

Research Article

Assessment of genetic variability, heritability and selection response for morph-yield traits in brassica

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Abstract

An experiment was conducted at The University of Agricultural Peshawar during 2015-16 to determine heritability and genetic advance of morph-yield traits to set up suitable selection criteria for further improvement. The experimental material comprised of 27 genotypes i.e. nine each of *Brassica napus*, *Brassica campestris* and *Brassica juncea* were evaluated in RCB design with three replication. Data were recorded on plant height, main raceme length, pods on main raceme, pod length, pod width, seed pod⁻¹, 100 seed weight and seed yield plant⁻¹. Significant differences ($p \leq 0.01$) were observed in all genotypes for all traits. Tallest plant height (237.1) was recorded for N-550, maximum main raceme length (114.5) was noted for C-136, maximum pods on main raceme (94 pods) was observed for N-531, longest pod length (7.0) was recorded for N-514 and N-531, broader pod width (0.54) was recorded for N-548, maximum seed pod⁻¹ (28) was noted for J-133, maximum 100 seed weight (61g) and seed yield plant⁻¹ (37.30) was recorded for C-117. Pods on main raceme and pod length exhibited high heritability (0.87) followed by Seed pod⁻¹ (0.86), Main raceme length (0.83), Primary branches plant⁻¹ (0.80), Pod width (0.79), Seed yield plant⁻¹ (0.77), 100 seeds weight (0.71) and Plant height (0.66). Maximum selection response as percent of mean was noted for Seed pod⁻¹ (47.27%) followed by Seed yield plant⁻¹ (36.41%), Primary branches plant⁻¹ (34.47%), pods on main raceme (27.25%), pod length (25.95%), Main raceme length (19.89%), Pod width (12.23%) and Plant height (10.99%). Considerable genetic variances, high heritability estimates and enviable selection response implied that the mentioned genotypes could be used in future brassica breeding programs.

Keywords: Brassica; Morph-yield traits; Genetic variability; Heritability; Selection response

Introduction

Brassica belongs to family *Brassicaceae* also known as *cruciferae*, the mustard family. Family *Brassicaceae* is one of the ten most important economically plant family [1, 2].

Rapeseed (*B. napus* L.) oil ranks third following soybean and palm oil around the world. Apart from straight human and animal consumption, industrial uses include the manufacture of rapeseed oil and converting

biomass to bio-energy. Rapeseed oil is also used for metilester, which is an essential component for biodiesel production [3].

Pakistan has been facing edible oil scarcity for years regardless of unassuming progress made in agricultural sector. Local production of edible oil shared only 23% (662 thousand tons) of total country's need, while the remaining 77 % was met through imports by spending huge foreign exchange (i.e. 2.0 billion US\$). Cotton seed and brassica (different species of genera Brassica) are the major contributors in local oilseed production [4]. Of more than 300 cultivated species of Brassica, *B. rapa*, *B. juncea* and *B. napus* are major sources of edible oil in the county. Non-availability of better-adapted genotypes and decrease in area under oilseed crops could be the main reasons for lower edible oil production in the country. The need for increased yield is felt because the country's population is increasing and the demand for oil in the country is expected to grow by 3-4% per year [5].

Information of genetic variability heritability and selection response helps in many crop improvement programs. Genetic variability is the differences in plants on the bases of diverse characters. Plant breeder are always trying to explore and induce genetic variability in the existing genetic material. This diversity helps in the selection of desirable lines and development of such cultivars which are adoptable to diverse agro-climatic conditions. Hence diversity in plant genetic resources is vital for the crop improvement [6, 7]. The estimation of heritability is easy and less time taking in the selection procedure and greater is the genetic development. The heritability of a trait determines the degree to which it is passing on from one generation to the next one and it is most priceless tool when used in concurrence with other traits in calculating genetic advance that follows the selection for that traits [8]. Therefore the present studies

was conducted to investigate genetic variability, heritability and selection response for morph yield traits in brassica

Materials and methods

The experiment was directed at The University of Agriculture Peshawar during 2015-2016 to study genetic variability, heritability and selection response in brassica genotypes for morph-yield traits.

Experimental materials

The experimental materials were comprised of 27 genetically diverse genotypes of brassica viz: Nine genotypes each of *B. napus* (N-502, N-509, N-510, N-514, N-531, N-533, N-547, N-548, N-550), *B. campestris* (C-108, C-117, C-21, C-22, C-134, C-136, C-139, C-144, C-148) and *B. juncea* (J-104, J-105, J-110, J-126, J-132, J-133, J-144, J-145, J-149). The genotypes were collected across the Pakistan.

Field layout

B. napus, *B. campestris* and *B. juncea* genotypes were evaluated in Randomized Complete Block (RCB) design with three replications. Each replication comprised of 27 entries. Three rows were allotted to each entry, where each row was 5 meter in length. Plant to plant and row to row spacing was 30 and 60 cm respectively. All cultural practices like fertilizer, irrigation and weeding were carried out according to the standard recommendations

Data collection

Data were taken on randomly selected plants of each genotype on the morph-yield traits viz: Plant Height, main raceme length, number of pods on main raceme, pod length, pod width, seeds pod⁻¹, 100 seeds weight and seed yield plant⁻¹.

Statistical analysis

Data recorded on morph-yield traits were subjected to analysis of variance according to [9]. Broad sense heritability (bs) was calculated as ratio of genotypic variance to phenotypic variance [10] and selection response were calculated according to [11].

Results and discussion

Plant height (cm)

Analysis of variance showed significant difference ($p < 0.01$) among brassica genotypes for plant height (Table 1). Mean values varied from 168.4 to 237.1 cm with an overall mean of 191.6 cm. N-550 was noted as tallest plant, while N-509 was recorded as dwarf plant (Table 2). For plant height, the

heritability value was high (0.66). The genetic advance was 21.30 and as a percent mean the value was 10.99% (Table 3). Our findings of high heritability (0.66) for plant height are in conformity with the earlier findings in *Brassica rapa L.* by [12]. While [13] noted moderate heritability for this trait in brassica cultivars.

Table 1. Mean squares of Brassica genotypes for morph-yield traits.

Parameters	Replications (df=2)	Genotypes (df=26)	Error (df=52)	Coefficient of Variation (%)
Plant height (cm)	54.23	789.38**	61.15	5.55
Main raceme length (cm)	72.24	325.56**	21.30	9.71
Pods on main raceme	14.81	482.68**	23.08	8.51
Pod length (cm)	0.10	2.44**	0.11	6.07
Pod width (cm)	0.0005	0.0042**	0.0003	4.07
Seed pod ⁻¹	34.79	88.61**	4.59	11.76
100 seeds weight (g)	0.01	0.01**	0.001	6.55
Seed yield plant ⁻¹ (g)	16.23	119.54**	10.77	12.87

** = significant at 1% probability level

Main raceme length (cm)

Lengthier the main raceme length is expected to have more number of pods. Data regarding main raceme length showed significant difference ($p < 0.01$) among genotypes for pod length (Table 1). Mean values varied from 64.9 to 114.5 cm with an overall mean of 89.7 cm. maximum value was recorded for C-136 while minimum value was observed in C-134 (Table 2). For main raceme length, the variance due to genes was (101.42) was five times higher than environmental variance (21.30). The heritability estimates of main raceme length was high (0.83) with genetic advance of 16.07, and as a percent mean the value was 19.89% (Table 3). High heritability estimate and genetic advance for

main raceme length are in accordance with the results of [14, 15]. They also noted high value of heritability and genetic advance for main raceme length in brown sarson (*Brassica rapa L.*) and Ethiopian mustard.

Pods on main raceme

Productive pods are expected to bear more seeds. Mean square revealed significant difference ($p < 0.01$) among the genotypes for number of pods on main raceme (Table 1). Mean values of pods on main raceme ranged from 58 to 94 pods. Maximum pods on main raceme were produced by N-531 and J-149 (94 pods), while minimum pods were recorded for N-547 (58 pods) (Table 2). For the number of pods on main raceme, the heritability estimates was high (0.87) and the

expected selection response was 20.34 with percent value of 27.25% (Table 3). Our results of number of pods on main raceme are in line with [16]. They conveyed high

heritability but low genetic advance for pods on main raceme in rapeseed. High heritability for pods on main raceme in $F_{3:4}$ *brassica* populations was also noted by [17].

Table 2. Mean performance of Brassica genotypes for morph-yield traits

Genotypes	Plant height (cm)	Main raceme length (cm)	Pods on main raceme	Pod Length (cm)	Pod Width (cm)	Seeds Pod ⁻¹	100 Seeds Weight (g)	Seed Yield Plant ⁻¹ (g)
N-502	193.0	81.7	69	6.1	0.53	23	0.46	34.65
N-509	168.4	70.9	61	6.0	0.46	20	0.49	32.32
N-510	193.0	68.9	60	5.7	0.42	20	0.48	32.57
N-514	183.1	68.3	71	7.0	0.53	21	0.37	23.05
N-531	193.6	88.9	94	7.0	0.47	19	0.54	24.29
N-533	182.1	80.1	75	6.6	0.51	12	0.59	32.12
N-547	181.2	86.8	58	5.1	0.43	18	0.57	18.78
N-548	192.3	83.8	88	6.6	0.54	20	0.59	25.16
N-550	237.1	76.6	70	4.6	0.44	12	0.49	21.72
C-108	192.4	84.2	66	6.1	0.41	13	0.56	26.5
C-117	200.7	69.9	71	5.7	0.46	16	0.61	37.30
C-21	196.6	84.7	62	6.0	0.42	23	0.50	22.95
C-22	204.2	85.8	92	4.1	0.43	12	0.51	9.2
C-134	177.1	64.9	46	5.8	0.44	10	0.44	18.68
C-136	214.1	114.5	88	3.9	0.40	10	0.47	17.56
C-139	170.8	76.6	85	4.9	0.43	22	0.49	25.60
C-144	214.4	75.1	75	4.1	0.45	16	0.46	28.80
C-148	179.0	79.6	67	5.0	0.45	14	0.50	20.33
J-104	224.7	90.6	66	5.6	0.45	11	0.48	31.90
J-105	205.5	91.8	90	5.4	0.44	26	0.49	21.86
J-110	187.8	81.2	70	4.1	0.45	13	0.48	29.44
J-126	188.5	82.0	78	6.3	0.42	24	0.50	16.89
J-132	191.5	60.9	64	5.0	0.47	23	0.57	27.88
J-133	185.1	77.9	93	6.5	0.46	28	0.60	29.26
J-144	192.1	85.6	86	4.8	0.48	27	0.52	29.26
J-145	209.9	87.1	77	6.2	0.47	19	0.53	27.07
J-149	174.9	82.3	94	6.1	0.48	22	0.56	22.95
Mean	193.3	80.2	74	5.7	0.46	18	0.51	26.01
LSD_(0.01)	12.16	7.55	7.39	0.55	0.05	1.45	0.05	2.32

Pod length (cm)

Data regarding pod length showed significant difference ($p < 0.01$) among genotypes for pod length (Table 1). Mean values ranged from 64.9 to 114.5 cm with an overall mean of 89.7

cm. longest pod length was recorded for N-514 and N-531 while shortest pod length was observed in C-136 (Table 2). For pod length, Genetic and environmental variances was 0.78 and 0.11 respectively. The heritability

estimates for the studied trait was also very high (0.87), the response from selection was 1.44 with the percent value of 25.95% (Table 3). Our results are in line with [16, 18]. They

also conveyed high heritability and low genetic advance value for pod length in *B. napus* L.

Table 3. Variance components, heritability and selection response of morph-yield traits of Brassica

Parameters	Vg	Ve	Vp	H	Re	Re (%)
Plant height (cm)	223.73	116.03	339.76	0.66	21.30	10.99
Primary branches plant ⁻¹	4.13	1.037	5.17	0.80	3.19	34.47
Main raceme length (cm)	101.42	21.30	122.72	0.83	16.07	19.89
Pods on main raceme	154.88	23.69	178.57	0.87	20.34	27.25
Pod length (cm)	0.78	0.11	0.89	0.87	1.44	25.95
Pod width (cm)	0.001	0.0003	0.002	0.79	0.05	12.23
Seed pod ⁻¹	28.01	4.59	32.59	0.86	8.61	47.27
100 seeds weight (g)	0.003	0.001	0.004	0.71	0.08	15.05
Seed yield plant ⁻¹ (g)	32.57	12.96	45.53	0.71	8.47	33.07

Pod width (cm)

Significant differences ($p < 0.01$) were found among the brassica genotypes for pod width (Table 1). Means values varied from 0.40 to 0.54 cm. Broad pods were noticed in N-548 while narrow pods were found in C-136 (Table 2). In case of pod width, the heritability was high 0.79, with genetic advance of 0.05 and as a percent mean the values was 12.23% (Table 3). Our results for pod width are in conformity with [19]. Similar [20] also conveyed high heritability for pod width in rapeseed.

Number of seed pod⁻¹

Mean squares data revealed significant difference ($p < 0.01$) among genotypes for seed pod⁻¹ (Table 1). Mean values varied from 10 to 28 seeds. Minimum seed pod⁻¹ was recorded for C-134 and C-136 (10 seeds) while the maximum seed pod⁻¹ was noticed for J-133 (28 seeds) (Table 2). High heritability (bs) estimates (0.86) and selection response value of 8.61 with the percent mean of (47.27%) were recorded for seed pod⁻¹. The genetic variance (32.57) was two times greater than the variance related to environment (12.96) for seed yield plant⁻¹ (Table 3). Our findings are in correspondence with [21, 22]. They conveyed high

heritability and genetic advance for seed pod⁻¹ in Indian mustard (*B. juncea* L.). While the findings of [23] are not in correspondence to our findings, he reported low heritability value for seed pod⁻¹ in *B. rapa* L.

100 Seeds weight (g)

Results regarding 100 seed weight revealed significant difference ($p < 0.01$) among brassica genotypes (Table 1). 100 seed weight ranged from 0.37 (N-514) to 0.61g (C-117) among genotypes, showing a net difference of 0.24g (Table 2). In yield associated traits, heritability for 100 seed weight was 0.71 with selection response of 0.08 and as a percent means the value was 15.05% (Table 3). Our findings for 100 seeds weight are in conformity with the earlier findings in mustard by [13] and in winter rapeseed by [24].

Seed yield plant⁻¹ (g)

Analysis of variance exhibited significant difference ($p < 0.01$) among the genotypes for seed yield plant⁻¹ (Table 1). Means of seed yield plant⁻¹ varied from 20.33 to 37.30 g. The maximum seed yield plant⁻¹ was displayed by C-117, while the minimum seed yield plant⁻¹ was noticed for C-148 (Table 2). The heritability value for the said trait was found high (0.71). For seed yield plant⁻¹

selection response was 8.47 and its value in percent was 33.07% (Table 3). [13, 25] conveyed moderate to high heritability estimates for seed yield plant⁻¹. While moderate heritability for seed yield plant⁻¹ was noted by [26].

Conclusions and recommendations

The genotypes used in present studies were of diverse nature and produced more yield. High heritability and genetic advance were noted for most of the traits which is the room for further improvement. The genotype C-117 followed by N-502 exhibited better performance in terms of seed yield plant⁻¹ and should be further tested at multi-location for possible release as a new cultivars.

Authors' contributions

Conceived and designed the experiments: Farhatullah, Performed the experiments: S Shah, Analyzed the data: A Sohail & A Izzam, Contributed reagents/ materials/ analysis tools: SMA Shah, S Ali & Q Hussain, Wrote the paper: A Sohail.

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