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Heritability $_{(BS)}$ and selection response estimates for yield and yield related traits in *Brassica napus* L.

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Abstract

Broad sense heritability and selection response were measured among fifteen rapeseed (*Brassica. napus* L. genotypes for seed yield and yield related traits during 2010-2011 at The University of Agricultural, Peshawar. The experiment was designed in Randomized Complete Block with three replications. Broad sense heritability estimates were higher (>60%) for primary branches plant^{-1}, pod length, seeds pod^{-1} and seed yield plant^{-1}. Moderate (30-60%) heritability values were observed for pods raceme^{-1} and 1000-seed weight. The expected response to selection was higher (≥20%) for seed yield plant^{-1} whereas, moderate values (10-20%) for selection response were recorded for primary branches plant^{-1}and seeds pod^{-1}. Pods raceme^{-1}, pod length and 1000-seed weight showed lower values **(**≤10%) for expected response to selection. Higher broad sense heritability estimates and considerable genetic advance could be a valuable tool for breeders to select improved genotypes of *Brassica napus* for higher seed yield. The genotypes J-35, J-38 and J-40 presented better results for studied traits and hence could be used in future breeding schemes.

Key words: Heritability, % Selection response, Genetic advance, *Brassica napus*.

Introduction

Rapeseed (*Brassica napus* L.) is relatively young species that resulted from spontaneous hybridizations between the diploid *Brassica rapa* L. (AA genome, 2n = 20) and *Brassica oleracea* L. (CC genome, 2n = 18) species [1]. It belongs to family Cruciferae and is an amphidiploid (AACC genome, 2n = 38). The time and location of origination of *Brassica napus* is not well clear and is believed that Mediterranean region is its place of origination as both wild *Brassica rapa* and *Brassica oleracea* originated there [2]. Its origin is fairly recent and repeatedly interspecific hybridization involving different genomes resulted in the development of *B. napus* L [3]. Rapeseed is the second most important oilseed crop in the world after soybean for oil while, in terms of area and production, rapeseed and mustard graded as the world's third most important edible oil crop. Canada, China, Northern Europe and the Indian sub-continent are the leading counties in the production of rapeseed. Rapeseed is considered as the most valuable source of vegetable oil in Europe. The seeds of present varieties normally contain 40-45% oil, 25% protein and 20% polysaccharides. These are used in the production of biodiesel (green diesel), industrial lubricants and hydraulic oils, detergents, soaps and recyclable plastics [4]. Rapeseed oil is primarily used in food and the oil cake contains high biological proteins as well as appropriate amounts of calcium and phosphorus. Oil and fat are a good source of energy and also comprises fat-soluble vitamins like A, D, E, and K. After oil extraction the remaining meal, having 38-44% high quality protein, is used as an animal feed and fertilizer for several crops [5].

The significant amount of genetic variability, higher heritability estimates and genetic potential studies of genotypes in terms of their expression for various morphological and yield related traits are very important for selection of best lines for successful and upcoming breeding programs. The effectiveness of heritability assessments increases as they are applied to calculate expected response to selection [6], which represents the amount of gain in a trait under particular selection intensity. Since selection response has an additional superiority over heritability, it can act as a directorial factor for plant breeders in selection programs. In order to estimate the selection effects, heritability along with selection response is much more useful than the heritability alone for the genetic improvement of a character. Broad sense heritability and expected response to selection along with its percentage was determined in this particular experiment among *Brassica napus* genotypes for seed yield and its related traits.

Materials and methods

The breeding material was provided by Plant Genetic Resources Institute, National Agricultural Research Centre, Islamabad containing fifteen *Brassica napus* genotypes viz., J-26 to J-40 that was sown in RCB design with 3 replications at The University of Agricultural, Peshawar during 2010-2011. Row length was kept as 5m whereas, 25cm plant to plant distance and 50cm row to row distance was maintained. Each genotype was sown in two rows in each replication. Data were recorded on 10 randomly selected plants on yield contributing traits and seed yield plant^{-1}. The collected data were statistically analysed by using computer package Statistix. Least Significant Differences (LSD) test was applied to find out the mean differences [7]. The genotypic, phenotypic and environmental variances, broad sense heritability and expected response to selection (Re) and its percentage were calculated [8].

Results and Discussion

Table 1 indicates means sum of squares for 6 traits. Highly significant differences were noted for primary branches plant^{-1}, pods raceme^{-1}, pod length (cm), seeds pod^{-1}, 1000-seed weight (g) and seed yield plant^{-1}(g) among *Brassica napus* genotypes. The co-efficient of variability was 9.7% for primary branches plant^{-1}, 6.82% for pods raceme^{-1}, 5.31% for pod length, 10.53% for seeds pod^{-1}, 8.04% for 1000-seed weight and 15.14% for seed yield plant^{-1} (Table 1). Data presented in Table 2 show that genotype J-33 produced minimum (5.1) primary branches plant^{-1} whereas J-35 produced maximum (8.7) primary branches plant^{-1} with a mean value of 7.1 branches. Mean values for pods main raceme^{-1} ranged from 63.1 to 88.0 with a mean value of 73.4. The genotype J-40 produced maximum pods main raceme^{-1} whereas genotype J-28 produced minimum pods. The data for pod length ranged from 6.3 to 8.5 cm indicating mean value of 7.1 cm. Maximum pod length (8.5 cm) was observed in genotype J-36 and minimum (6.3 cm) in genotype J-35. Mean values for seeds pod^{-1} ranged from 14.0 to 26.7 showing mean value of 20.4. The lowest seeds pod^{-1} recorded in genotype J-32 while the highest seeds pod^{-1} was observed in genotype J-40. The mean values for 1000-seed weight ranged from 4.2 to 5.7 g with mean value of 4.8 g. Maximum 1000-seed weight was observed in genotype J-38 while minimum was noted in genotype J-32. Maximum seed yield plant^{-1} was observed in genotype J-40 and lowest was recorded in genotype J-28. Seed yield plant^{-1} ranged from 12.1 to 37.6 g showing mean value of 23.8 g (Table 2).

Table 1: Mean squares for various yield related traits and seed yield of *Brassica napus* genotypes.

Parameters	Replications (df=2)	Genotypes (df=14)	Error (df=28)	CV (%)
Primary branches plant^{-1}	0.22	4.20**	0.48	9.70
Pods main raceme^{-1}	61.37	145.25**	25.07	6.82
Pod length (cm)	0.61	1.20**	0.14	5.31
Seeds pod^{-1}	4.07	36.25**	4.61	10.53
1000-seed weight (g)	0.15	0.40**	0.15	8.04
Seed yield plant^{-1} (g)	17.16	166.16**	12.94	15.14

CV= Coefficient of variation, df= Degree of freedom

Heritability estimates and genetic potential studies of genotypes in terms of their expression for yield and seed quality traits are very much important for selection of best lines for successful and upcoming breeding programs. In order to estimate the selection effects, heritability along with selection response is much more useful than the heritability alone. In the present study broad sense heritability and expected response to selection and its percentage for yield and yield contributing traits were determined. The genotypic, phenotypic and environmental variances, broad sense heritability and expected response to selection (Re) and its percentage were calculated [8]. Heritability values are categorized as low (≤30%), moderate (30-60%) and high (> 60%) [9]. While selection response/genetic advance as percent mean were considered as low (≤10%), moderate (10-20%) and high (≥20%) [6].

Table 2: Mean performance for various yield related traits and seed yield of *Brassica napus* genotypes.

Genotypes	**Primary branches plant^{-1}**	**Pods main raceme^{-1}**	**Pod length (cm)**	**Seeds pod^{-1}**	**1000-seed weight (g)**	**Seed yield plant^{-1} (g)**
J-26	7.1 bc	65.3 e	7.4 bc	20.7 bc	4.7 bcde	26.3 cde
J-27	8.4 a	66.4 e	6.9 cde	19.7 bcd	4.6 cde	24.8 de
J-28	8.2 a	63.1 e	6.6 e	15.7 e	4.9 bcd	12.1 i
J-29	7.0 bc	80.5 ab	7.3 bcd	21.0 b	4.9 bcd	34.3 ab
J-30	8.2 ab	66.8 e	7.3 bcd	22.0 b	4.5 cde	18.2 fgh
J-31	6.1 cd	75.7 bcd	6.7 de	17.3 cde	5.2 abc	23.2 ef
J-32	5.3 d	79.2 bc	6.8 cde	14.0 e	4.2 e	15.2 hi
J-33	5.1 d	68.7 de	6.9 cde	21.7 b	4.7 bcde	16.9 ghi
J-34	6.0 cd	68.0 de	6.6 e	20.3 bcd	4.9 bcde	15.2 hi
J-35	8.7 a	77.9 bc	6.3 e	26.3 a	4.6 cde	24.2 ef
J-36	7.0 bc	71.3 cde	8.5 a	22.7 b	4.8 bcde	24.5 de
J-37	7.7 ab	77.9 bc	6.7 de	17.0 de	5.1 abcd	31.5 bc
J-38	8.3 a	75.9 bcd	8.1 a	20.7 bc	5.7 a	30.3 bcd
J-39	6.0 cd	76.1 bcd	6.6 e	20.3 bcd	5.3 ab	22.1 efg
J-40	8.1 ab	88.0 a	7.9 ab	26.7 a	4.4 de	37.6 a
Mean	7.1	73.4	7.1	20.4	4.8	23.8
L.S.D$_{0.05}$	**1.16**	**8.37**	**0.63**	**3.59**	**0.65**	**6.02**

Results for heritability, selection response and selection response in terms of percent mean for yield and yield relating traits are presented in Table 3. The heritability (bs) estimates for primary branches plant^{-1} was higher (0.72) along with moderate expected selection response of 1.32 # indicating percent value of 18.51%. The primary branches plant^{-1} had genetic variance (1.24) and environmental variance (0.48). The results were in line with the findings of Sadat *et al*. [10] who observed moderate heritability and higher genetic advance for primary branches plant^{-1}. Lower broad sense heritability values and lower expected response to selection for primary branches plant^{-1} were found by Marjanovic *et al.* and Naazar *et al.* [11-12]. Higher genetic variance (40.06) was noted for pods main raceme^{-1} than the environmental variance (25.07). Pod length showed genetic variance (0.35) and environmental variance (0.14). Higher broad sense heritability estimates (0.62) and (0.71) were recorded for pods main raceme^{-1} and pod length, respectively. The expected response to selection was lower for both the traits with a value of 6.95# for pods main raceme^{-1} having percent calculation of 9.47 and 0.70 cm with percent mean of 9.84 for pod length. Higher broad sense heritability estimates and lower genetic advance for pods main raceme^{-1} and pod length were also observed by Khan *et al.* and Zehra and Kinaci [13-14] among rapeseed genotypes. The higher heritability values for pod length indicated that the trait is less influenced by the environmental conditions, so this parameter could be used for selection purposes in breeding schemes.

Table 3: Variance components, heritability $_{(BS)}$, and selection response $_{(Re)}$ for various yield related traits and seed yield of *Brassica napus* genotypes.

Traits	**Vg**	**Ve**	**Vp**	**$h^2_{(BS)}$**	**Re**	**Re (%)**
Primary branches plant^{-1}	1.24	0.48	1.72	0.72	1.32	18.51
Pods main raceme^{-1}	40.06	25.07	65.13	0.62	6.95	9.47
Pod length (cm)	0.35	0.14	0.49	0.71	0.70	9.84
Seeds pod^{-1}	10.54	4.61	15.16	0.70	3.79	18.59
1000-seed weight (g)	0.08	0.15	0.23	0.35	0.24	4.89
Seed yield plant^{-1} (g)	51.07	12.94	64.02	0.80	8.94	37.60

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

Seeds pod^{-1} presented higher heritability (bs) estimates (0.70) with genetic variance (10.54) almost two times greater than the environmental variance (4.61). The genetic advance for seeds pod^{-1} was 3.79 # with percent mean of 18.59. Naazar *et al.* [12] noted lower heritability and moderate selection response values for seeds pod^{-1} whereas lower selection response along with lower heritability estimates were observed by Naazar *et al.* [15] for seeds pod^{-1}. The expected selection response for 1000-seed weight was 0.24 g with lower percent mean of 4.89**.** The 1000-seed weight showed moderate broad sense heritability (0.35) estimates. The genetic variance (0.08) and environmental variance (0.15) were calculated for the mentioned trait. Moderate heritability for 1000-seed weight along with low genetic advance specifies that non-additive gene effects are more essential and mass selection on phenotypic basis may not be much effective to improve this trait. Moderate heritability and selection response for 1000-seed weight was noted by Sajid *et al.* [16]. Higher heritability (bs) estimates (0.80) were noted among genotypes for seed yield plant^{-1}. The genetic variance (51.07) was approximately 04 times greater than the environmental variance (12.94). The selection response for seed yield plant^{-1}was 8.94 g with higher percent value of 37.60. Seed yield plant^{-1} presented higher heritability estimates and higher selection response values. Similar findings were recorded by Guoqing and Weijun [17] and Naazar *et al.* [15] who found moderate heritability and selection response for seed yield among rapeseed genotypes.

Conclusion

1. Higher Heritability $_{(BS)}$ was presented by primary branches plant^{-1}, pod length, seeds pod^{-1} and seed yield plant^{-1}.
2. Genetic advance was higher for seed yield plant^{-1} while moderate for primary branches plant^{-1} and seeds pod^{-1}.
3. The genotypes J-35, J-38 and J-40 presented better results for yield and yield contributing traits and hence could be used in future breeding schemes.

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