Utilization of Genetic Variability for Yield Improvement in Indian mustard (*Brassica Juncea* L.) Under Medium Land Condition

Naresh prasad Yadav[1],* Birendra Kumar[2] and Uday Kumar Singh[3]

[1]PBG, ZRS, Darisai E Singhbhum, Birsa Agricultural University, Kanke, Ranchi, Jharkhand-834006
[2]Department of Agronomy, AICRP on Forage Crops, Birsa Agricultural University, Kanke, Ranchi, Jharkhand-834006
3 Scientist (Agronomy) KVK, Petarwad, Bokaro, Birsa Agricultural University, Kanke, Ranchi, Jharkhand-834006

Abstract
Twelve diverse Indian mustard (*Brassica juncea* L.) genotypes including three commercial check were evaluated in Zonal Research Station, Darisai of Birsa Agricultural University, Ranchi during *rabi* season of 2012-13 for the estimation of genetic variability, heritability and genetic advance for eleven quantitative characters. The genotypes differed significantly for all characters studied. Higher to moderate genotypic and phenotypic coefficient of variation was observed for primary branches/plant, secondary branches/plant, number of siliqua, seeds per siliqua, test weight, seed yield per hectare. Maximum heritability was recorded in siliqua length and test weight. High heritability coupled with high genetic advance was observed in siliqua length and test weight indicated the importance of the traits for yield improvement. Character association indicated that primary branches/plant, secondary branches per plant, number of siliqua and test weight were significant positive correlation with seed yield traits.

Keywords: Genetic variability, Indian mustard, Heritability, Genetic advance and correlation

*Correspondence
Author: Naresh prasad Yadav
Email: npybau3344@gmail.com

Introduction

India is a leading player in edible oils, being the world's largest importer (ahead of the EU and China) and the world's third-largest consumer (after China and the EU). Each year, India consumes over 10 million tonnes of edible oils. Per capita availability of edible oil reached around 11 kg per year during 2008 for which India had to import thousand tons of edible oil from other countries. So, it is imperative to take appropriate measures to increase the domestic production of edible oil for curtailing the import expenses. Among rapeseed and mustard, *raya* (*Brassica. juncea*) is very popular among the farmers due to higher seed yield and better tolerance against lodging, pests and heat. It can be successfully grown from end of August to end of October. Now efforts are underway to develop better *raya* genotypes. Such breeding efforts need critical evaluation of existing genetic variability, heritability, genetic advance and interrelationship between seed yield and agronomic traits. Present investigations were planned to measure extent of genetic variability, heritability and interrelationship of various traits to devise suitable selection criteria for further yield improvement.

Materials and Methods

The experimental materials for the present investigation comprised of twelve diverse genotypes of Indian mustard including the three commercial checks *viz*; Varuna (National check), JD-6 (Zonal check) and Shivani (Local check). The genotypes were of different sources *viz*. Indian Agriculture Research Institute, New Delhi, Chandrasekhar Azad University &Technology (Kanpur) and Birsa Agricultural University (Ranchi). The seeds were sown in randomized block design with three replications at Zonal Research Station, Darisai under Birsa Agricultural University, Ranchi, Jharkhand. There were ten rows of each genotype in a plot with a row spacing of 30 cm. Field and other post sowing operation were carried out as per recommendation. The soil health status was analyzed for availability of major nutrient and it was found that soil is moderately acidic and medium in topography. The nitrogen, sulphur and organic carbon content of the soil were low whereas, content of phosphorus was high and that of potassium is medium.

   Data were recorded on ten randomly selected plants from the rows excluding the border rows for each character under study. The mean ten plants were used for statistical analysis. The following twelve characters were measured during the course of the study: namely plant height (cm), primary branches per plant, secondary branches per plant, 50% flowering, number of siliquae per plant, siliqua length (cm), number of seed per siliqua, days to maturity, 1000

seed weight (g), seed yield per plant (g) seed yield per hectare (q/ha) and oil content (%). Oil content was estimated using a representative sample by Zeltex 800 NIR grain analyzer.

The mean value of each character under study were computed and subjected to analysis of variation. The phenotypic and genotypic variance was calculated as per the method described by [1]. The genotypic (GCV) and phenotypic (PCV) coefficient of variation were estimated according to the procedure outlined by [2]. Broad sense heritability (H^2) and genetic advance expected under selection, assuming the selection intensity of 5% were calculated as suggested by [3]. Heritability and genetic advance value categorized by [4] as low: less than 30%, moderate: 30-60%, high: more than 60% for heritability and low: less than 10%, moderate: 10 - 20%, high: more than 20% for genetic advance as percentage of mean.

Results and Discussion
Comparison of means

In the present study, the mean of all the traits under study are presented in **Table 1** and found a wide range of variation in performance of genotypes for all the traits.

Table 1 Mean performance of twelve genotypes of Indian mustard (*Brassica juncea* L.) under medium land condition

S.N	Genotype	50% flowering	Plant height (cm)	Pri. branch	Sec. branch	Number of siliqua	Siliqua Length (cm)
1	Varuna (NC)	45.00	149.67	4.53	5.00	131.63	4.41
2	BAUSM-92-1-I	39.67	137.67	4.73	5.73	146.40	4.47
3	Sej-2	40.00	142.00	4.67	5.40	138.00	4.42
4	Shivani (LC)	43.33	147.67	4.43	4.60	129.33	4.53
5	BAUSM-92-2-I	40.67	159.00	4.00	4.40	118.67	4.91
6	BAUSM-92-9-I	41.00	142.67	4.53	5.33	134.40	4.40
7	BAUSM-92-3-III	46.00	140.33	5.47	5.73	151.47	4.53
8	BAUSM-92-20-II	44.67	131.67	3.80	3.93	103.33	4.51
9	BAUSM-92-8-I	43.00	127.00	4.53	4.73	131.47	4.53
10	BAUSM-92-6-I	41.00	138.33	4.13	4.43	122.47	5.33
11	Pusa Agrani	33.33	117.00	4.40	4.47	128.27	4.44
12	JD-6 (ZC)	38.33	148.67	3.90	4.27	111.00	4.71
	MIN	33.33	117.00	3.80	3.93	103.33	4.40
	Max	46.00	159.00	5.47	5.73	151.47	5.33
	Mean	41.33	140.14	4.43	4.84	128.87	4.60
S.N	Genotype	Seeds/ siliqua	Days to maturity	Test weight (g)	Seed Yield/ plant (g)	Seed Yield (q/ha)	Oil content (%)
1	Varuna (NC)	12.80	110.00	3.27	10.39	8.97(5th)	38.30
2	BAUSM-92-1-I	12.60	106.00	3.53	11.43	9.47(2nd)	37.96
3	Sej-2	10.53	105.33	3.47	11.22	9.14(3rd)	38.32
4	Shivani (LC)	13.53	113.00	3.17	9.96	7.46	36.29
5	BAUSM-92-2-I	13.73	109.00	3.07	8.55	7.32	37.71
6	BAUSM-92-9-I	13.20	108.67	3.33	10.80	8.99(4th)	35.35
7	BAUSM-92-3-III	12.47	108.00	4.20	12.96	9.94(1st)	37.88
8	BAUSM-92-20-II	9.93	112.00	2.50	7.80	7.20	41.49
9	BAUSM-92-8-I	11.60	117.00	3.23	10.10	7.58	37.18
10	BAUSM-92-6-I	12.47	116.00	3.20	8.60	7.41	38.30
11	Pusa Agrani	12.20	101.00	3.20	9.93	7.40	37.88
12	JD-6 (ZC)	11.07	103.00	2.83	8.17	7.26	37.99
	MIN	9.93	101.00	2.50	7.80	7.20	35.35
	Max	13.73	117.00	4.20	12.96	9.94	41.49
	Mean	12.18	109.10	3.25	9.99	8.18	37.89

*NC- national check, ZC- zonal check and LC- local check

The 50% flowering ranged from 33.33 (Pusa Agrani) to 45.00 (Varuna) with population mean of 41.33, plant height 117.00 (Pusa Agrani) to 159.00 cm (BAUSM-92-2-I) with population mean of 140.14, primary branch 3.80 (BAUSM-92-20-II) to 5.47 (BAUSM-92-3-III) with population mean of 4.43, secondary branch 3.93 (BAUSM-92-

20-II) to 5.73 (BAUSM-92-3-III) with population mean of 4.84, number of siliqua 103.33 (BAUSM-92-20-II) to 151.47 (BAUSM-92-3-III) with population mean of 128.87, siliqua length 4.40 cm (BAUSM-92-9-I) to 5.33 cm (BAUSM-92-6-I) with population mean of 4.60, seeds per siliqua 9.93(BAUSM-92-2-II) to 13.73 (BAUSM-92-2-I) with population mean of 12.18, days to maturity 101.00 DAS (Pusa Agrani) to 117.00 DAS (BAUSM-92-8-I) with population mean of 109.10, test weight 2.50 g (BAUSM-92-2-II) to 4.20 g (BAUSM-92-3-III) with population mean of 3.25, seed yield per plant 7.80 g (BAUSM-92-2-II) to 12.96 g (BAUSM-92-3-III) with population mean of 9.99, seed yield 7.20 q ha^{-1} (BAUSM-92-2-II) to 9.94 q ha^{-1} (BAUSM-92-3-III) with population mean of 8.18, oil content 35.35 % (BAUSM-92-9-I) to 41.49 % (BAUSM-92-2-II) with population mean of 37.89.

Estimation of component of variance

Analysis of variance for different traits were estimated and it was found that genotypic mean sum of square was highly significant for all the traits suggesting differential performance of genotypes for all the traits (**Table 2**) similar findings was also reported by [5]. The variance component showed a wide range of phenotypic variation for all the characters in twelve genotypes of Indian mustard. Further, phenotypic component of variation (σ^2P) was invariably higher than genotypic component of variation (σ^2G), variation (σ^2e). There were large differences among genotypic and phenotypic variance for almost all the traits indicating the influence of environment. The results obtained are in accordance with the results of [5]. The highest phenotypic variation was observed for number of siliquae [5], while the lowest phenotypic variation was observed in test weight and siliqua length. On the other hand, highest and lowest genotypic variation was recorded in 50 % flowering and seeds siliqua^{-1} respectively. Again the highest and lowest value of environmental variance was observed in number of siliqua and test weight, respectively (**Table 3**).

Table 2 ANOVA for eleven traits of Indian mustard (*Brassica juncea* L.) under medium land condition

S.V	50% flowering	Plant height (cm)	Pri. branch	Sec. branch	Number of siliqua	Siliqua length (cm)	Seeds/ siliqua	Days to maturity	Test weight (g)	Seed Yield/ plant (g)	Seed Yield (q/ha)
Rep	2.33	38.52	0.17	0.46	171.36	0.05	1.74	0.75	0.12	0.60	0.20
Tre	35.81**	374.17**	0.60*	1.06*	562.73**	0.62**	4.18*	71.58**	0.49**	6.93**	3.16**
Err	0.78	23.38	0.23	0.31	181.13	0.10	1.97	1.99	0.10	1.03	0.84
SE (m) ±	0.51	3.09	0.28	0.32	7.77	0.18	0.63	0.81	0.19	0.59	0.53
C. D5%	1.50	8.70	0.83	0.94	22.79	0.54	1.85	2.39	0.56	1.72	1.56
C. V5%	2.15	3.32	11.03	11.53	10.44	6.97	8.99	1.30	10.08	10.19	11.24

Table 3 Analysis of genotypic, phenotypic and environmental variance

Genetic estimates	50% flowering	Plant Height (cm)	Pri. branch	Sec. branch	Number of siliqua	Siliqua length (cm)	Seeds/ siliqua	Days to maturity	Test weight (g)	Seed Yield/ plant (g)	Seed Yield (q/ha)
σ^2_P	1.11	23.69	0.44	0.55	181.36	0.38	2.15	2.31	0.37	1.31	1.08
σ^2_G	0.33	0.31	0.21	0.24	0.23	0.28	0.18	0.32	0.27	0.28	0.24
σ^2_E	0.78	23.38	0.23	0.31	181.13	0.11	1.97	1.99	0.10	1.03	0.84

Being a plant breeder, large genotypic value of any character is always helpful for effective selection. The character test weight and secondary branches plant^{-1} showed highest phenotypic coefficient of variance. Similar results were also reported by [6] and [7], while character days to maturity, showed lowest phenotypic coefficients of variance. The character test weight and number of siliqua showed highest and lowest genotypic coefficients of variance, respectively. Similar finding for test weight was also reported by [8]. The value of environmental coefficients of variance was recorded as the highest and lowest for seeds siliqua^{-1} and days to maturity, respectively (**Table 4**).

Estimate of heritability in broad sense and genetic advance

Genotypic coefficient of variation gives an idea of the quantum of genetic variability in given traits and provides a means to compare the variability in different quantitative characters. But, the same time it is not possible to estimate heritable variation with the help of genetic coefficient of variation alone. That is why [2], advocated that the genetic coefficient of variation together with heritability estimate give a better picture of the amount of advance to be expected by selection. Heritability estimates in the present study materials were generally low in almost all the traits due to larger phenotypic variance indicating great environmental influence (Table 4), the findings are in agreement

with [5], except siliqua length (73.65 %) and test weight (72.63 %) which exhibited higher heritability. Similar finding for test weight was also reported by [8]. Whereas, primary branch (47.19) and secondary branch (43.21) exhibited moderate heritability. The genetic advance measured as percentage of mean was also lower for all the traits except primary branches (14.48) and secondary branches (13.59) which exhibited moderate genetic advance. Whereas, siliqua length (20.32) and test weigh (27.82) exhibited high genetic advance as percentage of mean. (Table 4) [7] reported that, the siliqua length and test weight exhibited high heritability and high genetic advance so it is considered under control of additive genes, which highlights the usefulness of plant selection based on phenotypic performance thus mass selection, will be most suitable for improvement of these traits. Moderate heritability accompanied with low genetic advance as percentage of mean observed for primary branches and secondary branches indicated that non-additive gene effect was important and mass selection on phenotypic value may not be much effective to improve this trait.

Table 4 Estimates of genotypic (GCV) and phenotypic (PCV) coefficients of variance, heritability (H^2) and genetic advance (GA) in percentage

Genetic estimates	50% flowering	Plant height (cm)	Pri. branch	Sec. branch	Number of siliqua	Siliqua length (cm)	Seeds/ siliqua	Days to maturity	Test weight (g)	Seed Yield/ plant (g)	Seed Yield (q/ha)
PCV	2.54	3.47	14.90	15.26	10.45	13.39	12.03	1.39	18.60	11.47	12.73
GCV	1.38	0.40	10.23	10.03	0.37	11.49	3.45	0.52	15.85	5.33	6.05
ECV	2.14	3.45	10.83	11.50	10.44	6.87	11.52	1.29	9.73	10.16	11.20
H	29.48	1.32	47.19	43.21	0.12	73.65	8.21	14.00	72.63	21.60	22.56
GA	0.64	0.13	0.64	0.66	0.03	0.93	0.25	0.44	0.90	0.51	0.48
GA%	1.55	0.09	14.48	13.59	0.03	20.32	2.03	0.40	27.82	5.11	5.92

Table 5 Association study between different quantitative characters of Indian mustard under medium land condition

	50% Flowering	Plant height	Primary branch	Secondary branch	Number Of siliqua	Siliqua Length (cm)	Seeds/ siliqua	Days to maturity	Test Weight (g)	Seed Yield/ Plant (g)	Seed Yield (q/ha)
Days to 50% flowering	1.00										
Plant height	0.35	1.00									
Primary branch	0.27	-0.11	1.00								
Secondary branch	0.17	0.07	0.88**	1.00							
Number of siliqua	0.11	-0.07	0.95**	0.94**	1.00						
Siliqua length (cm)	-0.05	0.24	-0.41	-0.42	-0.36	1.00					
Seeds/siliqua	0.02	0.41	0.24	0.25	0.36	0.17	1.00				
Days to maturity	0.65*	0.05	-0.10	-0.21	-0.13	0.38	0.12	1.00			
Test weight (g)	0.18	0.01	0.96**	0.87**	0.94**	-0.18	0.36	-0.13	1.00		
Seed Yield/plant(g)	0.19	-0.09	0.98**	0.94**	0.97**	-0.51	0.24	-0.19	0.93**	1.00	
Seed Yield (q/ha)	0.30	0.12	0.84**	0.96**	0.85**	-0.46	0.14	-0.23	0.82**	0.90**	1.00

*Significant at 5% and **significant at 1%.

Association study

The correlation coefficient was analyzed for all the quantitative characters under study and presented in **Table 5**. Significant positive correlation was observed in yield traits with primary branches, secondary branches, number of siliqua and test weight. The relationships between yield traits and plant height was found positive but non significant. These results confirm the finding of [9-11]. Similar observation were also reported by [12].

References

[1] Lush, J.L. (1949). Heritability of quantitative characters in farm animals. Proceeding of. International. Congress of. Genetic. Herediates (Suppl.), pp. 356-357.

[2] Burton, G.M. (1952). Quantitative inheritance in grasses. Proc. 6th Ins. Grassland Cong. 1: 277-282.

[3] Allard, R.W. 1960. Principles of Plant Breeding. J Wiley and Sons. Inc. New York and London.

[4] Johnson, H.W., Robison, H.F. and Comstock, R.E. (1995). Estimates of genetic and environmental variability in soybeans. Agronomy Journal. 47: 314-318.

[5]   Ali, N. Javidfar, F. and Attary, A.A. 2002. Genetic variability, correlation and path analysis of yield and its component in winter rapeseed (Brassica napus L.), Pakistan. Journal of. Botany, 34(2):145-150.

[6]   Patel,J. M., Patel, K. M., Patel, C. J. and Prajapeti, K. P. 2006. Genetic parameters and inter-relationship analysis in Indian mustard, (Brassica juncea L.) (Czern and Coss), Journal of Oilseeds Research. 23: 159-160.

[7]   Dar,Z.A., Wani, S. A., Zaffar,G., Habib,M., Wani, M.A., Ishfaq,A., Khan,M.H. and Razvi, S.M. 2010. Variability Studies in Brown sarson (Brassica rapa L.), Research Journal of Agricultural Sciences., 1(3): 273-274.

[8]   Akbar, M., Saleem, U., Tahira., Yaqub,M. and Iqbal, N. 2007. Utilization of genetic variability, correlation and path analysis for seed yield improvement in mustard, (Brassica juncea), Journal of Agricultural. Research. 45(1).

[9]   Singh, D.P. 1974. Correlation in India Colza. Indian Journal of Agricultural Science, 44(3): 142-144.

[10] Özer, H., E, Oral and Doğru,U. 1999. Relationships between yield and yield components on currently improved spring rapeseed cultivars. Tr. Journal.of Agriculture and Forestry, 23: 603-609.

[11] Çalışkan, M.E., Mert,A., Mert,M and İşler,N. 1998. Important agronomic characters of some rapeseed cultivars and effects of these characters on yield formation in Hatay ecological conditions, Journal of Agricultural Faculty MKU., 3(2): 127-142

[12] Algan, N. and Aygün,H. 2001.Correlation between yield and yield components in some winter rape genotypes (In Turkish). The journal of Ege University, Agricultural Faculty, 38(1): 9-15.