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Assessment of genetic variability, heritability and genetic advance in Indian mustard (*Brassica juncea* L.)

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Abstract

Forty-five genotypes of Indian mustard (*Brassica juncea* L.) were evaluated during *rabi* 2021-22 under four environments created through different dates of sowing (timely sown 20 Oct. and late sown 20 Nov.) and row to row spacing (normal 30 × 10 cm and reduced 20 × 10 cm) *i.e*. timely sown, normal spacing (E_1), timely sown, reduced spacing (E_2), late sown, normal spacing (E_3), late sown, reduced spacing (E_4). Pooled analysis of variance revealed significant differences among genotypes, environments and G × E for all the traits. Therefore, analysis of variance carried out separately for each environment which indicated significant difference among all the genotypes for 14 traits under all environments. The variability studies showed high phenotypic (PCV) and genotypic (GCV) coefficient of variation for number of siliquae per plant, seed yield per plant and first branch initiation height in all the environments (except in E_4 for first branch initiation height), whereas, moderate GCV and PCV were recorded for plant height, primary branches per plant, 1000-seed weight, number of seeds per siliqua and harvest index in all the environments. Estimate of high heritability along with high genetic advance as per cent of mean were observed for number of siliquae per plant, seed yield per plant, first branch initiation height, plant height, number of primary branches per plant, 1000-seed weight, number of seeds per siliqua and harvest index in all the environments. Likewise, siliqua length had high heritability along with moderate genetic advance as per cent of mean considered for all the four environments. Thus, these characters might be under the control of additive gene action and direct selection based on these traits could be advantageous.

Keywords: *Genetic advance, genetic variability, heritability, Indian mustard*

Introduction

Oilseed crops are one of the most important crops in the world. These crops occupy prime importance in Indian economy, which is evident from the impact created by yellow revolution. Mustard is grown in diverse agro-climatic conditions ranging from North-Eastern/North-Western hills to down South under irrigated/rainfed, timely/late-sown, saline soils and mixed cropping. Rapeseed-mustard crops fit well in the rainfed cropping system of resource-poor farmers because of their low water requirement. India is the third largest oilseed economy after Canada and China in the world. In India mainly seven oilseed crops are grown among which rapeseed-mustard accounts nearly one-third of total oilseed production in India (Singh and Bansal, 2020) and ranks second after groundnut. In India, Rajasthan occupies first position in area 3.59 mha and production 6.19 mt with the productivity of 1724 kg/ha (Anonymous, 2022). The existence of genetic variability for selection of superior genotype is a basic requirement for any crop improvement programme (Lakra *et al*., 2020). For the success of the crop improvement programme, the characters for which variability is present, it should be highly heritable as progress due to selection depends on heritability, selection intensity and genetic advance of the character. Heritability and genetic advance estimates for different targeted traits help the breeder to apply appropriate breeding methodology in the crop improvement programme. Hence, the present study planned to assess the variability, heritability and genetic advance for yield and other characters in different environments.

Materials and Methods

The experiment was conducted at the Instructional Farm, Collage of Agriculture, Jodhpur during *rabi* 2021-22 in four environments created through different dates of sowing (timely sown 20 Oct. and late sown 20 Nov.) and row to row spacing (normal 30 × 10 cm and reduced 20 × 10 cm) *i.e.* normal sown and normal spacing (E_1), normal sown and reduced spacing (E_2), late sown and normal spacing (E_3), late sown and reduced spacing (E_4). The materials for present study comprised 45 genotypes of Indian mustard (*Brassica juncea* L.), among which 35 genotypes namely TM 301-1, TM 301-2, TM 301-3, TM 302, TM 303-1, TM 303-2, TM 303-3, TM 304-1, TM 304-2, TM 305-1, TM 305-2, TM 306-1, TM 306-2, TM 307-1, TM 307-2, TM 308-1, TM 308-2, TM 308-3, TM 309-1, TM 309-2, TM 309-3, TM 310-1, TM 310-2, TM 310-3, TM 311, TM 312-1, TM 312-2, TM 313, TM 314-1, TM 314-2, TM 315-1, TM 315-2, TM 316, TM 317-1 and TM 317-2, were short heighted (obtained from BARC, Trombay) and ten were released varieties *viz.* PM 25, PM 26, PM 31, JD 6, GDM 4, Navgold, Bio 902, Kranti, NRCHB 101 and RH 0749 which were sown in randomized block design with two replications. Each replication consisted two rows of four meter length in normal spacing conditions and three row of same length in case of reduced spacingwith a plot size of 0.6 × 4 m^2. The observations were recorded on fourteen traits, *viz*. days to 50% flowering, days to maturity, plant height (cm), first branch initiation height (cm), number of primary branches per plant, siliqua density of main shoot (%), number of siliquae per plant, siliqua length (cm), number of seeds per siliqua, 1000-seed weight (g), seed yield per plant (g), harvest index (%) and oil content (%). Except days to 50% flowering and days to maturity where, data were recorded on whole plot basis, data on rest of the morphological traits was recorded on randomly selected five competitive plants. The data were subjected to analysis of variance as per the procedure suggested by Panse and Sukhatme (1985), genotypic and phenotypic coefficient of variation (Burton and de vane, 1953), heritability in broad sense (Johnson *et al*., 1955) and genetic advance as percent of mean (Johnson *et al*., 1955).

Results and Discussion

Pooled analysis of variance over the four environments was carried out in order to verify presence of G × E interactions. G × E interaction variance was significant for all the observed parameters. Variance due to genotype and environments was also significant for all the observed parameters. These results indicated presence of substantial amount of G × E interaction (Table 1). Therefore, analysis of variance was carried out environment wise which revealed significant variance due to genotypes for all the characters indicating the presence of ample amount of variability in the genotypes (Table 2). These results are in the conformity with the earlier findings of Singh *et al.* (2022), Chaurasiya *et al.* (2019) and Meena *et al.* (2017).

Comparative study of different environments depicted that mean values in E_3 and E_4 were lower in relation to E_1 and E_2 for all the traits except siliqua density of main shoot indicated that delay in sowing date had adverse effect on the performance of genotypes for most of the traits. Further it was also observed that E_2 had higher mean in comparison to E_1 for plant height, first branch initiation height, number of siliquae per plant, number of seeds per siliqua 1000-seed weight and seed yield per plant whereas, E_4 in comparison to E_3 had similar trend for days to maturity, plant height, siliqua density of main

Table 1: Pooled analysis of variance for seed yield and its ancillary traits in mustard

Characters	Environment (df= 3)	Rep/Env (df= 4)	Genotype (df= 44)	G×E (df= 132)	Pooled error (df= 176)
Days to 50% flowering	813.7**	2.1	55.1**	4.5*	3.2
Days to maturity	2207.9**	4.7	33.6**	10.1**	5.2
Plant height (cm)	5513.6**	49.4	2918.9**	85.7**	51.4
First branch initiation height (cm)	173.1**	8.8	134.5**	34.8**	3.9
Primary branches per plant	1.7**	0.2	2.4**	0.4**	0.1
Siliqua density of main shoot (%)	390.7**	26.1	161.1**	31.6**	13.8
Siliquae per plant	4299.7**	54.8	12218.2**	198.4**	98.9
Siliqua length (cm)	1.7**	0.6	15.1**	1.7**	0.3
Seeds per siliqua	5.6**	0.1	3.4**	0.2**	0.1
1000-seed weight (g)	81.6**	1.3	62.6**	3.2**	0.6
Seed yield per plant (g)	68.2**	2.1	40.5**	22.8**	2.5
Harvest index (%)	77.2**	0.9	13.8**	0.6*	0.5
Oil content (%)	0.3**	0.1	1.3**	0.1**	0.04

*Significant at p = 0.05, **significant at p = 0.01

Table 2: Environment wise analysis of variance for seed yield and its ancillary traits in mustard

Characters	Environments											
	E_1			E_2			E_3			E_4		
	Rep. (df = 1)	Geno. (df= 44)	Error (df= 44)	Rep. (df = 1)	Geno. (df= 44)	Error (df= 44)	Rep. (df = 1)	Geno. (df= 44)	Error (df= 44)	Rep. (df = 1)	Geno. (df= 44)	Error (df= 44)
Days to 50% flowering	1.3	25.9**	4.0	2.2	16.2**	3.4	2.8	18.9**	3.1	1.9	7.7**	2.2
Days to maturity	8.1	16.8**	6.4	1.3	14.4**	6.4	5.9	18.1**	4.2	3.6	14.7**	3.9
Plant height (cm)	16.5	1014.3**	56.4	90.5	745.4**	70.3	3.2	726.7**	41.2	87.5	689.7**	37.7
First branch initiation height (cm)	9.5	59.1**	4.3	17.7	74.7**	4.5	7.3	71.5**	4.6	0.7	33.7**	2.5
Primary branches per plant	0.2	1.1**	0.1	0.3	1.0**	0.1	0.1	0.7**	0.1	0.2	0.7**	0.1
Siliqua density of main shoot (%)	57.6	98.4**	17.9	23.1	64.6**	13.9	11.1	57.8**	14.1	12.5	35.1**	9.3
Siliquae per plant	36.4	4589.8**	113.3	50.9	3169.2**	107.4	106.0	2788.2**	91.0	27	2264.8**	83.8
Siliqua length (cm)	0.12	0.4**	0.04	0.04	0.3**	0.03	0.1	0.4**	0.04	0.1	0.5**	0.04
Seeds per siliqua	0.4	5.2**	0.3	1.1	5.9**	0.3	0.2	4.5**	0.3	0.7	4.7**	0.3
1000-seed weight (g)	0.2	1.0**	0.1	0.1	1.1**	0.1	0.03	1.0**	0.04	0.1	0.9**	0.03
Seed yield per plant (g)	1.5	28.7**	0.6	0.9	14.8**	0.7	1.1	15.8**	0.6	1.7	12.9**	0.5
Harvest index (%)	1.9	24.5**	2.8	2.1	25.4**	2.3	2.1	35.5**	2.5	2.1	23.4**	2.3
Oil content (%)	0.2	2.9**	0.5	0.6	2.5**	0.7	0.5	2.2**	0.4	0.4	2.7*	0.46

*Significant at p = 0.05, **Significant at p = 0.01

Table 3: Range and mean performance for seed yield and its ancillary traits in different environments

Characters	Range				Mean			
	E_1	E_2	E_3	E_4	E_1	E_2	E_3	E_4
Days to 50 % flowering	32-48	33-46	26-42	27-36	39	38	34	33
Days to maturity	118-130	117-130	108-124	109-126	124	123	114	115
Plant height (cm)	70-171	80.6-167.6	60.2-158	63.2-169.6	104.7	115.5	97.4	101.9
First branch initiation height (cm)	13.6-40.6	12.2-40.8	13.8-46	16-40.2	24.3	25.4	24.1	22.1
Number of primary branches per plant	2.6-7.2	3-7.2	3-7.2	3-6.2	4.3	4.1	4.1	4.0
Silique density of main shoot (%)	45.2-78.5	47.6-76.9	50.7-77.2	54.1-75.4	60.7	58.9	62.2	63.8
Number of siliquae per plant	96-301	101-272	101-254	97.5-237	150.4	154.7	143.6	139.2
Silique length (cm)	3.5-6.1	3.6-5.9	3.2-5.9	3.28-6	4.7	4.7	4.6	4.6
Number of seeds per siliqua	8.5-18.2	9.7-17.2	8.5-17.1	8.5-17.1	13.3	13.4	13.2	13.1
1000-seed weight (g)	3.1-6.9	3.4-6.9	3.3-6.3	3.4-6.2	5.1	5.1	4.6	4.7
Seed yield per plant (g)	7.2-21.3	8.4-19.2	6.8-18	6.1-15.8	12.0	13.00	11.3	10.7
Harvest index (%)	22.2-42.8	21.9-38.5	20.4-38.1	19.1-36.3	28.9	27.7	28.8	27.2
Oil content (%)	37.2-43.5	37.2-44.5	36-41.25	35.25-43.0	40.1	40.0	38.7	38.5

shoot and 1000- seed weight (Table 3). These results indicated that reduced spacing in short heighted genotypes is more advantageous. The mean oil content was almost same across the environments indicating that this character was least influenced by environmental fluctuations.

Comparison of range over environments for all the traits indicated that E_1 was most favourable for the expression of traits *viz*. days to 50% flowering, number of primary branches per plant, siliqua density of main shoot, number of siliquae per plant, number of seeds per siliqua, 1000-seed weight, seed yield per plant and harvest index which revealed that these traits had higher range in this environment. Similarly, E_3 was favourable for expression of first branch initiation height, siliqua length, number of seeds per siliqua and harvest index and E_4 had wider range for the traits days to maturity, plant height and oil content (Table 3). Conclusively it can be advocated that to obtain clear-cut discrimination in screening of mustard genotypes for different traits should be carried out under timely sown, normal spacing (E_1) conditions.

Further, phenotypic coefficient of variation was higher than genotypic coefficient of variation for all the observed characters in all the environments. There was less difference between PCV and GCV which indicated less influence of environment on the expression of trait. High PCV and GCV were observed for number of siliquae per plant, seed yield per plant and first branch initiation height (except in E_4 for first branch initiation height) in all the four environments (Table 4). Similar findings pertaining to presence of high genetic variability were reported by Yadav *et al*. (2011) for first branch initiation height, Rai *et al*. (2017) for seed yield per plant and siliquae per plant, whereas, moderate GCV and PCV were recorded for plant height, primary branches per plant, 1000-seed weight, number of seeds per siliqua and harvest index. Similar findings have also been reported by Tripathi *et al*. (2019) for number of primary branches per plant and number of seeds per siliqua, Synrem *et al*. (2014) for number of seeds per siliqua, Gadi *et al*. (2020) for 1000-seed weight, Kumar *et al*. (2019) and Ray *et al*. (2019) for harvest index. Results revealed presence of high amount of genetic variability in the evaluated genotypes for the major yield contributing characters along with seed yield which indicated that further improvement for these traits is possible. Likewise, lower GCV and PCV were recorded for silique density of main shoot, siliqua length, days to 50 per cent flowering, oil content and days to maturity in all the four environments indicated lower genetic variations for these traits (Table 4). These results are in agreement with the finding of Tripathi *et al*. (2019) for

Table 4: Genotypic and phenotypic coefficient of variation, heritability and genetic advance as percent of mean for seed yield and its ancillary traits in different environments

Characters	Genotypic coefficient of variation (%)				Phenotypic coefficient of variation (%)				Heritability (bs) %				Genetic Advance as percent of mean 5%			
	E_1	E_2	E_3	E_4	E_1	E_2	E_3	E_4	E_1	E_2	E_3	E_4	E_1	E_2	E_3	E_4
Days to 50 % flowering	8.57	6.61	8.30	5.06	10.03	8.18	9.18	6.70	73.02	65.33	71.53	55.74	15.09	11.01	14.46	7.78
Days to maturity	1.84	1.61	2.31	2.00	2.75	2.61	2.92	2.64	44.61	38.09	62.62	57.50	2.53	2.05	3.76	3.13
Plant height (cm)	20.88	15.90	19.01	17.88	22.08	17.48	20.12	18.89	89.46	82.76	89.26	89.64	40.70	29.81	36.03	34.88
First branch initiation height (cm)	21.49	23.33	23.97	17.91	23.11	24.79	25.57	19.28	86.47	88.60	87.86	86.28	41.17	45.25	46.29	34.28
Number of primary branches per plant	16.16	16.50	13.55	13.80	17.82	18.14	15.58	15.48	82.28	82.71	75.61	79.57	30.21	30.91	24.27	25.37
Siliqua density of main shoot (%)	10.44	8.53	7.51	5.62	12.56	10.62	9.63	7.36	69.04	64.64	60.77	58.26	17.87	14.14	12.06	8.83
Number of siliquae per plant	31.44	25.29	25.56	23.72	32.23	26.16	26.41	24.62	95.18	93.45	93.68	92.86	63.20	50.36	50.96	47.09
Silique length (cm)	8.91	7.92	9.25	10.36	9.85	8.94	10.21	11.30	81.81	78.34	82.26	84.03	16.60	14.44	17.03	19.57
Number of seeds per siliqua	11.80	12.58	10.89	11.43	12.54	13.18	11.69	12.06	88.50	91.08	86.76	89.78	22.87	24.74	20.90	22.31
1000-seed weight (g)	13.92	14.24	14.86	13.80	14.58	14.99	15.49	14.34	90.91	90.30	92.06	92.56	27.35	27.88	29.37	27.35
Seed yield per plant (g)	31.17	20.50	24.43	23.17	31.88	21.44	25.44	24.07	95.59	91.49	92.21	92.67	62.79	40.40	48.32	45.96
Harvest index (%)	11.42	12.26	14.07	11.95	12.80	13.44	15.10	13.19	79.71	83.21	86.75	82.00	21.00	23.04	27.05	22.30
Oil content (%)	2.73	2.37	2.37	2.74	3.27	3.12	3.01	3.31	69.98	57.78	61.90	66.65	4.71	3.71	3.84	4.56

days to 50% flowering, days to maturity and oil content, Sikarwar *et al.* (2017) for days to 50% flowering and siliqua length, Synrem *et al*. (2014) for siliqua length and days to maturity, Doddamhimappa *et al*. (2011) for harvest index.

Heritability estimates along with genetic advance would be more useful in predicting yield under phenotypic selection than heritability estimates alone as suggested by Johnson *et al*. (1955). In the present investigation, estimate of high heritability along with high genetic advance as per cent of mean were reported for number of siliquae per plant, seed yield per plant, first branch initiation height, plant height, number of primary branches per plant, 1000-seed weight, number of seeds per siliqua and harvest index in all the environments (Table 4). Therefore, inheritance of these traits might be under the control of additive gene action hence, the improvement of these traits can be made through direct phenotypic selection. Similar findings have been reported by Yadav *et al*. (2011) for first branch initiation height, Chaurasiya *et al*. (2019) and Rout *et al*. (2019) for number of siliquae per plant, seed yield per plant, number of primary branches per plant, 1000-seed weight, Doddamhimappa *et al*. (2011) for siliquae per plant, seed yield per plant, number of seeds per siliqua and Tripathi *et al*. (2019) for harvest index. The trait siliqua length showed high heritability along with moderate genetic advance. This result was also reported by Yadav *et al*. (2011) and Rai *et al*. (2017). The trait oil content had high heritability with low genetic advance as per cent of mean in all the four environments. Such result has also reported by Tripathi *et al*. (2019) and Doddamhimappa *et al*. (2011).

Conclusion

It was concluded from the present investigation that sufficient genetic variability was present in the experimental material for most of the traits in all the environments. Therefore, this variability could be further exploited for creating segregating generations using these genotypes for timely as well as late sown condition. High heritability coupled with high genetic advance was observed for number of siliquae per plant, seed yield per plant, first branch initiation height, plant height, number of primary branches per plant, 1000-seed weight, number of seeds per siliqua and harvest index which indicated that these characters governed by additive gene action and direct selection based on these traits could be advantageous.

References

Anonymous. 2022. Rajasthan agriculture statistics at a glance 2020-21. Commissionerate of agriculture, Rajasthan, Jaipur.

Burton GN and Devane EM. 1953. Estimating heritability in fall fescue (*Festuca arundiancea* L.) from replicated clonal materials. *Agron J* **45**: 478-481.

Chaurasiya JP, Singh M and Tomar P. 2019. Genetic variability, heritability, genetic advance and character association of Indian mustard (*B. juncea* L.). *J Oilseed Brassica* **10**: 80-86.

Doddadhimappa R, Gangapur B, Prakash G and Hiremath CP. 2011. Genetic variability studies of germplasm accessions in Indian mustard under protected and unprotected conditions at Bijapur, Karnataka. *Int J Agric Sci* **7**: 54-57.

Gadi J, Chakraborty NR and Imam Z. 2020. To study the genetic variability, heritability and genetic advance for different quantitative characters in Indian Mustard (*B. juncea*). *Int J Curr Microbiol Appl Sci* **9**: 1557-1563.

Johnson HW, Robinson HF and Comstock RE. 1955. Estimates of genetic and environmental variability in soybean. *Agron J* **47**: 314–318.

Kumar R, Kaur S, Bala K, Kaur S and Sharma L. 2019. Assessment of genetic variability, correlation and path analysis for yield traits in F_1 hybrids of Indian mustard (*B. juncea*). *Agriways* **7**: 1-7.

Lakra A, Tantuway G, Tirkey AE and Srivastava K. 2020. Genetic variability and trait association studies in Indian mustard (*B. juncea*). *Int J Curr Microbiol App Sci* **9**: 2556-2563.

Meena HS, Kumar A, Singh VV, Meena PD, Ram B and Kulshrestha S. 2017. Genetic variability and inter-relation of seed yield with contributing traits in Indian mustard (*B. juncea*). *J Oilseed Brassica* **81**:131-137.

Panse VG and Sukhatme, PV. 1985. Statistical methods for agricultural workers. 3rd Revised Edition, ICAR Publication, New Delhi.

Rai PK, Ambawat S, Gurjar N, Singh VV, Singh S and Singh D. 2017. Estimation of genetic variability among drought tolerant RILs population of Indian mustard (*B. juncea*) derived from Rohini x RH819. *Int J Dev Res* **7**: 10929-10934.

Ray J, Singh OP, Pathak VN and Verma SP. 2019. Assessment of genetic variability, heritability, genetic advance and selection indices for yield contributing traits in Indian mustard (*B. juncea*). *Int J Chem Stud* **7**: 1096-1099.

Rout S, Kerkhi SA and Gupta A. 2019. Estimation of genetic variability, heritability and genetic advance in relation to seed yield and its attributing traits in Indian mustard (*B. juncea*). *J Pharmacogn Phytochem* **8**: 4119-4123.

Sikarwar RS, Satankar N, Kushwah MK and Singh AK. 2017. Genetic variability, heritability and genetic advance studies in yellow sarson (*B. rapa var.* Yellow Sarson). *Int J Agric Innov Res* **5**: 2319-1473.

Singh L and Bansal S. 2020. Status of rapeseed and mustard crop in India: Trend and decomposition analysis. *J Krishi Vigyan* **8**: 279-284.

Singh S, Kumar V, Singh SK and Daneva V. 2022. Genetic variability, interrelation and path analysis for yield & yield characters in Indian mustard (*B. juncea*). *J Oilseed Brassica* **13**:112-118.

Synrem GJ, Rangare NR, Myrthong I and Bahadure DM. 2014. Variability studies in Intra specific crosses of Indian mustard (*B. juncea*) genotypes. *J Agric Vet Sci* **7**: 29-32.

Tripathi N, Kumar K and Verma OP. 2019. Assessing genetic variability in Indian mustard (*B. juncea*) for seed yield and its contributing attributes under normal and saline/alkaline condition. *J Pharmacogn Phytochem* **8**: 1322-1324.

Yadav DK, Giri SC, Vignesh M, Vasudev S, Yadav AK, Dass B, Singh R, Singh N, Mohapatra T and Prabhu KV. 2011. Genetic variability and trait association studies in Indian mustard (*B. juncea*). *Indian J Agric Sci* **81**: 712-716.