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# Morphological characterization and association of various yield and yield contributing traits in *Brassica* genotypes

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## Abstract

An experiment was conducted to evaluate eighteen *Brassica* genotypes for various morphological characters and estimate association for yield and yield contributing traits. The experimented was executed following Randomized complete block design (RCBD) with three replications in the experimental farm of the department of Genetics and Plant Breeding, Bangladesh Agricultural University Mymensingh-2202. The nine yield attributing characters are studied in the experiment. The genotypes differed significantly for all the traits *viz*., days to 1st flowering, days to maturity, plant height, number of branches/plant, number of pod/plant, length of pod, number of seeds/pod, 1000-seed weight (g) and seed yield/plant (g).Considering the two most important traits like early maturity and yield /plant, BD-7114 performed best among the studied genotypes. Correlation coefficients among the characters were studied to determine the association between yield and it attributing components. A significant positive correlation was found between yield and its attributing characters namely with number of seeds/pod and 1000-seed weight. Path analysis revealed both direct and indirect effects on seed yield and revealed that number of seeds/pod had the highest direct effect on seed yield. The findings of the research could be exploited in future breeding programs for improving *Brassica* genotypes.

**Key words**: Morphological characterization, yield, yield contributing traits, *Brassica* genotypes

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## Introduction

*Brassica* is the world's third most important sources of edible vegetable oils. It is an important genus of plant kingdom consisting of over 3200 species with high diverse morphology. *Brassica* belongs to the family Brassicaceae originated primarily from near Himalayan region and secondarily from European-Mediterranean area and Asia (Downey and Robelen, 1989). The genus *Brassica* has generally been divided into three groups namely – rapeseed, mustard and cole. Mustard and rapeseed seeds contain 42% oil and 25% protein (Khaleque, 1985). They are the third highest source of edible oils supply in the world after soybean (FAO, 2017). The production of rapeseed and mustard in the worldwide is 69.6 million tones (FAO, 2017).The mustard oil is used not only for edible purpose but also is used in hair dressing, body massaging and in different types of pickles preparation. The oil cake contains proteins of high biological value and applicable quantities of calcium and phosphorus. It is not only a high energy food but also a carrier for fat soluble vitamins (A, D, E and K) in the body. It is used as a very good animal feed as well as organic manure for various crops.

In Bangladesh various species of *Brassica* are grown. The genomic constitutions of the three diploid elemental species of *Brassica* are AA for *Brassica campestris*, BB for *Brassica nigra* and CC for *Brassica oleracea* having diploid chromosome number of 20, 16 and 18 respectively. On the other hand the species *Brassica juncea* (AABB), *Brassica carinata* (BBCC) and *Brassica napus* (AACC) are the amphidiploids.

Rapeseed and mustard occupy the first position in respect of area and production among the oil crops grown. Though a range of *Brassica* oilseed are grown in the country, the local production of edible oil meets only fourth of the required quantity, the rest is being imported by spending valuable foreign currency. Major cultivation of this crop is done with the traditional cultivars in the marginal lands. There is limited scope to increase yield of *Brassica* due to cultivation of existing low yielding varieties with low input and management and almost all cultivars are brown seeded and smaller in size (2-2.5 g/1000 seeds). There should be an attempt to develop short duration and high yielding varieties of mustard with more oil percentage in seed, tolerant to biotic and abiotic stress to fulfill the requirement of edible oils of the country by increasing the production. A plant breeding program can be divided into three steps, building up a gene pool of variable germplasm, selection of individual from the gene pool and utilization of selected individual to evolve a superior variety (Chauhan and Singh, 1985). The knowledge of genetic variability present in the population, heritability of economically important characters and correlation coefficients of those characters is very important before launching an effective breeding program.

Determination of correlation co-efficient between the characters has a considerable importance in selecting breeding materials. The path co-efficient analysis has been found to give more specific information on the direct and indirect influence of each of the component characters upon seed yield (Behl *et al.,* 1992). Multivariate analysis is a useful tool in quantifying the degree of divergence between biological population at genotypic level and to assess relative contribution of different component to the total divergence both at intra- and inter-cluster levels (Murty and Arunchalam, 1966; Ram and Panwar, 1970; Sachan, 2014). Therefore, the present study was undertaken to characterize and assess the variability range, to study the relationship among different traits and the direct and indirect contribution of each trait towards yield in the *Brassica* species.

## Materials and Methods

***Plant materials*:** The experiment was conducted with 18 genotypes of rapeseed in the experimental farm of the department of Genetics and Plant Breeding, Bangladesh Agricultural University, Mymensingh. The genotypes were collected from Bangladesh Agricultural Research Institute (BARI) and Sher-e-Bangla Agricultural University (SAU). Name and source of 18 genotypes are presented in the Table 1.

***Data collection and analysis*:** Data were collected on the following traits-days to 1st flowering, days to maturity, plant height, number of branches/plant, number of pod/plant, length of pod, number of seeds/pod, 1000-seed weight (g) and seed yield/plant (g). The experiment was designed followed by Randomized Complete Block Design (RCBD) with three replications. Analysis of variance (ANOVA) was performed using the plant breeding statistical program (Utzzal, MSTATC and PLABSTAT, Version 2N, 2007) with the following methods:

$$Yij = gi + rj + \epsilon ij$$

Where,

Yij = Observation of genotype i in replication j
gi = Effects of genotype i
ri =Effects of replication j
$\epsilon ij$ = The residual error of genotype i in replicate j

***Simple correlation co-efficient and path analysis*:** Simple correlation co-efficient (r) was estimated with the formula followed by Singh and Chaudhary

(1985).Path co-efficient analysis was done according to the procedure employed by Dewey and Lu (1995) also quoted in Singh and Chaudhary (1985) and Dabholkar (1992), using simple correlation values.

**Table 1.** List of *Brassica* genotypes with their source of collection.

| Sl No. | Genotype (code name) | Source |
|---|---|---|
| 1 | BARI Sarisa-8 | BARI, BD |
| 2 | BARI Sarisa-16 | BARI,BD |
| 3 | BD-7104 | BARI, BD |
| 4 | Tori-7 | BARI, BD |
| 5 | BARI Sarisa-10 | BARI, BD |
| 6 | BARI Sarisa-11 | BARI, BD |
| 7 | SAU-01 | SAU, BD |
| 8 | BD-10111 | BARI, BD |
| 9 | BD-6950 | BARI, BD |
| 10 | BD-10115 | BARI, BD |
| 11 | JUN-536 | BARI, BD |
| 12 | Nap-0567 | BARI, BD |
| 13 | Nap-0564 | BARI, BD |
| 14 | BDJH-12 | BARI, BD |
| 15 | BD-7114 | BARI, BD |
| 16 | BD-7115 | BARI, BD |
| 17 | BD-6957 | BARI, BD |
| 18 | BD-6952 | BARI, BD |

**NB:**BARI=Bangladesh Agricultural Research Institute, BD=Bangladesh, SAU=Sher-e-Bangla Agricultural University, Bangladesh.

## Results and Discussion

The Analysis of variance indicated that the difference among genotypes for all the yield and yield contributing traits under study *viz.,* days to first flowering, days to maturity, plant height (cm), number of branches/plant, number of pod/plant, length of pod (cm), number of seeds/pod, 1000 seed weight (g) and seed yield/ plant (g) were significant (Table 2). Rameeh (2013) observed significant variation among genotypes for different morphological traits. Belete *et al*. (2012) also observed significant difference among the genotypes for traits except plant height and seed yield. These results suggest that all the genotypes under study had significant variation with each other. The mean performances of eighteen brassica genotypes for various morphological traits are shown in Table 3.

***Mean performance of the genotypes*:** Being an important character to assess early maturity, days to flowering was taken to an account for the genotypes. Days to first flowering among the genotypes ranged from 22.60 to 36.00 days with a mean value of 28.39 days. BD-7114 took the lowest days to first flowering (22.60 days) and BDJH-12 took the highest days to first flowering (36.00 days). Early maturity is the most desirable character of *Brassica* in present situation. Days to maturity among the genotypes ranged from 76.93 to 104.7 days with a mean value of 94.64 days. BD-7114 took the lowest days to maturity (76.93 days).

Plant height in *Brassica* is a complex character and is the end product of several genetically controlled factors (Cheema *et al.,* 1987).The average range of plant height among the genotypes was 70.60 cm to 144.7 cm with a mean value of 109.91cm. The higher number of branches is preferable for achieving high yield. In this study, the average number of branches ranged from 3.733 to 7.500 with a mean value of 5.14. SAU-01 had the maximum number of branches/plant (7.500) and BARI Sar-16 had the minimum number of branches/plant (3.733). The yield of the plant is related to number of pod/plant. Number of pod/plant among the genotypes ranged from 183.6 to 69.47 with a mean value of 121.39. Nap-0567 had the highest pod length (6.620 cm) and BD-6950 had the lowest pod length (4.053 cm).Maximum number of seed/pods a positive attribute towards higher yield. In this study, number of seed/pod among the genotypes ranged from 18.93 to 10.33 with a mean value of 13.24. BD-7114 had the highest number of seed/pod (18.93).

There was a significant difference in 1000-seed weight among the lines depending on the size and shape of grains. The highest 1000-seed weight was recorded in BD-7114 (3.62 g) and JUN-536 had minimum 1000-seed weight (2.52 g). There was significant difference in yield/plant among the studied lines. Yield/plant (g) ranged from 5.513g to 1.657 g with a mean value of 2.84. BD-7114 had maximum yield/plant (5.51 g).

**Table 2.** Analysis of variance for different morphological characters of 18 *Brassica* genotypes.

| Source of variation | df | First flowering | Days to maturity | Plant height (cm) | No. of branches/ plant | No. of pod/plant | Pod length (cm) | No. of seeds/pod | 1000-seed wt. (g) | Yield/ plant (g) |
|---|---|---|---|---|---|---|---|---|---|---|
| Replication | 2 | 20.327 | 6.161 | 99.22 | 0.117 | 11.84 | 0.037 | 0.448 | 0.009 | 0.016 |
| Genotypes | 17 | 38.611** | 205.567** | 1401.04** | 4.161** | 2573.75** | 1.715** | 19.895** | 0.337** | 2.399** |
| Error | 34 | 3.542 | 35.438 | 210.43 | 0.297 | 63.41 | 0.120 | 0.369 | 0.013 | 0.011 |

** = Significant at 1% level of probability

**Table 3.** Mean performance of 18 *Brassica* genotypes on different morphological traits.

| Genotypes | Days to First flowering | Days to maturity | Plant height (cm) | No. of branches/ plant | No. of pod/plant | Pod length (cm) | No. of seeds/pod | 1000-seed wt. (g) | Yield/ plant (g) |
|---|---|---|---|---|---|---|---|---|---|
| BARI Sar-8 | 26.47fgh | 95.33abc | 98.7cde | 4.700defgh | 118.4gh | 4.58ghi | 11.87fg | 3.57ab | 2.61fg |
| BARI Sar-16 | 28.00defgh | 97.33abc | 144.7a | 3.733 h | 82.47ij | 5.54cde | 13.67e | 3.48ab | 3.10 e |
| BD-7104 | 27.67efgh | 100.0ab | 107.8bcde | 4.533defgh | 130.2defg | 4.773gh | 12.80ef | 3.08cd | 3.17 e |
| Tori-7 | 22.73 i | 82.00de | 80.33ef | 4.800defg | 116.9gh | 5.067efg | 15.73 cd | 2.88 de | 3.35 d |
| BARI Sar-10 | 29.93cdef | 98.33abc | 121.0abcd | 4.067efgh | 69.47 j | 4.84fgh | 12.00fg | 2.59fg | 2.20 i |
| BARI Sar-11 | 31.40bcd | 98.67abc | 125.9abc | 3.80gh | 126.7efgh | 4.78gh | 11.87fg | 2.66fg | 2.68fg |
| SAU-01 | 27.47efgh | 88.00 cd | 101.7bcde | 7.50a | 113.3 h | 6.120abc | 12.67ef | 3.00cd | 1.65k |
| BD-10111 | 26.93efgh | 90.20bcd | 107.3bcde | 6.667ab | 160.3b | 4.673ghi | 12.93ef | 2.80ef | 3.56 c |
| BD-6950 | 33.13abc | 102.7 a | 124.9abc | 4.133efgh | 113.3h | 4.053 i | 11.40gh | 3.05cd | 2.58 g |
| BD-10115 | 33.73ab | 104.3 a | 140.3 a | 6.283bc | 183.6 a | 4.287hi | 10.33 h | 2.72efg | 2.79 f |
| JUN-536 | 30.20cde | 100.9ab | 128.3ab | 4.00fgh | 119.3gh | 4.687ghi | 12.87ef | 2.52 g | 1.98 j |
| Nap-0567 | 27.53efgh | 95.33abc | 95.27def | 4.333efgh | 74.20 j | 6.620a | 16.53 c | 2.66fg | 2.20 i |
| Nap-0.564 | 26.20gh | 90.67bcd | 97.80cde | 7.20ab | 137.7cde | 6.407ab | 15.40 d | 3.19c | 3.77 b |
| BDJH-12 | 36.00a | 104.7a | 143.7 a | 6.333bc | 145.6c | 4.273hi | 10.60 h | 3.38b | 3.08 e |
| BD-7114 | 22.60 i | 76.93e | 70.60f | 5.40cd | 143.5cd | 5.467def | 18.93a | 3.62a | 5.51a |
| BD-7115 | 24.73 hi | 93.27abc | 84.87ef | 5.067de | 90.99i | 5.953bcd | 17.60 b | 3.10c | 2.41 h |

| Genotypes | Days to First flowering | Days to maturity | Plant height (cm) | No. of branches/ plant | No. of pod/plant | Pod length (cm) | No. of seeds/pod | 1000-seed wt. (g) | Yield/plant (g) |
|---|---|---|---|---|---|---|---|---|---|
| BD-6957 | 26.87efgh | 81.60de | 104.8bcde | 5.00def | 136.3cdef | 4.910fgh | 10.62h | 3.14c | 2.75fg |
| BD-6952 | 29.40fghdefg | 103.3a | 100.6bcde | 4.933def | 122.7fgh | 4.620ghi | 10.47h | 3.07cd | 1.71k |
| LSD(0.05) | 3.12 | 9.87 | 24.70 | 0.904 | 13.21 | 0.574 | 1.01 | 0.189 | 0.174 |
| Mean | 28.39 | 94.64 | 109.91 | 5.14 | 121.39 | 5.09 | 13.24 | 3.03 | 2.84 |
| SE (±) | 0.85 | 1.95 | 5.09 | 0.28 | 6.90 | 0.18 | 0.61 | 0.08 | 0.21 |
| SD | 3.59 | 8.28 | 21.61 | 1.18 | 29.29 | 0.76 | 2.58 | 0.34 | 0.89 |
| Minimum | 22.60 | 76.93 | 70.60 | 3.73 | 69.47 | 4.05 | 10.33 | 2.52 | 1.66 |
| Maximum | 36.00 | 104.67 | 44.67 | 7.50 | 183.58 | 6.62 | 18.93 | 3.62 | 5.51 |
| Level of significance | ** | ** | ** | ** | ** | ** | ** | ** | ** |
| CV (%) | 6.63 | 6.29 | 13.20 | 10.60 | 6.56 | 6.80 | 4.59 | 3.83 | 3.64 |

** = Significant at 1% level of probability

***Association study among various traits*:** Yield is the result of combined effect of several contributing characters and environment. Understanding of the interaction of characters among themselves and with the environment has been of great use in plant breeding. Relationships among yield and yield contributing traits were studied through analysis of correlation and path coefficient among them.

***Estimation of correlation coefficients*:** Correlation studies provide information on the nature and extent of association between any two pairs of metric characters. From this, it would be possible to bring about genetic up-gradation in one character by selection of the other of a pair. Genotypic and phenotypic correlation co-efficient among different traits of 18 *Brassica* genotypes are presented in Table 4 and 5.

In the present study out of 36 associations, 14 associations were significant at genotypic level and 13 associations were significant at phenotypic level. Among the 14 associations, 7 associations were positively significant and the rest 7 were negatively significant at genotypic level. Among 13 associations, 7 associations were positively significant and rest 6 associations were negatively significant at phenotypic level. Besides, 11 associations were positive and non-significant at genotypic level and 11 associations were positive and non-significant at phenotypic level. On the other hand, 11 relationships were found negative and non-significant at genotypic level and 12 relationships were found negative and non-significant at phenotypic level.

The significant and positive association between the traits suggested additive genetic model thereby less affected by the environmental fluctuation. The positive and non-significant association referred information of inherent relation among the pairs of combination. The negative and non-significant association referred a complex linked of relation among the pair of combinations. The results of correlation coefficients implied that significant positive correlations at both the levels were recorded for yield/plant with number of seeds/pod and 1000-seed weight and significant negative correlations at both the levels were recorded for yield/plant with days to maturity only. Very close values of genotypic and phenotypic correlations were also observed between some character combinations which might be due to reduction in error (environmental) variance to minor proportions as reported by Dewey and Lu (1959).

**Table 4.** Coefficients of genotypic correlation among different yield and yield contributing traits.

| Characters | Days to maturity | Plant height (cm) | No. of branches/ plant | No. of pod/plant | Pod length (cm) | No. of seeds/pod | 1000-seed wt. (g) | Yield/ plant (g) |
|---|---|---|---|---|---|---|---|---|
| Days to first flowering | 0.835** | 0.904** | -0.048 | 0.211 | -0.583* | -0.766** | -0.283 | -0.407 |
| Days to maturity | | 0.748** | -0.244 | -0.045 | -0.499* | -0.605** | -0.288 | -0.553* |
| Plant height (cm) | | | -0.157 | 0.103 | -0.521* | -0.716** | -0.218 | -0.325 |
| No. of branches/ plant | | | | 0.576* | 0.249 | 0.012 | 0.150 | 0.200 |
| No. of pod/plant | | | | | -0.442 | -0.295 | 0.104 | 0.413 |
| Pod length (cm) | | | | | | 0.719** | 0.048 | 0.058 |
| No. of seeds/pod | | | | | | | 0.196 | 0.508* |
| 1000-seed wt. (g) | | | | | | | | 0.505* |

* and ** indicate significant at 5% and 1% level of probability, respectability.

**Table 5.** Coefficients of phenotypic correlation among different yield and yield contributing traits.

| Characters | Days to maturity | Plant height (cm) | No. of branches/ plant | No. of pod/plant | Pod length (cm) | No. of seeds/pod | 1000-seed wt. (g) | Yield/pla nt (g) |
|---|---|---|---|---|---|---|---|---|
| Days to first flowering | 0.827** | 0.860** | -0.042 | 0.206 | -0.572* | -0.743** | -0.265 | -0.400 |
| Days to maturity | | 0.737** | -0.243 | -0.038 | -0.454 | -0.589* | -0.278 | -0.537* |
| Plant height (cm) | | | -0.160 | 0.103 | -0.493* | -0.690** | -0.202 | -0.317 |
| No. of branches/ plant | | | | 0.561* | 0.232 | 0.009 | 0.159 | 0.192 |
| No. of pod/plant | | | | | -0.437 | -0.294 | 0.100 | 0.411 |
| Pod length (cm) | | | | | | 0.705** | 0.055 | 0.059 |
| No. of seeds/pod | | | | | | | 0.183 | 0.508* |
| 1000-seed wt. (g) | | | | | | | | 0.499* |

* and ** indicate significant at 5% and 1% level of probability, respectability.

***Estimation of path co-efficient*:** Path analysis technique furnishes a method portioning the correlation coefficients into direct and indirect effects provide the information on actual contribution of the independent variables on the dependent variable. In the present study, all the eight traits were considered as causal variables of yield/plant and phenotypic correlation coefficients of these traits with yield/plant were partitioned into the direct and indirect effects through path coefficient analysis.

The correlation value denotes only the nature and extent of association existing between pairs of characters. The yield is dependent on several contributing characters that are mutually associated which will in turn impair the true association existing between a yield contributing characters and economic characters and change in any one component is likely to disturb the whole network of cause and effect. Each contributing characters has two parts of action *viz.,* the direct effect and the indirect effects through yield contributing characters on economic characters which are not revealed from the correlation studies. The relations between yield and yield contributing characters were studied in detail by path co-efficient analysis is presented in Table 6 and 7. Plant height, number of pod/plant, number of seeds/pod and 100-seed weight had direct positive effect on seed yield at both phenotypic and genotypic level. Therefore, these characters would be reliable criteria for improving yield. Hosen *et al*., (2008) found that number of branches/plant, number of seeds/pod, 1000-seed weight had positive direct effect on yield. Rashid (2007) found that seeds/pod, number of pod/plant and number of primary branches/plant and number of secondary branches/plant had positive direct inputs on seed yield. The residual effect determines how best the causal factors account for the variability of the dependent factor, the yield/plant in this case. In case of the present study the residual effect was 0.1622 and 0.1304 at phenotypic and genotypic level respectively. The reason seems to be very low and non-significant correlation of some traits with yield. Besides, some other factors which have not been considered here need to be included in this analysis to account fully for the variation in yield.

**Table 6.** Partitioning of genotypic correlation coefficient into direct and indirect effects of 9 important traits of 18 *Brassica* genotypes by path analysis (bolded number = direct effect).

| Characters | Days to first flowering | Days to maturity | Plant height (cm) | No. of branches/ plant | No. of pod/plant | Pod length (cm) | No. of seeds/pod | 1000-seed wt. (g) | Yield/ plant (g) |
|---|---|---|---|---|---|---|---|---|---|
| Days to first flowering | **-0.175** | -0.340 | 0.548 | -0.00015 | 0.089 | 0.261 | -0.718 | -0.073 | -0.407 |
| Days to maturity | -0.146 | **-0.408** | 0.454 | -0.0008 | -0.019 | 0.223 | -0.582 | -0.074 | -0.553* |
| Plant height (cm) | -0.158 | -0.305 | **0.607** | -0.00049 | 0.044 | 0.234 | -0.689 | -0.056 | -0.325 |
| No. of branches/ plant | 0.0084 | 0.099 | -0.095 | **0.003** | 0.245 | -0.111 | 0.012 | 0.039 | 0.200 |
| No. of pod/plant | -0.037 | 0.018 | 0.062 | 0.0018 | **0.426** | 0.198 | -0.284 | 0.027 | 0.413 |
| Pod length (cm) | 0.102 | 0.203 | -0.316 | 0.00079 | -0.188 | **-0.448** | 0.692 | 0.0124 | 0.058 |
| No. of seeds/pod | 0.130 | 0.247 | -0.434 | 0.00004 | -0.126 | -0.322 | **0.962** | 0.051 | 0.508* |
| 1000-seed wt. (g) | 0.049 | 0.117 | -0.132 | 0.0005 | 0.044 | -0.022 | 0.189 | **0.258** | 0.505* |

Residual effect = 0.1304

**Table 7.** Partitioning of phenotypic correlation coefficient into direct and indirect effects of 9 important traits of 18 *Brassica* genotypes by path analysis (bolded number = direct effect).

| Characters | Days to first flowering | Days to maturity | Plant height (cm) | No. of branches/ plant | No. of pod/plant | Pod length (cm) | No. of seeds/pod | 1000-seed wt. (g) | Yield/ plant (g) |
|---|---|---|---|---|---|---|---|---|---|
| Days to first flowering | **0.067** | -0.333 | 0.325 | 0.0053 | 0.107 | 0.157 | -0.648 | -0.081 | -0.400 |
| Days to maturity | 0.055 | **-0.405** | 0.278 | 0.031 | -0.020 | 0.125 | -0.514 | -0.085 | -0.537* |
| Plant height (cm) | 0.058 | -0.298 | **0.377** | 0.020 | 0.054 | 0.136 | -0.602 | -0.061 | -0.317 |
| No. of branches/ plant | -0.0028 | 0.098 | -0.060 | **-0.127** | 0.292 | -0.064 | 0.0078 | 0.048 | 0.192 |
| No. of pod/plant | 0.014 | 0.015 | 0.039 | -0.071 | **0.520** | 0.120 | -0.256 | 0.030 | 0.411 |
| Pod length (cm) | -0.038 | 0.184 | -0.186 | -0.029 | -0.227 | **-0.275** | 0.615 | 0.017 | 0.059 |
| No. of seeds/pod | -0.050 | 0.238 | -0.260 | -0.0011 | -0.153 | -0.194 | **0.872** | 0.056 | 0.508* |
| 1000-seed wt. (g) | -0.018 | 0.113 | -0.076 | -0.020 | 0.052 | -0.015 | 0.160 | **0.304** | 0.499* |

Residual effect = 0.1622

## Conclusion

The present study revealed the morphological characterization and association among various traits in eighteen genotypes of brassica. From the analysis of variance (ANOVA), significant variations were observed for all the characters among the genotypes. Significant variation among genotypes indicated existence of wide genetic diversity that would provide better scope of selection. Considering the two most important traits like early maturity and yield /plant, BD-7114 performed best among all the genotypes which would be released as variety after further trials. Number of seeds/pod and 1000-seed weight would be most prominent traits for increasing yield in *Brassica*. Yield is significant but negatively correlated with days to maturity. Path coefficient analysis revealed all the characters whether they had positive direct or indirect or negative direct or indirect effect on seed yield. That would be helpful for character selection program for better yield.

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