International Journal of Chemical Studies

Joohi Ray
Department of Genetics and
Plant Breeding SMM Town PG
College, Ballia, Uttar Pradesh,
India

OP Singh
Department of Genetics and
Plant Breeding SMM Town PG
College, Ballia, Uttar Pradesh,
India

VN Pathak
Department of Genetics and
Plant Breeding SMM Town PG
College, Ballia, Uttar Pradesh,
India

Samar Pratap Verma
Department of Genetics and
Plant Breeding SMM Town PG
College, Ballia, Uttar Pradesh,
India

Assessment of genetic variability, heritability, genetic advance and selection indices for yield contributing traits in Indian mustard [*Brassica juncea*]

Joohi Ray, OP Singh, VN Pathak and Samar Pratap Verma

Abstract
Nineteen genotypes of Indian mustard were evaluated at agricultural research farm Nidharia of S.M.M. Town Post Graduate College, Ballia during *Rabi* 2017-2018 in a randomized block design (RBD) with three replication to study of genetic variability, heritability, genetic advance and selection indices. The data was recorded on five randomly selected plants for 12 characters. Analysis of variance (ANOVA) express significant for all characters except siliqua length and volumetric seed weight. The highest mean was observed for number of siliqua per plant followed by plant height and days to maturity. Highest genotypic and phenotypic coefficient of variation was recorded for number of secondary branches, number of siliqua per plant and seed yield per plant. High heritability coupled with high genetic advance for number of secondary branches, number of siliquae per plant, seed yield per plant and biological yield. Sixty-three selection indices involving seed yield and five yield components *viz;* days to 50%flowering, plant height, number of siliqua per plant, biological yield per plant and harvest index were constructed using the discriminant function technique. The single character without any combination had highest genetic advance as well as relative efficiency for number of siliquae per plant. The index based on five characters *viz*; seed yield per plant, plant height, number of siliquae per plant, biological yield per plant and harvest index revealed the highest genetic advance as well as a relative efficiency.

Keywords: mustard *Brasica Juncea* genetic var. heritability and selection indices

Introduction
Rapeseed mustard is second most important oil seed crops of our country. Mustard is a member of family *Brassiceae,* amphidiploid, chromosome number 36. Presently rapeseed mustard covers 35.44 million ha. With production and productivity of 73.95 mitric tones and 2.09 tones/ha. respectively. In India, the total cultivated area of repeseed-mustard 6.50 million ha. with the production 5.70 metric tons and productivity 1 tone/ha. The important state of India producing rapeseed and mustard are Rajasthan, Haryana, Madhya Pradesh, Uttar Pradesh and West Bengal. *Brassica* is high in dry matter digestibility @ 85 to 95% which contrasts with good alfalfa, @ 70%. Its leaves contain 18 to 25% crude protein, while the root contains about 10% crude protein. Due to their rich nutritional contents, these leaf and root crops have been commonly grown as nutritional fodder for sheep and cattle. It also improves the fertility of the soil and allow farmers to increase their grazing season. It provides good soil cover over winter to prevent soil erosion, produces large amounts of biomass, suppresses weeds and can improve soil tilth with its root system.

Material and Method
The experimental consisting 18 genotypes and one check i.e, total 19 treatment were sown in randomized block design with three replications. The genotypes was sown with spacing 0.4 m row to row and 0.3m. plant to plant distance. The soil type of experimental site was sandy loam (pH= 8.6) EC=1.009 rich in potash and low organic carbon, nitrogen and phosphorus. Five competitive plants from each plot were randomly selected for recording observations for all the quantitative characters except days to flowering and maturity, which was recorded on the plot basis. The data were recorded for the following characters; days to 50% flowering, days to maturity, plant height (cm), number of primary branches, number of secondary branches, number of siliquae per plant, siliquae length, number of seed per siliqua, biological

Correspondence
Samar Pratap Verma
Department of Genetics and
Plant Breeding SMM Town PG
College, Ballia, Uttar Pradesh,
India

Yield per plant, volumetric seed weight and harvest index. The analysis of variance and covariance's for different characters were computed according to Panse and shukhatme (1961) [7].The genotypic and phenotypic co-efficient of variation calculated with the help of formula suggested by Burton (1952) [3]. Heritability (broad sense) and expected genetic advance were estimated as suggested by Allard (1960) and selection indices were constructed using method developed by Smith (1936) [9] based on discriminate function of Fisher (1936) [5].

Result and Discussion

Analysis of variance was carried out for yield contributing characters and presented in Table-1 which showed that treatments differ significantly for all the characters except volumetric seed weight and siliqua length. The mean value of any populations sample provide on idea about the center of variability of any traits. While, the range of traits provides maximum and minimum limits of that variable genotypes. Mean, range, critical differences, coefficient of variation, heritability and genetic advance presented in Table 2. The genotypic and phenotypic coefficient of variation were highest for number of secondary branches per plant (25.71-24.96) followed by number of siliquae per plant (24.16-24.14), seed yield per plant (23.20-22.49) and biological yield per plant (20.51-20.43), while the lower magnitudes were days to 50% flowering (6.19-6.30) and plant height (9.14-9.10). In general noted phenotypic coefficient of variation were higher than genotypic coefficient of variation. The result indicate that breeders have opportunity for selection of desirable plants through the attributes had higher magnitudes of PCV/GCV. A similar results were reported by Kumar et al. (2003) and Bind et al. (2014) [2].

The heritability in broad sense or the degree of genetic determination is the ratio V_g/V_p expresses the extent to which individual phenotypes are determined by their genotype (Falconer, 1985) [4]. Heritability plays a role in an improvement of the crop yield, with the help of heritability estimates we can find out. The fundamental requirement of selection is the heritable variation of genotypes. The characters which are more heritable and yield contributing can ameliorate the yield potential by their few cyclic selection. The present study revealed that estimates of broad sense heritability were high for all the traits. The expected genetic advance is a prediction of breeders that is upto which extant, a character can be improved in coming generation after 9-10% of better heritable individual selection. Heritability estimates together with genetic advance are generally regarded to be more useful in predicting the grain through selection. High heritability coupled with high genetic advance in percent of mean. Where, observed for number of siliqua per plant,

number of secondary branches per plant, biological yield per plant and seeds per siliqua indicate the character were predominantly governed by additive gene action and may be exploited directly in selection. Similer result found Bind et al. (2014) [2] and Akabari and Niranjana (2015) [1].

Total sixty-three selection indices (Table 3) based on six characters constructed in all possible combination revealed that the selection efficiency was higher over straight selection were based on individual component number of siliquae per plant exhibited a genetic advance of 67.70% which was highest than those calculated for other characters including seed yield per plant, suggested that number of siliqua per plant prove to be better index selection based on one character. The selection indices was simultaneously based on discriminate function of two characters eg; number of siliqua per plant (X_4) and biological yield (X_5) recorded highest genetic gain of 73.17%. Similarly The Three characters viz; seed yield per plant (X_1), number of siliqua per plant (X_4) and biological yield per plant (X_5) genetic advance increase to 75.36%. Combination of four characters ie; seed yield per plant (X_1), plant height (X_3), number of siliqua per plant (X_4) and biological yield per plant(X_5) were taken together the genetic advance showed 75.34% which was lesser than combination three (X_1,X_4,X_5).Among The six combination of seed yield per plant (X_1), plant height (X_3), number of siliqua per plant (X_4), biological yield per plant (X_5) and harvest index (X_6) had given maximum genetic advance (76.35%). The six combination of characters viz; seed yield per plant (X_1), days to 50% flowering (X_2), plant height (X_3), number of siliqua per plant (X_4), biological yield per plant (X_5) and harvest index (X_6) showed the highest genetic advance (76.12%) in this combination. The study revealed the index which included more than one character gave high genetic advance suggested the utility of construction of selection indices for effecting simultaneous improvement of several characters. The present study showed the selection indices increased based on increasing the number of characters under selection. Singh et al.1979 [10] and Rao 1974 [8] were given the same opinion that an increase in characters result in an increase in genetic gain and that the selection indices improve the efficiency directly selection yield alone.

Selection efficiency (Table 4) improve with number of characters in combination with yield except combination five (X_1, X_2, X_3, X_4, X_5, X_6). Average selection efficiency (1794.33%) was higher than rest other selection indices (X_1, X_2, X_3, X_4, X_5, X_6) when one character was included in selection function. Similarly the selection efficiency was 1939.37% for two character, 1997.36% for three characters, 1996.79% for four characters, 2023.69% for five characters and 2017.49% for six characters, But character six (2017.49%) was lower than character five (2023.69%).

Table 1: Analysis of variance for 12 characters in Indian mustard

S. No.	Characters/d.f	Source of variation		
		Replication	Treatment	Error
		2	18	36
1	Days to 50% flowering	0.158	40.81**	0.732
2	No of primary branches	0.072	3.144*	0.446
3	No of secondary branches	0.160	33.581**	0.664
4	Plant height (cm)	5.867*	842.202**	2.667
5	No of siliquae per plant	19.383*	13785.065**	9.153
6	Siliqua length (cm)	0.0744	1.167	0.045
7	Days to maturity	0.9123	541.161**	1.542
8	Seeds per siliqua	0.318	12.468**	0.416
9	Biological yield(g)	0.674	558.411**	1.367

10	Test weight (g)	0.424	1.294	0.262
11	Harvest index (%)	0.599	38.065**	1.597
12	Seed yield(g)	0.455	46.459**	0.984

* Significant at 5% probability level ** Significant at 1% probability level

Table 2: Mean, Range, critical difference, phenotypic co-efficient of variation and genotypic co-efficient of variation, heritability and genetic advance of Indian Mustard

Characters	Mean	Range	Critical difference	Phenotypic coefficient of variation	Genotypic coefficient of variation	Heritability h2(b)	Genetic advance	Genetic advance in percentage of mean
Days to 50% flowering	60.63	49.60-66.67	1.41	6.19	6.03	95	7.33	12.09
No of primary branches	7.22	5.00-10.00	1.10	17.22	14.52	71	1.82	25.23
No of secondary branches	13.27	8.73-22.80	1.34	25.71	24.96	94	6.63	49.93
Plant height (cm)	183.86	138.22-223.62	2.70	9.14	9.10	99	34.30	18.65
No of sliquae per plant	280.71	168.33-434.00	5.00	24.16	24.14	100	139.46	49.68
Sliqua length (cm)	5.02	3.54-6.11	0.35	12.88	12.17	89	1.19	23.69
Days to maturity	116.49	105.00-147.33	2.06	11.56	11.51	99	27.51	23.62
Seeds per sliqua	12.79	9.33-17.77	1.06	16.46	15.67	91	3.93	30.73
Biological yield(g)	66.69	43.34-99.29	1.93	20.51	20.43	99	27.97	41.94
Test weight (g)	13.54	12.43-15.33	0.84	5.75	4.33	57	0.91	6.72
Harvest index (%)	26.10	15.86-32.43	2.80	14.21	13.36	88	6.75	25.87
Seed yield(g)	17.32	10.85-25.00	2.20	23.20	22.49	94	7.77	44.89

Table 3: Selection indices of phenotypicaly significant character to the yield

S.N.	Selection index	Discriminant function	Ex. Genetic advance	Relative eff.
1	X_1 seed yield per plant	$0.9390X_1$	3.77	100.00
2	X_2 days to 50% flowering	$0.9481X_2$	3.56	94.33
3	X_3 plant height	$0.9906X_3$	16.65	441.30
4	X_4 number of siliquae per plant	$0.9980X_4$	67.70	1794.33
5	X_5 biological yield per plant	$0.9927X_5$	13.58	359.85
6	X_6 harvest index	$0.8839X_6$	6.75	86.88
7	$X_1.X_2$	$0.9522X_1 +0.9683X_2$	6.01	159.39
8	$X_1.X_3$	$0.9548X_1 +0.9944X_3$	18.29	484.82
9	$X_1.X_4$	$0.9514X_1 +0.9992X_4$	69.44	1840.68
10	$X_1.X_5$	$0.8582X_1 +1.0240X_5$	16.85	446.62
11	$X_1.X_6$	$0.9376X_1 + 0.8287X_6$	5.84	154.87
12	$X_2.X_3$	$0.9658X_2 + 0.9963X_3$	19.51	517.20
13	$X_2.X_4$	$0.9778X_2 + 0.9977X_4$	66.59	1764.89
14	$X_2.X_5$	$0.9454X_2+ 0.9924X_5$	14.02	371.13
15	$X_2.X_6$	$1.0072X_2 +0.8894X_6$	6.06	160.60
16	$X_3.X_4$	$0.9869X_3 + 0.9974X_4$	66.91	1773.50
17	$X_3.X_5$	$0.9918X_3 + 0.9951X_5$	22.82	604.98
18	$X_3.X_6$	$0.9981X_3 + 0.9002X_6$	18.09	479.60
19	$X_4.X_5$	$0.9985X_4 + 0.9877X_5$	73.17	1939.37
20	$X_4.X_6$	$0.9990X_4 + 0.9310X_6$	68.61	1818.41
21	$X_5.X_6$	$0.9871X_5 + 0.8811X_6$	13.28	351.98
22	$X_1.X_2.X_3$	$0.9607X_1 + 0.9790X_2 +0.9977X_3$	21.15	560.65
23	$X_1.X_2.X_4$	$0.9513X_1 + 0.0085X_2 + 0.9995X_4$	68.43	1813.75
24	$X_1.X_2.X_5$	$0.8790X_1 + 0.9889X_2 +1.0213X_5$	17.48	463.23
25	$X_1.X_2.X_6$	$0.9308X_1 + 1.071X_2 + 0.8073X_6$	8.33	220.87
26	$X_1.X_3.X_4$	$0.9842X_1 + 0.9889X_3 +0.9978X_4$	68.99	1828.65
27	$X_1.X_3.X_5$	$0.8752X_1 + 0.9990X_3 + 1.0213X_5$	25.76	682.85
28	$X_1.X_3.X_6$	$0.9336X_1 + 1.0082X_3 +0.8327X_6$	19.85	526.09
29	$X_1.X_4.X_5$	$0.9325X_1 + 0.9994X_4 + 0.9790X_5$	75.36	1997.36
30	$X_1.X_4.X_6$	$0.9118X_1 + 1.0018X_4 + 0.8771X_6$	70.39	1865.84
31	$X_1.X_5.X_6$	$-0.8132X_1 + 1.4623X_5 + 2.0166X_6$	16.89	447.74
32	$X_2.X_3.X_4$	$1.0524X_2 + 0.9793X_3 +0.9981X_4$	66.47	1761.94
33	$X_2.X_3.X_5$	$0.9505X_2 + 1.0002X_3 + 0.9935X_5$	24.98	662.18
34	$X_2.X_3.X_6$	$1.0268X_2 + 0.9939X_3 + 0.9023X_6$	21.08	558.70
35	$X_2.X_4.X_5$	$0.9776X_2 + 0.9932X_4 + 0.9879X_5$	72.14	1912.10
36	$X_2.X_4.X_6$	$1.0356X_2 + 0.9999X_4 +0.9196X_6$	67.61	1792.00
37	$X_2.X_5.X_6$	$1.0050X_2 + 0.9875X_5 +0.8877X_6$	14.21	376.61
38	$X_3.X_4.X_5$	$0.9886X_3 + 0.9976X_4 +0.9919X_5$	72.85	1930.96
39	$X_3.X_4.X_6$	$0.9907X_3 + 0.9918X_4 + 0.9612X_6$	68.12	1805.56
40	$X_3.X_5.X_6$	$1.0003X_3 + 0.9889X_5 +0.8956X_6$	23.50	622.98
41	$X_4.X_5.X_6$	$1.0000X_2 + 0.9818X_5 + 0.9206X_6$	73.88	1958.32
42	$X_1.X_2.X_3.X_4$	$0.9713X_1 +1.0721X_2 +0.9795X_3 +0.9992X_4$	68.64	1819.23

43	$X_1.X_2.X_3.X_5$	$0.8923X_1 + 0.9912X_2 + 0.9998X_3 + 1.0170X_5$	27.86	738.42
44	$X_1.X_2.X_3.X_6$	$0.9368X_1 + 1.0850X_2 + 0.9956X_3 + 0.8178X_6$	22.81	604.51
45	$X_1.X_2.X_4.X_5$	$0.9324X_1 + 1.0132X_2 + 0.9998X_4 + 0.9997X_5$	74.42	1972.54
46	$X_1.X_2.X_4.X_6$	$0.8559X_2 + 1.1829X_2 + 1.0074X_4 + 0.8051X_6$	69.49	1841.92
47	$X_1.X_2.X_5.X_6$	$-1.0015X_1 + 1.0985X_2 + 1.5101X_5 + 2.1050X_6$	17.90	474.37
48	$X_1.X_3.X_4.X_5$	$0.9771X_1 + 0.9909X_3 + 0.9981X_4 + 0.9946X_5$	75.34	1996.79
49	$X_1.X_3.X_4.X_6$	$0.9089X_1 + 1.0060X_3 + 1.0019X_4 + 0.8831X_6$	70.23	1861.48
50	$X_1.X_3.X_5.X_6$	$-1.2504X_1 + 1.0126X_3 + 1.5771X_5 + 2.3070X_6$	26.55	703.68
51	$X_1.X_4.X_5.X_6$	$-0.0904X_1 + 1.0008X_4 + 1.2637X_5 + 1.5632X_6$	76.11	2017.36
52	$X_2.X_3.X_4.X_5$	$1.0368X_2 + 0.9835X_3 + 0.9982X_4 + 0.9916X_5$	72.45	1920.27
53	$X_2.X_3.X_4.X_6$	$1.1157X_2 + 0.9760X_3 + 1.0001X_4 + 0.9285X_6$	67.79	1796.83
54	$X_2.X_3.X_5.X_6$	$1.0082X_2 + 0.9987X_3 + 0.9893X_5 + 0.9031X_6$	25.86	685.53
55	$X_2.X_4.X_5.X_6$	$1.0546X_2 + 1.0017X_4 + 0.9776X_5 + 0.8941X_6$	72.96	1933.75
56	$X_3.X_4.X_5.X_6$	$0.9941X_3 + 0.9989X_4 + 0.9870X_5 + 0.9505X_6$	73.84	1957.09
57	$X_1.X_2.X_3.X_4.X_5$	$0.9504X_1 + 1.0666X_2 + 0.9829X_3 + 0.9995X_4 + 0.9998X_5$	75.01	1988.10
58	$X_1.X_2.X_3.X_4.X_6$	$-0.8762X_1 + 1.2523X_2 + 0.9767X_3 + 1.0070X_4 + 0.8106X_6$	69.98	1854.80
59	$X_1.X_2.X_3.X_5.X_6$	$-1.4083X_1 + 1.1195X_2 + 0.9953X_3 + 1.6205X_5 + 2.3920X_6$	28.82	763.93
60	$X_1.X_2.X_4.X_5.X_6$	$-0.2470X_1 + 1.1845X_2 + 1.0063X_4 + 1.2907X_5 + 1.5589X_6$	75.27	1995.19
61	$X_1.X_3.X_4.X_5.X_6$	$-0.5150X_1 + 1.0074X_3 + 1.0006X_4 + 1.3768X_5 + 1.8545X_6$	76.35	2023.69
62	$X_2.X_3.X_4.X_5.X_6$	$1.1067X_2 + 0.9814X_3 + 1.0010X_4 + 0.9837X_5 + 0.9163X_6$	73.53	1948.96
63	$X_1.X_2.X_3.X_4.X_5.X_6$	$-0.6945X_1 + 1.2521X_2 + 0.9781X_3 + 1.0055X_4 + 1.4165X_5 + 1.8825X_6$	76.12	2017.49

Table 4: Highest selection efficiency with character combination in Indian Mustard

Characters	Selection efficiency
Number of siliquae per plant	1794.33
Number of siliquae per plant + Biological yield	1939.37
Seed yield per plant + Number of siliquae per plant	1840.68
Seed yield per plant + Number of siliquae per plant + Biological yield	1997.36
Number of siliquae per plant + Biological yield + Harvest index	1958.32
Seed yield per plant + Plant height + Number of siliqua per plant + Biological yield	1996.79
Seed yield per plant + days to 50% flowering + Number of siliquae per plant + Biological yield	1972.54
Seed yield per plant + Plant height + Number of siliquae per plant + Biological yield + Harvest index	2023.69
Seed yield per plant + Days to 50% flowering + number of siliquae per plant + Biological yield + Harvest index	1995.19
Seed yield per plant + days to flowering + plant height + number of siliquae per plant + Biological yield + Harvest index	2017.43

Conclusion

Thus it may be concluded that there is sufficient genetic variability for most of the economic traits studied in the above genetic material and a combination of various traits contributes to seed yield. In this study it is find that number of siliqua per plant, number of secondary branches, biological yield per plant and yield per plant showed maximum potential for effectiveness of selection. Because these traits showed high genotypic and phenotypic coefficient of variation, heritability and genetic advance. This would help us in designing the selection methodology which can further be utilized in the breeding programme for improvement of seed yield in Indian mustard. In the present study there was a consistent increase in the relative efficiency of the succeeding index with the simultaneous inclusion of each characters. Therefore, in practice the plant breeders might be interested in maximum gain with minimum number of characters considering the basic philosophy of saving time and labour in selection program.

References
1. Akabari RV, Niranjana M. Genetic variability and trait association studies in Indian mustard. International J. of Agri. Sciences. 2015; 11(1):35-39.
2. Bind Devimani, Dhirendra and Dwivedi VK. Genetic variability and character association in Indian mustard, Agric. Sci. Digest. 2014; 34(3):183-188.
3. Burton. Quantitative inheritance in grasses. Proc. 6th Inst, Grassland Cong. 1952; 1:227-283.
4. Falconer DS. Introduction to quantitative genetics. ELBS Second Ed. Longman Group Ltd., London, P. 1985; 113:281-290.
5. Fisher RA. The use of multiple measurements in taxonomic problems. Ann. Eugen. 1936; 7:179.
6. Kumar Sushil, Chand Pooran, Sirohi Anil, Kumar Virendra, Kumar Pankaj. Studies on relationship among yield components and selection criteria for yield improvement in Indian mustard, Progressive Agri. 2013; 13(1):181-186.
7. Panse VG, Sukhatme PV. Statistical methods for Agriculture works, 2nd Ed., ICAR, New Delhi, 1961.
8. Rao L. Analysis of genetic variability and formulation of selection indices for yield in Soyabean. Mysore J. Agric. Sci. 1974; 8(1):156.
9. Smith HF. A discriminant function for plant selection. Ann. Eugen. 1936; 7:240-250.
10. Singh CB, Dalal MA. Index selection in soyabean. Indian J. Genet. 1979; 39(2):234-236.