* (2002), Singh *et al.,* (2002), Khan and Khan (2003), Mahmood *et al.,* (2003), Marinkovic *et al.,* (2003), Tahir *et al.,* (2006), Zhang and Zhou (2006), Khan *et al.,* (2008), Zehra and Kinaci (2009), Sadat *et al.,* (2010), Khan *et al.,* (2005) and Ali *et al.,* (2003).

Erucic acid content (%)

Analysis of variance showed highly significant differences ($P \leq 0.01$) among all the genotypes for erucic acid content. The coefficient of variation for erucic acid content was 6.61 % (Table 1). Aytac and Kinaci (2009) also reported significant difference among Brassica genotypes for erucic acid content. Data regarding erucic acid content ranged from 35.0 to 59.2 with the mean value of 48.6. Minimum erucic acid content (35.0 %) was recorded for genotype CH-2, followed by genotype CH-1(40.9 %) and genotype PGRI- 7(41.3 %), whereas, maximum erucic acid content were recorded for genotype CH-3 (59.2 %) followed by genotype CH-4 (57.6 %) and CHS-6 (57.3 %) (Table 2). Genetic and environmental variances for erucic acid content were 89.16 and 10.33 respectively. High broad sense heritability 0.90 was recorded for erucic acid content (Table 3). The present findings are in contrast with the earlier finding of Raj and Singh (1998), Khulbe *et al.,* (2000), Ali *et al.,* (2002), Singh *et al.,* (2002), Khan and Khan (2003), Mahmood *et al.,* (2003), Marinkovic *et al.,* (2003), Tahir *et al.,* (2006), Zhang and Zhou (2006), Khan *et al.,* (2008), Zehra and Kinaci (2009), Sadat *et al.,* (2010), Khan *et al.,* (2005) and Ali *et al.,* (2003).

Table 1. Mean squares for various quality traits of 8 *Brassica napus* genotypes evaluated at The University of Agriculture Peshawar during 2010-11.

Traits	Replication (df=2)	Genotypes (df=7)	Error (df=14)	CV (%)
Oil content	1.045	8.149^{NS}	5.130	4.51
Protein content	1.680	4.807*	1.380	5.71
Glucosinolate content	266.440	431.194**	99.585	13.50
Erucic acid content	7.545	277.793**	10.328	6.61

CV= Coefficient of variation and df = Degree of freedom

Table 2. Mean performance for quality traits of 8 *Brassica napus* genotypes evaluated at KP Agricultural University Peshawar during 2010-11.

Genotypes	Oil content (%)	Protein (%)	Glucosinolate (umolg^{-1})	Erucic acid (%)
CH-1	47.3	21.3	76.6	40.9
CH-2	50.3	18.4	49.0	35.0
CH-3	51.5	20.1	81.7	59.2
CH-4	52.0	20.4	85.4	57.6
CH-5	51.1	20.1	85.0	55.2
CH-6	51.1	21.5	74.7	57.3
PGRI-7	48.2	22.6	72.8	41.3
PGRI-8	50.5	20.0	72.8	42.3
Mean	50.2	20.5	74.7	48.6
LSD$_{0.05}$	NS	2.06	17.48	5.62

Table 3: Variance components and heritability $_{(BS)}$ for various quality traits of 8 *Brassica napus* genotypes evaluated at The University of Agriculture Peshawar during 2010-11.

Traits	Vg	Ve	Vp	h^2 (BS)
Oil content	1.01	5.13	6.14	0.16
Protein content	1.14	1.38	2.52	0.45
Glucosinolate content	110.54	99.59	210.12	0.53
Erucic acid content	89.16	10.33	99.48	0.90

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

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