Genetic variability studies of germplasm accessions in Indian mustard under protected and unprotected conditions at Bijapur, Karnataka

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ABSTRACT

At Regional Agricultural Research Station (RARS), Bijapur, 118 germplasm accessions from three years (2004-2006) study 46 Indian mustard genotypes were found promising. These promising genotypes were further tested vigorously with a view to identify best performing genotypes for this region especially from released varieties belonging to NRCRM, Bharatpur. An experiment comprising of 46 germplasm accessions was laid out in RBD with two replications separately under protected (against pests and diseases) and unprotected conditions under rainfed condition at RARS, Bijapur during *Rabi* season of 2007. Observations were recorded for 14 traits including aphid and powdery mildew reaction. The genetic variability parameters were computed. Seed yield per meter and seed yield per plant showed higher phenotypic and genotypic coefficient of variability in both conditions followed by biological yield per plant. Heritability and genetic advances were higher for seed yield per meter followed by number of siliquae per plant in both conditions.

Key words : Indian mustard, Variability, Heritability, Germplasm, Resistance

INTRODUCTION

Indian mustard [*B. juncea* (Linn) Czern and Coss] popularly known as rai, raya or laha is one of the most important oil seed crops of the country and it occupies considerably large acerage among the *Brassica* group of oil seed crops. India stands first both in acerage and production of rapeseed and mustard in Asia. The crops are cultivated in an area of 70 lakh ha with a production of 81 lakh tonnes and with an average yield of 1149 kg/ha (Anonymous, 2006). In India, mustard and rape seed are being grown largely in states like, Uttar Pradesh, Rajasthan, Haryana, Assam, Gujarat, Punjab, West Bengal and Madhya Pradesh. However, in Karnataka state, it is grown sporadically as a mixed crop in less acerage with mainly growing local varieties.

However, seed yield, a complex character is usually controlled by non-additive gene actions and it is not only influenced by a number of other morphological characters which are governed by a large numbers of genes, but also environment to a great extent. Thereby, the heritable variation creates difficulty in a selection programme. Therefore, it is necessary for the partition of overall variability into heritable and non-heritable components which enables the breeders to adopt suitable breeding procedure for further improvement of genetic stocks.

At Regional Agricultural Research Station, Bijapur,

out of 118 germplasm accessions from three years study, (2004-2006), 46 Indian mustard genotypes were found promising. These promising genotypes were further tested vigorously under protected and unprotected conditions separately with view of to identify best performing genotypes for this region especially varieties from NRCRM, Bharatpur, which were popular recently.

A comprehensive knowledge of genetic parameters with pathological and entomology aspects is indispensable for this region in a mustard improvement programme. The amount of work done on the genetic variability in some of the important quantitative and qualitative characters and breeding for improvement in rapeseed and mustard is very rare in southern parts of India. The present study was, therefore, envisaged with the objectives, to study the genetic variability the performance of different mustard germplasm accessions for yield, yield components and diseases and pests resistance under protected and unprotected condition of Bijapur district.

MATERIALS AND METHODS

An experiment comprising of 46 germplasm lines in Indian mustard received from NRCRM, Bharatpur was laid out in a Randomized Block Design with two replications separately under protected and unprotected conditions. Both the experiments were conducted under

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rainfed situations at Regional Agricultural Research Station, Bijapur during *Rabi* season 2007-08. The lines were sown in two rows each of 5.0 m length with spacing of 45 cm between rows and 15 cm between the plants. For protected condition, plant protection chemicals against diseases and pest were used as per recommendations while for unprotected conditions, plant protection chemicals were not used in spite of incidence of pest and diseases. Other package of practices were similarly to both the conditions.

Observations were recorded on five randomly selected plants for different characters *viz.,* days to maturity, plant height (cm), number of primary branches per plant, number of secondary branches per plant, number of siliquae per plant, number of seeds per siliqua, 1000-seed weight (g), oil content (%), seed yield per plant (g) biological yield per plant (g), harvest index (%), seed yield per meter (g) in each genotype and replication.

Range, mean, genotypic and phenotypic coefficient of variance were computed using standard statistical methods (Burton and Devane, 1953) whereas, heritability in broad sense and genetic advance was estimated by following method adopted by Johnson *et al.* (1955) and Allard (1960), respectively. The scoring for aphid resistance was done as proposed by Bakhetia and Sandhu (1973). Data on the powdery mildew disease severity was assessed on five plants of each genotype per replication using 0-9 scale as given by Mayee and Datar (1986).

RESULTS AND DISCUSSION

In the present investigation, the phenotypic and genotypic coefficients of variation were the highest for seed yield per metre followed by seed yield per plant,

number of secondary branches per plant, biological yield per plant, number of primary branches per plant in protected conditions (Table 1). Similarly, under unprotected conditions (Table 2) the phenotypic and genotypic coefficients of variation were highest for seed yield per meter followed by seed yield per plant, biological yield per plant, number of secondary branches per plant (Table 2). Similar results were also obtained by Singh *et al.* (1991) and Gupta *et al.* (1991) in Gobhi Sarson.

The observations indicated that substantial variability existed for these characters *viz.,* seed yield per metre, seed yield per plant, number of secondary branches per plant, biological yield per plant, number of primary branches per plant for both protected and unprotected conditions. Moderate values of PCV and GCV were observed for number of siliquae per plant, number of seeds per siliqua for protected condition. In unprotected condition also these characters exhibited moderate values of PCV and GCV. These coefficient values also indicated considerable amount of variability for these characters. Narrow differences between PCV and GCV suggested negligible influence of extraneous factors which were recorded for seed yield per meter, number of siliquae per plant, number of seeds per siliqua for both conditions. In general, phenotypic coefficient of variation was higher than genotypic coefficient of variation. It indicated the influence of environment for all the traits under study. Similar results were obtained by Kumar and Mishra (2006).

The coefficient of variation indicates only the extent of variability present for different characters and do not indicate the heritable portion. To obtain heritable portion of variability, it is essential to know the heritability estimates for different characters. The heritability estimates

Table 1 : Estimates of variability parameters for different quantitative traits in mustard under protected condition								
Sr. No.	Traits	Mean	Range	PCV	GCV	h² (%)	GA	GAM
1.	Days to maturity	107.54	103-112	3.20	3.15	96.80	6.87	6.38
2.	Plant height (cm)	117.15	112.18-122.1	3.29	1.19	13.00	1.03	0.87
3.	No. of primary branches/plant	5.51	4.0-7.7	22.55	12.07	28.60	0.73	13.24
4.	No. of secondary branches/plant	9.59	7.1-14.9	24.91	16.84	45.70	2.25	23.46
5.	No. of siliquae/plant	169.06	135.2-242.3	17.53	16.80	91.80	56.06	33.15
6.	No. of seeds/siliqua	10.97	8.2-13.7	15.99	13.38	70.10	2.53	23.06
7.	1000-seed weight (g)	3.50	2.92-4.11	10.30	7.39	51.50	0.38	10.85
8.	Oil content (%)	44.20	39.4-45.75	2.84	2.75	94.10	2.43	5.49
9.	Seed yield/plant (g)	6.02	3.71-9.19	31.29	24.05	59.10	2.29	38.03
10.	Biological yield/plant (g)	12.89	8.78-17.82	23.90	17.81	55.50	3.52	27.30
11.	Harvest index (%)	46.04	40.47-52.05	8.91	5.46	37.50	3.17	6.88
12.	Seed yield/metre (g)	31.51	18.55-50.05	31.60	29.74	88.60	18.17	57.66

separate the environmental influence from the total variability and indicate the accuracy with which a genotype can be identified by its phenotypic performance, thus making the selection more effective. As such the heritability in broad sense is the proportion of genotypic variability to the total variability, its importance has been emphasized by Lush (1949) in animals.

High heritability estimates were recorded for seed yield per meter, oil content, number of siliquae per plant, number of seeds per siliqua, days to maturity in protected condition, while under unprotected condition, high heritability was observed for days to maturity, seed yield per meter, oil content, number of siliquae per plant, biological yield per plant, seed yield per plant, number of seeds per siliqua and harvest index. Similar observations were also made by Singh (2004).

Moderate heritability values were observed for number of secondary branches per plant, 1000 seed weight, seed yield per plant, harvest index and biological yield per plant for protected condition. In unprotected condition moderate heritability values were observed for plant height, number of secondary branches per plant and 1000-seed weight. These results were in accordance with the results of Nagaraja (1990).

Singh *et al.* (1987) recorded low and medium heritability for number of primary branches per plant, plant height as similarly revealed from present study under protected condition and only number of primary branches per plant for unprotected condition. However, in contrast Narendrakumar *et al.* (1988) observed high heritability for all the traits except seed yield.

Heritability estimates in broad sense alone is not a true indicator of effectiveness of selection for the trait since their scope is restricted by their interaction with the environment (Johnson *et al.*, 1955). Hence, heritability values considered along with the predicted genetic gain increases the reliability of these parameters as a tool in selection programme.

High heritability was coupled with high genetic advance for number of siliquae per plant, seed yield per meter and number of seeds per siliqua under protected condition, while under unprotected condition, it was observed for number of siliquae per plant, seed yield per plant, seed yield per meter and number of seeds per siliqua, This implied that, these traits were not much influenced by environmental factors which in turn indicated that these traits are mostly controlled by additive and /or additive × additive gene interactions and is expected to respond to direct selection for improvement. These observations were in accordance with the results of Somu (2001) and Singh (2004). In contrast, Diwakar and Singh (1993) reported for high heritability with high genetic advance of days to flowering and plant height.

In contrast, Ghosh and Gulati (2001) observed that high heritability coupled with high genetic advance for oil content, harvest index, number of primary branches, number of siliquae on main shoot, main shoot length and number of seeds per siliqua and also Singh *et al.* (2003) reported high heritability coupled with high genetic advance was observed for days to flowering followed by 1000 seed weight, days to maturity and plant height.

Moderate heritability with moderate genetic gain was observed for number of secondary branches per plant, 1000-seed weight, seed yield per plant and biological yield per plant in protected conditions. While under unprotected condition, it was observed for number of secondary branches per plant and 1000-seed weight, hence these are conditioned by additive and non-additive gene

Table 2 : Estimates of variability parameters for different quantitative traits in mustard under unprotected condition

Sr. No.	Traits	Mean	Range	PCV	GCV	h² (%)	GA	GAM
1.	Days to maturity	108.51	104-113	3.15	3.09	96.5	6.79	6.25
2.	Plant height (cm)	114.19	108.5-121.4	2.82	1.72	36.9	2.41	2.11
3.	No. of primary branches/plant	5.21	3.7-6.8	22.59	12.22	29.3	0.71	13.62
4.	No. of secondary branches/plant	9.29	7.2-14.6	25.86	17.55	46.0	2.28	24.54
5.	No. of siliquae/plant	156.30	124.2-221.8	18.30	17.29	89.3	52.62	33.66
6.	No. of seeds/siliqua	10.57	7.8-13.3	16.62	13.89	69.8	2.53	23.93
7.	1000-seed weight (g)	3.49	2.89-4.08	10.09	7.28	52.1	0.38	10.88
8.	Oil content (%)	44.07	39.15-45.4	3.07	2.95	92.4	2.58	5.85
9.	Seed yield/plant (g)	4.52	2.21-7.69	39.90	34.09	73.0	2.72	60.17
10.	Biological yield/plant (g)	10.33	5.3-16.32	35.66	31.70	79.0	6.00	58.08
11.	Harvest index (%)	43.35	40.68-48.35	6.19	2.74	60.5	3.67	8.46
12.	Seed yield/metre (g)	24.12	11.50-42.36	39.81	38.40	93.0	18.40	76.28

components and selection based on phenotypic observations alone may not be very effective for these traits. High heritability values associated with moderate values of genetic gain was observed for number of seeds per siliqua for both protected and unprotected conditions.

Panse and Kharagonkar (1957) suggested that, if the heritability of a particular character is high in a specific environment coupled with low genetic advance, then it could be mainly due to non-additive gene action. Similarly in the present study, days to maturity and oil content showed high heritability coupled with low genetic advance in both conditions. This indicated lower proportion of genetic components in the total variability and suggested that these characters are controlled by non-additive gene components. Hence, direct selection based on phenotypic observations may not be effective for their improvement. The observations are also in accordance with the result of Somu (2001).

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