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Estimation of Genotypic and Phenotypic Coefficients Variation of Yield and its Contributing Characters of *Brassica rapa* L.

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Abstract: A research was conducted by using twenty one (21) F_9 populations derived from inter-varietal crosses of *Brassica rapa* L. Path co-efficient analysis revealed that plant height, number of primary branches per plant, number of siliqua per plant, seeds per siliqua and siliqua length had a positive direct effect on yield per plant and days to 50% flowering, number of secondary branches per plant and thousand seed weight had a negative direct effect on yield per plant.Correlation study revealed that yield per plant had a significant positive association with plant height, number of primary branches per plant, number of siliqua per plant, seeds per siliqua and siliqua length (genotypic or phenotypic level). Based on the variability study, some F_9 plants that showed high heritability for short duration and yield contributing characters were selected from some of the cross combinations of the intervarital crosses of *Brassica rapa* for further selection.

Key words: Genotype · Phenotypic · Heritability · Correlation coefficients · Siliqua · *Brassica rapa* L.

INTRODUCTION

Brassica oil is the world's third most important sources of edible vegetable oils [1]. Oleiferous *Brassica species* can be classified into three groups *viz* the cole, the rapeseed and the mustard. The mustard groups include species like *Brassica juncea* Czern and Coss, *Brassica nigra* Koch and *Brassica carinata* Braun; while the rapeseed groups include *Brassica rapa* L. and *Brassica napus* L. [2]. The genomic constitutions of the three diploid elemental species of *Brassica* are AA for *Brassica rapa,* 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.

The coles are consumed as vegetables and the other two are the valuable sources of edible oils and proteins. The mustard oil is not used only for edible cooking purpose but also is used in hair dressing, body massing and in different types of pickles preparation. It has also several medicinal values. Oil cake is the most important feed for livestock and is also used as organic manure. The important regions growing these crops include Canada, China, Northern Europe and the Indian subcontinent. In Bangladesh, local cultivars/varieties like *B. juncea* and *B. napus* are high yielding but not short durated. Thats why *B. rapa* is widely grown and it gives moderate yield but early cultivars produce high yield and it is drought stress resistant. In Bangladesh, *Brassica* is the most important oilseed crop. The country is facing huge shortage in edible oils. Almost one fourth of the total edible oil consumed annually is imported. The import cost was about 690 million US dollar in 2003 [3]. On Recommended Dietary Allowance (RAD) basis, Bangladesh requires 0.29 million tons of oils which is equivalent to 0.8 million tons of oilseeds; but she produces only about 0.254 million tons, which covers only 45% of the domestic need [4]. This crop covers the highest acreage which is 78% of the total oilseed acreage of Bangladesh [3].The average yield of *Brassica* oilseed in Bangladesh is around 963 kg/hectare [4].

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In Bangladesh there is limited scope to increase acreage due to pressure of other crops and to increase yield due to cultivation of the existing low yielding varieties with low inputs, *B. rapa* is the most popular cultivated species. Short duration variety Tori-7 of *B. rapa* is still popular in Bangladesh because it can fit well into the T.Aman-Mustard-Boro cropping pattern.Early maturity line (SAU sarisha 2 X SAU sarisha 1), combination SAU sarisha 2 X BARI sarisha 6 gave higher number of primary branches and number of siliquae / plant. No improved short duration variety of *B. napus* is available to replace this short duration variety. So *B. rapa* is the most popular variety to the farmers.There should be an attempt to develop short duration and high yielding varieties of rapeseed to meet the challenge of edible oils of the country by increasing the production. Segregating materials obtained through different inter-varietal crosses of the species *B. rapa* will give an opportunity to select the desired plant types to meet the existing demand. Therefore, this study was carried out with following objectives: (i) to study the variability among F_9 generation materials for selection of desired lines, (ii) to study the inter-relationship and effect of characters on yield and (iii) to select early maturing, high yielding lines for release.

MATERIALS AND METHODS

The present research work was carried out in the experimental farm, Sher-e-Bangla Agricultural University (SAU), Dhaka during Rabi season. A total number of 19 (nineteen) materials were used in this experiment. Where (19) were F_9 segregating generation materials and six check varieties. The seeds of checks and F_9 materials were laid out in a randomized complete block design (RCBD) with three replications. The size of plot was 5m x 25m. A distance of 1.5 m from block to block, 30 cm from row to row and 10 cm from plant to plant was maintained. For studying different genetic parameters and inter-relationships the ten characters were taken into consideration. Plant height (cm), Number of primary branches/plant, Number of secondary branches/plant, Days to 50% flowering, Siliqua length (cm), Number of siliquae/plant, Number of seeds/siliqua, 1000 seeds weight (gm), Seed yield/plant (gm) and Days of maturity.

Statistical Analysis: The data were analyzed for different components. Phenotypic and genotypic variances were estimated by the formula used by Johnson *et al.* [5]. Heritability and genetic advance were measured using the formula given by Singh and Chaudhary [6] and Allard [7]. Genotypic and phenotypic co-efficient of variation was calculated by the formula of Burton [8]. Simple correlation coefficient was obtained using the formula suggested by Clarke [9] Singh and Chaudhary [6] and path co-efficient analysis was done following the method outlined by Dewey and Lu [10].

Estimation of Genotypic and Phenotypic Variances: Genotypic and phenotypic variances were estimated according to the formula of Johnson *et al.* [5].

$$\text{Genotypic variance, } \delta^2 g = \frac{MSG - MSE}{r}$$

Where, MSG = Mean sum of square for genotypes

MSE= Mean sum of square for error and

r = Number of replication

δ^2_p Phenotypic variance, $\delta^2 p = \delta^2 g + \delta^2 e$

Where, $\delta^2 g$ = Genotypic variance,

$\delta^2 e$ = Environmental variance = Mean square of error/r

Estimation of Genotypic and Phenotypic Co-efficient of Variation: Genotypic and phenotypic co-efficient of variation were calculated by the following formula [8].

$$GCV = \frac{\delta g \times 100}{\bar{x}}$$

$$PCV = \frac{\delta p \times 100}{\bar{x}}$$

Where, GCV= Genotypic co-efficient of variation

PCV = Phenotypic co-efficient of variation

δg = Genotypic standard deviation

δp = Phenotypic standard deviation

$\bar{x}$ = Population mean

Estimation of Heritability: Broad sense heritability was estimated by the formula suggested by Singh and Chaudhary [6].

h^2b (%) = $(\delta^2 g / \delta^2 p)$ x100

Where, h^2b = Heritability in broad- sense.

$\delta^2 g$ = Genotypic variance

$\delta^2 p$ = Phenotypic variance

RESULTS AND DISCUSSION

Genotypic and Phenotypic Coefficient of Variation: The highest genotypic and phenotypic coefficient of variation was observed for number of secondary

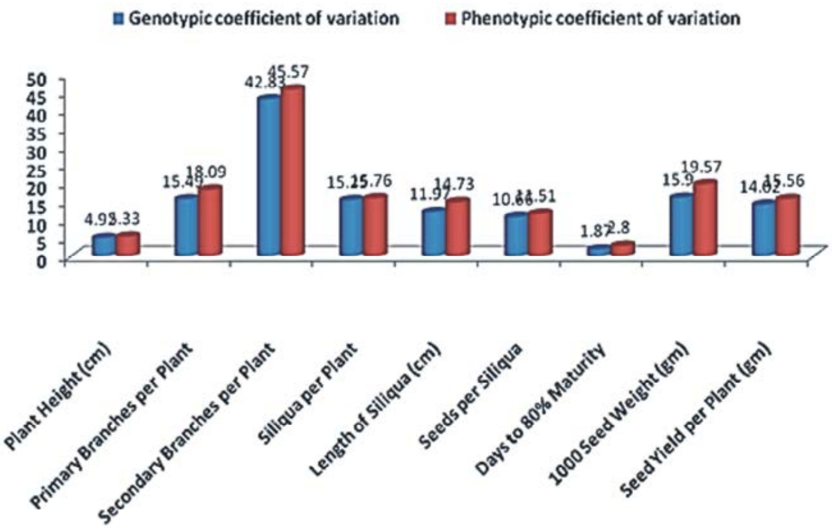

Fig. 1: Genotypic and phenotypic coefficient of variation in *Brassica rapa* L.

Table 1: Estimation of genetic parameters among nine characters of 25 genotypes in *Brassica rapa* L

Parameters	Phenotypic coefficient of variation%	Genotypic coefficient of variation%	Heritability %	Genetic advance (5%)	Genetic advance (% mean)
Plant height (cm)	5.33	4.92	85.34	9.32	9.37
Primary branches per Plant	18.09	15.49	73.35	1.27	27.34
Secondary branches per Plant	45.57	42.83	88.32	1.42	82.71
Siliqua per plant	15.76	15.25	93.63	26.19	30.40
Length of siliqua(cm)	14.73	11.97	66.10	0.94	20.05
Seeds per siliqua	11.51	10.66	85.83	2.58	20.34
Days to 80% maturity	2.80	1.87	44.68	2.15	2.57
1000- seed weight(gm)	19.57	15.90	66.05	0.85	26.65
Seed yield per plant(gm)	15.56	14.02	81.12	1.07	26.04

branches/plant (Table 1) whereas the minimum was th number of days to 80% maturity. Number of secondary branches showed moderate difference between phenotypic coefficient (45.57) and genotypic coefficient (42.83%) of variances (Fig. 1). Days to 80% maturity showed moderate difference between phenotypic coefficient (2.8%) and genotypic coefficient (1.87%) of variances. Lekh *et al.* [11] reported a similar result.

Heritability and Genetic Advance from Selection: The extent of heritability, genetic advance, genetic advance in percentage of mean among the genotypes in respect of ten characters were studied and have been presented in Table 1.

Plant Height (cm): Plant height showed moderately high (85.34 %) heritability in broad sense (h^2_b) with medium genetic advance (9.37 %) (Table 1), indicating the possibility of additive genes effect for the expression of this character. Therefore selection would be effective for improving this character. Shen *et al.* [12] found moderate h^2_b (58.22), medium genetic advance (12.61) and medium genetic advance in percentage of mean (14.38) which supported the present findings.

Number of Primary Branches per Plant: Number of primary branches per plant exhibited moderate heritability (73.35 %) in broad sense (h^2_b) coupled with moderate genetic advance in percentage of mean (27.34 %) (Table 1), indicating that this character was highly influenced by environmental effects and selection for such trait might not be rewarding. Li *et al.* [13] and Singh *et al.* [14] obtained similar conclusion.

Number of Secondary Branches per Plant: Number of secondary branches per plant exhibited high heritability (88.82 %) in broad sense (h^2_b) coupledwith high genetic advance in percentage of mean (82.71 %) (Table 1) which revealed the possibility of predominance of both additive and non-additive gene action in the inheritance of this character.

Number of Siliquae per Plant: The magnitude of heritability (93.63 %) in broad sense (h^2_b) for number of siliqua per plant was high coupled with moderate medium genetic advance in percentage of mean (30.4 %) (Table 1) indicating that this character was governed by additive gene and selection might be effective. Moderate h^2_b (54.97) was reported by Rashid [15].

Length of Siliqua (cm): Length of siliqua exhibited moderately low heritability (66.1 %) in broad sense (h^2_b) with moderate (20.05 %) genetic advance in percentage of mean (Table 1). In that case the high values of heritability are not always indication of high genetic advance i.e. this character is governed by non-additive gene. The low heritability was due to the favorable influence of environment rather than genotype and selection for such trait might not be effective. It differs with the findings by Rashid [15] but similar with the findings of Singh *et al.* [16], Kown *et al.* [17] and Labana *et al.* [18].

Number of Seeds per Siliqua: Number of siliqua exhibited high heritability (85.83 %) in broad sense (h^2_b) with moderate (20.34 %) genetic advance in percentage of mean (Table 1). indicating that this character was governed by additive gene and selection might be effective. Malik *et al.* [19] reported high heritability for this trait.

Days to 80% Maturity: The magnitude of heritability (44.68 %) in broad sense (h^2_b) for days to maturity was moderately high with low genetic advance in percentage of mean (2.57 %) (Table 1) indicating this character is governed by non-additive genes and lower possibility of selecting genotypes.

Thousand Seed Weight (g): The magnitude of low heritability (66.05 %) in broad sense (h^2_b) with moderately (26.65 %) genetic advance in percentage of mean (Table 1), indicating that, this character was highly influenced by environmental effect and selection would not be in effective. Similar findings were observed by Singh *et al.* [16], Li *et al.* [13] and Yadav [20].

Seed Yield per Plant (g): Yield per plant exhibited moderately high heritability (81.12 %) in broad sense (h^2_b) with moderate (26.04 %) genetic advance in percentage of mean (Table 1) indicating that this character were influenced by environmental effect and selection for such trait might not be rewarding. These results support the reports of Liang and Walter [21] but Singh *et al.* [14] found high heritability for this trait.

Genotypic and Phenotypic Correlation Coefficient of Yield

Plant Height (cm): Plant height showed positive phenotypic and genotypic correlation coefficients being 0.263 and 0.292, respectively with relatively high differences between them indicating large environmental influences on this character (Fig. 2). Tyagi *et al.* [22] observed highest variation in plant height among parent and their hybrid.

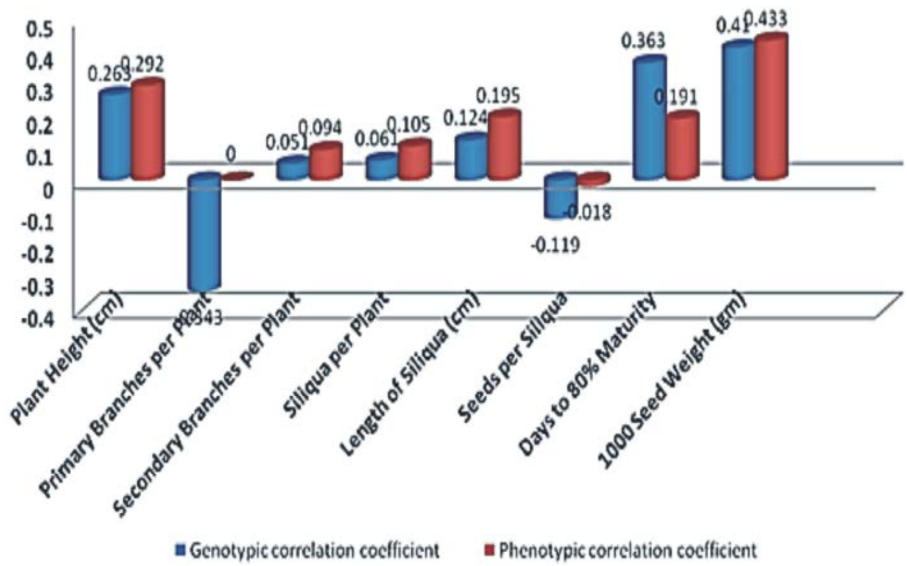

Fig. 2: Genotypic and phenotypic correlation coefficient of yield with other characters of *Brassica Rapa* L.

Number of Primary Branches per Plant: Number of primary branches per plant showed negative phenotypic correlation coefficient (-0.343) (Fig. 2). Chowdhary *et al.* [23] found significant differences for number of primary branches per plant.

Number of Secondary Branches per Plant: Number of secondary branches showed positive phenotypic correlation coefficient (0.051) and genotypic correlation coefficient (0.105) (Fig. 2). Lekh *et al.* [12] reported a similar result.

Number of Siliquae per Plant: Number of siliquae/plant showed positive phenotypic correlation coefficient (0.061) and genotypic correlation coefficient (0.105) (Fig 2). Higher genotypic variances indicate the better transmissibility of a character from parent to the offspring [24].

Length of Siliqua (cm): Length of siliqua showed positive phenotypic (0.124) and genotypic correlation coefficient (0.195) (Fig 2). Labowitz [25] studied *Brassica campestris* population for siliqua length and observed high genetic variation on this trait.

Number of Seeds per Siliqua: Number of seeds per siliqua showed negative phenotypic correlation coefficient (-0.119) and genotypic correlation coefficient (-0.018) (Fig. 2). Banerzee *et al.* [26] observed 35.85 % GCV in *Brassica campestris*.

Days to 80% Maturity: Days to 80% maturity showed positive phenotypic (0.363) and genotypic correlation coefficient (0.191) (Fig. 2). Labowitz [25] studied *Brassica campestris* population for days to 80% maturity and observed high genetic variation on this trait.

Thousand Seed Weight (g): The phenotypic and genotypic correlation coefficients for this trait were (0.41) and (0.433), respectively. The phenotypic correlation coefficient appeared to be much higher than the genotypic correlation coefficient suggesting considerable highly significant influences of environment on the expression of the genes controlling this trait. Banerzee *et al.* [26] reported values of 11.8% and 18.9% of GCV and PCVfor thousand seed weight in *Brassica campestris*. Similarly Tak and Patnaik [27] reported values of 13.1% and 16.5% of GCV and PCV, respectively for *Brassica campestris*.

CONCLUSION

The phenotypic variance of the twenty five materials was considerably higher than the genotypic variances for all the traits studied. Highest genotypic and phenotypic coefficient of variation was observed for number of secondary branches per plant and was minimum for number of day to 80% maturity. Seed yield of the genotypes varied from 3.19 to 4.30 g in parents and from 4.23 to 5.70 g in hybrids. The highest seed yield of the parent was found in Tori 7 (4.30) whereas lowest in BARI sarisha 15 (3.19 g). Based on the variability studied, some F_9 genotypes that showed high heritability for short duration and yield contributing characters were selected from some of the cross combinations of the intervarital crosses of *Brassica rapa* for further selection.

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