

ESTIMATION OF SELECTION INDICES IN *BRASSICA JUNCEA* L. AND *BRASSICA NAPUS* L.

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Abstract

Genetic selection indices were studied for six productive traits in two varieties (S-9 and S-95) of *Brassica juncea* and four varieties (Canola-I, II, III and Canola standard) of *B. napus*. Correlation analysis indicated that seed yield/plant had strong positive association with plant height, branches/plant, siliqua/plant, seeds/siliqua and dry matter yield/plant. Path analysis and selection indices also confirmed that all the traits contributed significantly towards seed yield/plant. The direct and indirect effects were found to be regulating the character association in all the traits. Magnitude of genetic and phenotypic variance ranged between 0.555 (seed yield/plant) to 960.63 (siliqua/plant), respectively. Heritability (b s) showed high estimates (ranging from 97.70% to 60.24%) for all the traits, indicating the involvement of additive gene action. Dry matter yield/plant, seeds/siliqua and plant height exhibited low genetic advance irrespective of their high heritability estimates, probably due to non-additive gene (dominance and epistasis) effects. On the basis of selection indices, it is concluded that branches/plant and siliqua/plant are the most important yield components, therefore, selection based on these traits could be exploited for the improvement of yield in present genotypes.

Introduction

Rape (*Brassica napus*) and mustard (*B. juncea*) belonging to family Cruciferae are the most important source of oil and contribute one third of Pakistan's domestic oil production (Khan *et al.*, 1987). Although the oil of rape and mustard is an important commodity in the tropics and sub-tropics, very little attention has been paid towards the quantitative breeding aspects of this economically important oil seed crops (Rajput, 1997).

The seed yield in rape and mustard is a complex and quantitatively inherited character and is likely to be highly influenced by the environmental fluctuations unlike other yield components (Larik *et al.*, 1999). The expected improvement in such component characters primarily depends on the nature and magnitude of heritable variation. Further, the component characters may show different types of association with seed yield. Therefore, undesirable associations between the desired traits under selection may result in genetic slippage (Dickerson, 1955) and limit the genetic gain (Larik *et al.*, 1997). The path analysis, however, quantifies the direct and indirect effects of characters and thus allows relative weightage of importance to be given to such characters which are to be selected and manipulated.

In the present study, this problem has been approached in three ways: (I) Correlation analysis (ii) Path coefficient analysis, and (iii) Genetic selection indices. Such information can profitably be exploited in expanding our knowledge of developmental allometry (Hamid & Grafius, 1978) and can further be helpful in formulating efficient selection programme for synthesis and development of new rape and mustard ideotypes with improved yield potential.

Material and Methods

The investigations pertaining to selection indices in two varieties of *B. juncea* (viz., S-9 and S-95) and four varieties of *B. napus* (viz., Canola- I, II, III and Canola Standard) for six productive traits were undertaken at the Department of Plant Breeding & Genetics, Sindh Agriculture University, Tandojam Pakistan during Rabi 1997-98 in a randomized complete block design with four replications. Seeds were drilled in rows 45cm apart by single coulter hand driven drill @ 3.5 kg/ha. Before first irrigation the seedlings were thinned to maintain plant to plant distance of 22.5cm. A 2x3 meter plot size was maintained in all the plots throughout the growth period. Ten plants per replication from two central rows of each genotypes were selected at random and tagged for recording the data on six productive traits (Table 1). Data thus obtained for each character was subjected to statistical analysis (Gomez & Gomez, 1984). The analysis of variance (ANOVA) for all the traits was carried out separately. The pertinent mean squares were then partitioned into the genotypic and error variance according to the method suggested by Breese (1972) as under:

| Item | d.f | M.S. | Mean Square expectation |
|------------|------------|------|--------------------------|
| Replicates | (r-1) | | |
| Genotypes | (g-1) | MSG | $\delta^2e + r\delta^2G$ |
| Error | (r-1)(g-1) | MSE | δ^2e |

Genetic selection indices were determined using above analysis similar to Larik *et al.*, (1997).

1. Genotypic variance = $\delta^2g = (MSG - MSE)/r$
2. Phenotypic variance = $\delta^2pH = MSG/r$
3. Heritability (hw) = $\frac{\delta^2g}{\delta^2pH}$
4. Selection index (s) = $K \times \sqrt{\sigma^2 ph}$
5. Genetic advance (Gs) = $hw \times s$
6. Genetic advance % of means = $\frac{Gs}{x} \times 100$

where MSG and MSE are the genotype and the error mean squares respectively from analysis of variance, r is the number of replications and K is constant = 2.06 at 5% selection intensity. Phenotypic and genotypic correlations were calculated by using the formula given by Falconer (1989). Path coefficient analysis was computed according to Dewey & Lu (1959), using phenotypic correlations.

Results and Discussion

Mean performance and ANOVA regarding seed yield and its components for six *Brassica* varieties is shown in Table 1. Variety S-95 of *B. juncea* displayed overall superiority for all the productive traits. However, all the varieties of *B. napus* exhibited significantly more seeds per siliqua. ANOVA displayed highly significant ($p \geq 0.01$)

Table 1. Average expression and ANOVA (mean squares) for six quantitative characters of *Brassica juncea* L. and *B. napus* L.

| Trait/genotype | Plant height (cm) | Branches/ plant | Siliqua/ plant | Seeds/ siliqua | Dry matter yield/plant (gm) | Seed yield/ plant (gm) |
|---------------------------|----------------------|-----------------------|---------------------|------------------------|-----------------------------------|---------------------------|
| <i>Brassica juncea</i> L. | | | | | | |
| S - 9 | 170.65b | 7.98b | 101.06b | 12.46b | 16.50a | 3.34b |
| S - 95 | 180.88a | 11.14a | 146.26a | 12.55d | 16.89a | 3.16a |
| <i>Brassica napus</i> L. | | | | | | |
| Canola-I | 110.35d | 3.60c | 71.79c | 19.69a | 12.08a | 2.16b |
| Canola-II | 127.19c | 5.62bc | 75.19c | 16.85c | 10.56a | 1.65c |
| Canola-III | 128.84c | 5.27bc | 59.77d | 17.25abc | 12.86a | 1.70c |
| Canola | | | | | | |
| Standard | 125.71c | 5.23bc | 82.71c | 16.62c | 14.95a | 1.50c |
| Mean Squares | | | | | | |
| Item | d. f. | | | | | |
| Reps | 3 | 89.43 ^{n.s} | 1.46 ^{n.s} | 1095.34 ^{n.s} | 1.12 ^{n.s} | 3.99 ^{n.s} |
| Genotypes | 5 | 3183.76 ^{**} | 28.85 ^{**} | 3842.55 ^{**} | 32.65 ^{**} | 24.96 ^{n.s} |
| Error | 15 | 79.02 | 1.65 | 363.86 | 3.17 | 9.92 |
| | | | | | | 0.156 ^{n.s} |
| | | | | | | 2.57 ^{**} |
| | | | | | | 0.348 |

* ** = Significant at 5% and 1% level, n.s. = Non-significant.

differences among genotypes for all the traits except dry matter yield per plant, indicating that the substantial genetic variability existed among the genotypes the traits under study. The correlation coefficients highlight the pattern of association among seed yield and its components (Table-2). Results demonstrated that seed yield/plant was positively and significantly associated with all the productive traits at phenotypic level, whereas at genotypic level all the traits revealed negative non-significant association. Phenotypic correlation coefficients (PCC) were lower in magnitude in 50% of the cases than their corresponding genotypic correlation coefficients (GCC). However, negative non-significant GCC could be either due to the modifying effect of the environment or the strong inherent association of the characters at genic level (Sharma & Tyagi, 1991).

The difference in nature of correlation coefficient at genotypic and phenotypic level suggests that either the environment or non-additive genetic effects or the interaction of both influenced the associations of these characters. Such environmental influences on association of seed yield with its components have been reported by Das *et al.*, (1984) in *B. juncea* and *B. campestris*, Khan *et al.*, (1992) in *Raya* and Larik *et al.*, (1999) in *rape* and *mustard*.

Correlation studies suggests that all traits were important in determining the seed yield/plant in *rape* and *mustard*. Branches/plant expressed significant positive PCC with siliqua/plant and seed yield/plant ($r=0.690^*$ and 0.519^*) respectively. Plant height displayed positive significant PCC ($r=0.438^*$) with branches/plant and seed yield/plant ($r=0.50^*$), indicating that there is a mutual relationship of these characters with seed yield arising from the combined effects of genotype and environment, while these traits showed negative non-significant association at genotypic level, indicating the absence of either linkage or pleiotropy between them. Two characters having a common physiological or biochemical chain may also show negative GCC (Hohenboken, 1985). No significant association could be detected between plant height v/s siliqua/plant and siliqua/plant v/s seeds/siliqua either genotypically or phenotypically except for the observation that the association between these traits remained positive. The non-significant association between these characters suggests that they are independent of each other and could be selected separately as these are components of seed yield (Sharma & Tyagi, 1991). Seeds/siliqua displayed non-significant negative PCC with plant height and branches/plant. Such a negative association occurs when two developing structures of a plant compete for a common nutrient supply and negative correlation may arise if one structure is favoured over the other in the amount of nutrient supply (Adams, 1967). However, the issue needs further investigation before such a relationship could be established.

Pathways through which the yield components operate to produce their associations with seed yield are depicted in Table 3. Path analysis revealed that branches/plant exhibited highest direct effect (0.1880) on seed yield with its largest indirect effect (0.1776) through plant height. Siliqua/plant had the next highest positive direct effect (0.1870) on seed yield with its largest effect via branches/plant (0.1829) and plant height (0.1566). The direct effects of all the yield components were lesser than their PCC with seed yield and were counter balanced by positive indirect effects via other yield components. The positive indirect effects of these traits are in agreement with their strong positive PCC. Therefore, selection based on branches/plant and siliqua/plant could be more rewarding and will equally improve seed yield in *rape* and *mustard*. However, plant height, seeds/siliqua and dry matter yield also displayed positive direct effects on seed

Table 2. Genotypic (G) and Phenotypic (P) correlation coefficient among six productive traits in *Brassica juncea* L. and *B. napus* L.

| Character | Plant height (cm) | Branches/plant | Siliqua/plant | Seeds/siliqua | Dry matter yield/plant (gm) | Seed yield/plant (gm) |
|------------------------|-------------------|------------------------|-----------------------|------------------------|-----------------------------|------------------------|
| Plant height | G 1.000 | -0.502 ^{n.s.} | 0.492 ^{n.s.} | 0.001 ^{n.s.} | -0.270 ^{n.s.} | -0.390 ^{n.s.} |
| | P 1.000 | 0.438* | 0.223 ^{n.s.} | -0.009 ^{n.s.} | 0.237 ^{n.s.} | 0.501** |
| Branches/plant | G 1.000 | 1.000 | 0.560 ^{n.s.} | 0.073 ^{n.s.} | -0.387 ^{n.s.} | -0.456 ^{n.s.} |
| | P 1.000 | 1.000 | 0.690** | -0.064 | 0.286 ^{n.s.} | 0.519** |
| Siliqua/plant | G 1.000 | 1.000 | 1.000 | 0.003 ^{n.s.} | -0.121 ^{n.s.} | -0.603 |
| | P 1.000 | 1.000 | 1.000 | 0.176 ^{n.s.} | 0.564** | 0.726** |
| Seed/siliqua | G 1.000 | 1.000 | 1.000 | 1.000 | 0.212 ^{n.s.} | 0.369 ^{n.s.} |
| | P 1.000 | 1.000 | 1.000 | 1.000 | 0.261 ^{n.s.} | 0.698** |
| Dry matter yield/plant | G 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | -0.416 ^{n.s.} |
| | P 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 0.621** |
| Seed yield/plant | G 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 |
| | P 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 |

*** = Significant at 5% and 1% level, n.s. = Non-significant.

Table 3. Direct and indirect effects of different quantitative traits on seed yield per plant in *Brassica juncea* L. and *B. napus* L.

| Character | Plant height | Branches/plant | Siliqua/plant | Seeds/siliqua | Dry matter yield/plant | Phenotypic correlation with seed yield |
|------------------------|--------------|----------------|---------------|---------------|------------------------|--|
| Plant height | 0.1450 | 0.1280 | 0.1135 | 0.1380 | 0.0565 | 0.6210** |
| Branches/plant | 0.1776 | 0.1880 | 0.0022 | 0.0895 | 0.0624 | 0.5197** |
| Siliqua/plant | 0.1566 | 0.1829 | 0.1870 | 0.1150 | 0.0845 | 0.7260** |
| Seeds/siliqua | 0.1875 | 0.1624 | 0.0895 | 0.1301 | 0.1290 | 0.6985** |
| Dry matter yield/plant | 0.1260 | 0.1301 | 0.0148 | 0.1064 | 0.1241 | 0.5014** |

** Significant at 1% level, values in Italic denote direct effects.

Table 4. Selection indices in six quantitative traits of *Brassica juncea* L. and *B. napus* L.

| Character | Genotypic variance | Phenotypic variance | Heritability % (b.s) | Selection index (s) at 5% | Genetic advance % of means |
|------------------------|--------------------|---------------------|----------------------|---------------------------|----------------------------|
| Plant height | 777.68 | 795.94 | 97.70 | 57.83 | 40.18 |
| Branches/plant | 6.80 | 7.21 | 94.27 | 05.50 | 80.20 |
| Siliqua/plant | 869.67 | 960.63 | 90.53 | 63.53 | 64.29 |
| Seeds/siliqua | 7.36 | 8.16 | 90.28 | 05.85 | 33.25 |
| Dry matter yield/plant | 3.75 | 6.24 | 60.24 | 05.12 | 22.08 |
| Seed yield/plant | 0.555 | 0.642 | 86.44 | 1.64 | 67.78 |

yield indicating their importance in determining seed yield/plant. Several workers have reported similar results (Khan *et al.*, 1992 b; Kumar *et al.*, 1988; Singh *et al.*, 1988). The effect of residual factors on seed yield/plant (0.421) suggests that though the characters under study influenced the seed yield considerably, however, their might be a few more components, which might have been responsible to influence seed yield/plant.

Estimation of selection indices are shown in Table 4. All the metrical traits exhibited very wide range of genotypic and phenotypic variances ranging from 0.555 (seed yield/plant) to 960.63 (Siliqua/plant). Second maximum genotypic (777.68) and phenotypic variances were shown by the trait plant height. Heritability in broad sense indicates the effectiveness with which the selection of a genotype can be based on phenotypic performance and prediction of genetic advance associated with breeding method is one of the important goals of quantitative genetics. The traits branches/plant, siliqua/plant exhibited higher estimates of broad sense heritability coupled with high genetic advance indicating the importance of additive gene action. Results also suggests that these traits are more amenable to selection and could be improved by simple selection method and single round of selection in selfing series should be ample to fix all major genes.

Although the yield is a complex polygenic character its inheritance has been characterized as the most fluctuative (Larik *et al.*, 1999) displayed high heritability estimates (86.44%) which were biased upward due to contribution of non-additive genetic variance and GXE interaction as the genotypes were evaluated at one location in single macro-environment. Normally non additive type of gene action does not contribute tangibly in the improvement of cross pollinated crops as it is a non fixable component of genetic variance (Allard, 1960). However, complementary interaction is fixable and utilizable genetic variance (Sachan & Singh, 1988). Higher estimates of heritability for seed yield from variance most likely resulted from within plot competition in the present studies. It is, therefore, suggested that narrow sense heritability should be computed which is less biased by GXE interaction and may be calculated in standard units which is more reliable (Ali & Wynne, 1994). The traits seeds/siliqua and dry matter yield were highly heritable (90.18% and 60.24%, respectively) but failed to show higher estimates of expected genetic advance (33.25% and 22.08%, respectively) expressed as percentage of means. This indicates that higher heritability in broad sense does not necessarily provide higher values of genetic advance and hence heritability alone provide no indication for the amount of genetic progress that can be achieved through selection (Larik *et al.*, 1997). High heritability associated with low genetic advance for these traits is probably due to non additive gene (dominance and epistasis) effects (Sharma & Tyagi, 1990, 1991). The traits showing high heritability with low genetic gain expected through selection will take several selection cycles to materially change the productive traits of the genotypes used in this study.

On the basis of correlation, path coefficient analysis and other selection indices, the present investigations, therefore, suggests that the branches/plant and siliqua/plant are the most important yield components, therefore, maximum weightage should be given to these traits in selection programme in accelerating the seed yield in present rape and mustard genotypes.

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