



Morphological evaluation and variability analysis of *Brassica rapa* germplasm accessions collected from Uttarakhand Hills

Tabassum*¹, AS Jeena², Arvind Singh Negi³ and Deepak Kaujalagi⁴

^{1,2}College of Agriculture, Govind Ballabh Pant University of Agriculture and Technology, Pantnagar-263145, Uttarakhand, India

³School of Agriculture, Graphic Era Hill University, Dehradun, Uttarakhand, India

⁴Karnataka State Department of Agriculture, Bangalore

*Corresponding author: tabassum12081992@gmail.com

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Abstract

The present experiment was conducted to estimate genetic variability, heritability and genetic advance among thirty *Brassica rapa* germplasm accessions. These accessions were evaluated in randomized block design in two replications with three checks to identify genetically diverse accessions for the improvement of yield and other traits in *Brassica rapa*. Data was recorded on 8 quantitative traits viz., plant height, shoot length, siliqua length, beak length, number of siliqua, number of seeds per siliqua, siliqua density and seed yield per plant. Higher values of GCV and PCV were observed for seed yield per plant followed by siliqua density, number of seeds per siliqua, beak length and shoot length. Higher GCV indicated stability in the expression of these traits and better transmissibility of the traits from parents to the progeny. High heritability coupled with high genetic advance as percent of mean was observed for all the traits under study indicated the predominance of additive gene action in the inheritance of these traits. Therefore, selection would be effective for the improvement of these traits in following generations.

Key words: *Brassica rapa*, genetic advance, genetic variability, heritability

Introduction

For increasing the production of *Brassica rapa*, there is a need to expand the area under cultivation and per unit area production. But the scope of area increase under cultivation is limited therefore one way to increase production is to enhance production per unit area. Moreover the crop should fit in the cropping pattern. Therefore, high yielding and short duration *Brassica rapa* varieties should be developed to fit into the existing cropping pattern (Naznin *et al.*, 2015). According to a report of national mission on oilseeds and oil palm (NMOOP), the production of all oilseeds has increased from 24.35 million tonnes in 2004-05 to 26.68 million tonnes in 2014-15. The oilseeds yield which was 885 kg per hectare in 2004-05 increased to 1037 kg per hectare in 2014-15 (Annual report, 2015-16). Globally, India is third largest producer of edible oils and among them *Brassica* accounts for almost 5% gross national product and 10% of the value of agricultural products. India is the third largest producer of rapeseed and mustard after China and Canada. In India the production of all *Brassica* species was 6.31 million tonnes from an area of 5.79 million hectares with average productivity of 1089 kg/ha (Anonymous, 2015). Major rapeseed and mustard

growing states are Rajasthan, Uttar Pradesh, Madhya Pradesh, Haryana, Assam, Gujarat, Punjab and West Bengal.

In any breeding programme, the existence of genetic variability is of great value. Variability provides the degree of diversity between lines and estimated on the basis of different quantitative traits. For the development of superior improved cultivar, utilization of existing germplasm, the sum total of existing variability in a crop species and its related species is important to fulfil different kinds of needs of the present day and future. It is important for the selection of desirable lines with suitable traits and these lines can be used as a donor in future crop improvement programmes (Sohail *et al.*, 2018). It is also important to divide existing variability into its heritable and non heritable components by estimating phenotypic and genotypic coefficient of variation. The heritability estimation provides the degree to which a trait is passing on to the next generation, therefore add to the selection and use in the calculation of genetic advance under selection (Khan *et al.*, 2016). Existing genetic variability for important characters plays an important role in plant breeding as selection will be effective and more diverse lines when used in hybridization programme

generally display a great heterosis than those between less diverse lines. Therefore the present study was carried out with the objective of analysing the genetic variability among genotypes in respect of qualitative characters and to estimate the genetic variability, heritability and genetic advance to screen out the suitable genotypes for future use.

Materials and methods

Thirty *Brassica* germplasm accessions collected from different districts of Uttarakhand hills were used in this experiment. These accessions along with three check varieties viz., Kranti (*B. juncea*), PPS-1 (*B. rapa var campestris*) and PT-303 (*B. rapa var toria*) were grown in Randomized Block Design (RBD) with two replications at the experimental field of Pantnagar Centre of Plant Genetic Resources, Govind Ballabh Pant University of Agriculture and Technology, Pantnagar. Each accession was sown in a single row of 3m with row to row spacing of 30 cm. Data were recorded on 5 plants from each plot for eight quantitative characters viz., plant height (cm), shoot length (cm), siliqua length (cm), beak length (cm), number of siliqua, number of seeds per siliqua, siliqua density and seed yield per plant. Four qualitative characters namely siliqua texture, siliqua angle, seed colour and seed size were also recorded. Distribution of these accessions for different qualitative characters was done as described in *Brassica* descriptor downloaded from NBPGR site. Genotypic (GCV) and phenotypic (PCV) coefficients of variation were calculated as per formulae given by Burton (1952). GCV and PCV values were categorized as low (0-10%), moderate (10-20%) and high (above 20%) as indicated by Sivasubramanian and Menon (1973). Broad Sense Heritability (h^2b) was estimated by using formula suggested by Lush (1949). The heritability was categorized as low (0-30%), moderate (30-60%) and high (60 and above) as given by Robinson *et al.* (1949). Genetic advance (GA) for each character was computed by adopting the formulae given by Johnson *et al.* (1955). Genetic advance as per cent mean (GAM) was categorized as low (0-10%), moderate (10-20%) and high (20 and above) as given by Johnson *et al.* (1955).

Results and Discussion

Evaluation of genotypes based on qualitative traits

The observations on four qualitative traits were recorded for all the thirty germplasm accessions and results are presented in table 1. For siliqua texture, the maximum number of germplasm accessions were fall in undulated (18) class followed by constricted (12) and smooth (2). For siliqua angle, majority of the germplasms (20) were

Table 1: Distribution of *Brassica rapa* accessions for different qualitative characters

S. No.	Character	Class	Accessions
1	Siliqua texture	Constricted	12
		Smooth	2
		Undulated	18
2	Siliqua angle	Appressed	20
		Semi- appressed	5
		Open	7
3	Seed colour	Yellow	20
		Reddish brown	2
		Brown	3
		Dark brown	4
		Black	3
4	Seed size	Small	32
		Medium	-
		Bold	-

observed with appressed type followed by open (7) and semi- appressed (5). For seed colour, maximum accessions showed yellow (20), followed by dark brown (4), brown (3), black (3) and reddish brown (2). All the germplasm accessions were found having small seed.

Genetic variability parameters estimation

Mean, range, phenotypic and genotypic coefficients of variation, heritability and genetic advance were estimated for the various yield contributing traits in *Brassica* and results are presented in table 2. For all the traits, a wide mean range was found indicated that a good amount of genetic variability was present in the experimental material. For plant height, mean values ranged from 78.00 cm to 164.00 cm with overall mean of 128.46 cm. Moderate values of GCV (16.58) and PCV (16.63) were obtained with higher heritability (99%) and GAM (34.04%). Our findings are in conformity with the earlier recorded by Jahan *et al.* (2014) and Ara *et al.* (2013) in *Brassica rapa*. For shoot length, the mean values ranged from 20.60 cm to 80.00 cm with grand mean of 49.05 cm. High values of GCV (23.66) and PCV (23.85) were observed with high heritability (98%) and GAM (48.34%). For siliqua length, mean was ranged from 2.58 cm to 6.72 cm with 5.15 cm grand mean. Moderate values of GCV (16.11) and PCV (17.85) were obtained along with higher heritability (81%) and GAM (29.94%). Islam *et al.* (2015) also observed moderate values of GCV and PCV for the trait in F9 population derived from inter varietal crosses of *Brassica rapa*. The mean values for beak length ranged from 0.44 cm to 2.07 cm with overall mean of 1.38 cm. GCV (25.39), PCV (29.50), heritability (74%) and GAM (45.01%) were found to be higher for this trait. For number of siliqua per plant, mean was ranged from 15.00 to 45.00 with 30.26 grand mean.

Table 2: Mean, range, genetic (GCV), phenotypic (PCV) coefficient of variability, heritability (h^2b) and genetic advance as percent of mean (GAM) for different quantitative characters in *Brassica rapa*.

S.No.	Characters	GM	Range	GCV(%)	PCV(%)	GA	GAM	H ² b
1	Plant height (cm)	128.46	78.00-164.00	16.58	16.63	43.73	34.04	0.99
2	Shoot length (cm)	49.05	20.60-80.00	23.66	23.85	23.71	48.34	0.98
3	Silique length (cm)	5.15	2.58-6.72	16.11	17.85	1.54	29.94	0.81
4	Beak length (cm)	1.38	0.44-2.07	25.39	29.50	0.62	45.01	0.74
5	No of silique/plant	30.26	15.00-45.00	17.91	19.58	10.21	33.73	0.84
6	No of seeds/silique	17.18	7.00-39.00	27.96	30.89	8.96	52.15	0.82
7	Silique density (cm)	0.67	0.28-1.60	40.62	42.12	0.54	80.70	0.93
8	Seed yield/plant (gm)	38.32	5.40-71.00	44.93	45.24	35.22	91.91	0.99

Moderate values of GCV and PCV were obtained (17.91 and 19.58) along with higher heritability (84%) and GAM (33.73%). similar results were also obtained by Islam *et al.* (2015) and Hosen *et al.* (2010). For no of seeds per silique, the mean value ranged from 7.00 to 39.00 with 17.18 grand mean. Higher values of GCV and PCV were observed (27.96 and 30.89) with higher heritability (82%) and GAM (52.15). higher values for all the four were also obtained earlier by Rashid *et al.* (2010). For silique density range of mean values was from 0.28 to 1.60 and grand mean was 0.67. GCV (40.62) and PCV (42.12), heritability (93%) and GAM (80.70%) all were found to be higher. For seed yield per plant, the range of mean values was from 5.40 g to 71.00 g with grand mean of 38.32 g. Higher values of GCV and PCV were observed (44.93 and 45.24) along with high heritability (99%) and GAM (91.91%). These results are found to be similar with the earlier obtained by Jahan *et al.* (2014) and Sikarwar *et al.* (2017).

From the above results it was observed that for all the traits, contribution of GCV was higher to the total PCV and less differences between them indicating that they were less responsive to environmental factors for their phenotypic expression. Higher values of GCV and PCV were observed for seed yield per plant followed by silique density, number of seeds per silique, beak length and shoot length. Higher GCV indicated stability in the expression of these traits and better transmissibility of the traits from parents to the progeny. Moderate values of GCV and PCV were obtained for number of silique per plant, plant height and silique length. High heritability coupled with high genetic advance as percent of mean was observed for all the traits under study indicated the predominance of additive gene action in the inheritance of these traits. Therefore, selection would be effective for the improvement of these traits in following generations.

Conclusion

The results of the study indicated higher values of both GCV and PCV for seed yield per plant followed by silique density, number of seeds per silique, beak length and shoot length. Higher values of PCV indicated higher variability was present among germplasm accessions and higher GCV indicated that large amount of this variability was due to its genotype and these traits were less influenced by the environment. High heritability coupled with high genetic advance as percent of mean was recorded for all the traits studied indicated that additive gene action was involved in the inheritance of these traits. Therefore, selection for these yield contributing traits would be effective for the improvement of seed yield per plant in following generations.

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