



Assessment of Genetic Variability and Diversity in Indian Mustard (*Brassica juncea* L.) under Timely and Late Sown Conditions

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Authors' contributions

This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.

Article Information

DOI: <https://doi.org/10.9734/jabb/2024/v27i101457>

Open Peer Review History:

This journal follows the Advanced Open Peer Review policy. Identity of the Reviewers, Editor(s) and additional Reviewers, peer review comments, different versions of the manuscript, comments of the editors, etc are available here: <https://www.sdiarticle5.com/review-history/123635>

Original Research Article

Received: 19/07/2024

Accepted: 23/09/2024

Published: 26/09/2024

ABSTRACT

The present investigation was carried out at Research farm of Genetics and Plant Breeding, Birsa Agricultural University, Kanke, Ranchi, Jharkhand, India during Rabi 2022-2023. In this study two sets of field experiments were conducted with 43 genotypes of Indian mustard consisting 30 F1 hybrids and 13 parents to assess the genetic variability, heritability and genetic advance under timely (TS) and late sown (LS) conditions. The genotypes were evaluated for twelve quantitative

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Cite as: Perween, Shahina, Arun Kumar, Manigopa Chakraborty, Ekhlague Ahmad, CS Mahto, and MK Barnwal. 2024. "Assessment of Genetic Variability and Diversity in Indian Mustard (*Brassica Juncea* L.) under Timely and Late Sown Conditions". *Journal of Advances in Biology & Biotechnology* 27 (10):331-41. <https://doi.org/10.9734/jabb/2024/v27i101457>.

characters. The analysis of variance showed highly significant differences among the genotypes for all the characters. The maximum GCV and PCV were recorded for the characters, number of secondary branches / plant and seed yield / plant in both timely sown and late sown condition. High heritability coupled with high genetic advance was observed for 1000 seed weight and seed yield /plant¹ in both TS and LS conditions which suggested that these characters can be considered as favourable for improvement through selection. D² analysis grouped the 43 genotypes into 9 clusters in TS and 7 clusters in LS conditions. The distribution of genotypes in both the environments was different. Maximum genotypes (28) were present in TS while maximum genotypes (27) were present in cluster I. The maximum inter cluster distance was observed between clusters VI and IX in TS while in LS the clusters IV and VI showed maximum inter cluster distance. Therefore, it can be concluded that the genotypes in these clusters exhibit the highest degree of genetic diversification. This diversity makes them valuable for incorporation into a successful breeding program for development of new varieties.

Keywords: Genetic variability; GCV; PCV; heritability; genetic advance; cluster analysis.

1. INTRODUCTION

Indian mustard (*Brassica juncea* L.) is a cornerstone of India's oilseed industry, distinguished for its substantial oil content ranging from 38 to 42% and a protein level of 24%. Predominantly utilized in Northern India for cooking and frying, this crop plays a crucial role in the country's agricultural landscape. India leads globally in the cultivation and production of groundnut, castor, sesame, and niger, while securing the second position in safflower and rapeseed-mustard, and the third for linseed. *Brassica juncea* commonly known as rai or raya originates as a natural amphidiploid (2n=36) derived from *B. rapa* (2n=20) and *B. nigra* (2n=16), belonging to the Cruciferae family within the Brassicaceae genus. This crop commands a significant share of acreage among oilseed Brassica varieties [1]. During the 2018-19 growing season, Indian mustard was cultivated over approximately 75-80% of the 6.23 million hectares dedicated to these crops. The timing of planting is a critical factor influencing seed yield, as the yield of Brassica crops results from various components, each governed by multiple genes. Effective genetic improvement relies on understanding the genetic variability within a population. Cluster analysis offers insights into genetic relationships among genotypes, aiding in the selection of diverse parents for hybridization. Therefore, this study aimed to assess genetic variability, heritability, genetic advance, and diversity in Indian mustard under both timely and late sown conditions.

2. MATERIALS AND METHODS

The present investigation was carried out at Research farm of Genetics and Plant Breeding,

Birsa Agricultural University, Kanke, Ranchi, Jharkhand, India during Rabi 2022-2023. Geographically, this area is located at an altitude of 651 m above mean sea level and at 23.4345' N latitude and 85.3214' E longitude. The soil type is sandy loam and soil pH is 5.8. The area on an average receives 1400 mm of rainfall every year. Forty three genotypes of Indian mustard including thirty F1 hybrids and 13 parents were taken for study. These genotypes were grown under timely sown (E1) and late sown (E2) conditions in a Randomized Block Design using three replications each. Each plot consisted of two row of 3 meter in length, spaced 30 cm apart. The distance between plant to plant 10 cm was maintained by thinning. The recommended fertilizer doses viz.80:40:40:20kg/ha N:P:K:S respectively were applied and irrigated 4 times to raise a good crop.

Observations were made on five randomly chosen plants per plot for twelve distinct traits: days to 50% flowering, plant height (cm), number of primary branches per plant, number of secondary branches per plant, siliqua per plant, siliqua length (cm), distance to primary branch (cm), main shoot length (cm), days to maturity, number of seeds per siliqua, 1000-seed weight (g), and seed yield per plant (g). However, data for days to 50% flowering and days to maturity were recorded at the plot level. The recorded data for the various traits were analyzed using the variance analysis model outlined by Panse and Sukhatme [2] and the coefficient of variation was estimated according to Burton and de Vane [3]. Heritability in the broad sense was assessed using the methodology of Hanson et al. [4]. Additionally, genetic divergence was analyzed through the Mahalanobis D² statistic, as proposed by Rao in 1936.

3. RESULTS AND DISCUSSION

3.1 Analysis of Variance and Coefficient of Variation

The analysis of variance for all the characters under TS (timely sown) and LS (late sown) conditions is presented in Table 1. The analysis of variance indicated significant differences among the genotypes for all the characters studied in both environments. Further, parents and crosses (F1 hybrids) partitioned from genotypes were also found significant for most of the traits in both environmental conditions. The estimates of mean, range, genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) in E1 and E2 for various characters studied are presented in Table 2. For all character in both conditions (E1 and E2), the size of PCV generally surpasses GCV. The high values of GCV and PCV were recorded for the characters, number of secondary branches / plant (27.17 and 37.43) and seed yield / plant (27.26 and 30.27) under timely sown condition indicating better opportunity for improvement in these traits through selection. Moderate GCV and PCV were found in number of siliqua / plant and 1000 seed weight in both E1 and E2 condition, it indicates the influence of environment in the expression of these characters. Low GCV and PCV were observed in days to 50% flowering (5.83 and 6.20, siliqua length (4.78 and 6.97), days to maturity (2.11 and 2.25) and number of seeds / siliqua (3.93 and 6.07). The high values of genotypic and phenotypic coefficient of variation were recorded for the characters, number of secondary branches / plant (26.62 and 35.82) and seed yield / plant (27.28 and 30.65) under late sown condition. The value of PCV ranged from 2.25 for days to maturity to 37.43 for number of secondary branches / plant while GCV ranged from 2.11 for days to maturity to 27.26 for seed yield / plant in E1. Low values of PCV and GCV were observed in the characters, days to maturity, siliqua length and days to 50% flowering in both E1 and E2. Similar results on variability for different characters were reported by Sharma et al. [5], Akabari and Niranjana [6], Rout et al. [7], Kumar et al. [8] and Gupta et al. [9].

3.2 Heritability and Genetic Advance

The heritability in broad sense and genetic advance in / cent of mean were computed for all the characters and are presented in Table 2. The heritability ranged from 16.66% (Number of primary branches/plant) to 95.44% (1000 seed weight) in E1 while in E2 it ranged from 19.07% (main shoot length) to 95.02% (1000 seed weight). In general, higher estimates in broad sense were observed for all the characters in E1 and E2 except for plant height (56.65% in E1 and 50.32% in E2), secondary branches/plant (52.70% in E1 and 55.24% in E2), siliqua length (46.92% in E1 and 41.27% in E2), Point to primary branches (46.41% in E1 and 52.10% in E2) and number of seeds/siliqua (42.05% in E1 and 50.82% in E2) which showed moderate heritability in both E1 and in E2. The high heritability of these traits suggests that their development is primarily driven by genetic factors, with environmental influences playing a minimal role.

The Genetic advance in % of mean ranged from 4.07% (days to maturity) to 50.26% (seed yield/plant) in E1 and in E2 it ranged from 2.52% (number of primary branches/ plant) to 50.01% (seed yield/plant). In the timely sown (TS) conditions and in the late sown (LS) conditions, seed yield / plant exhibited the greatest genetic advance at 50.26% and 50.01% respectively. In TS, seed yield / plant showed higher genetic advance in /cent of mean (50.26%) followed by number of secondary branches/plant (40.64%), 1000 seed weight (38.71%) and point to primary branches (22.56%) where as in LS condition seed yield / plant (50.01%) showed higher genetic advance in /cent of mean followed by number of secondary branches/plant (40.77%), 1000 seed weight (38.81%), point to primary branches (26.49%).

High heritability coupled with high genetic advance was observed for 1000 seed weight and seed yield /plant in both E1 and E2 which suggested that these characters can be considered as favourable for improvement through selection. High heritability together with low genetic advance was noticed for days to 50% flowering and days to maturity for both in TS and LS conditions indicating the role of non-additive gene for inheritance of these characters. Similar findings were also reported by Pandey and Pandey [10], Maurya et al. [11] and Gupta et al. [9].

Table 1. Analysis of variance for 13 characters in Indian mustard under timely (E1) and late sown (E2) condition

Characters	Env/D.F	Replications	Genotypes	Parents	Parents vs. Crosses	Crosses	Error
		2	42	12	1	29	84
Days to 50% flowering	E1	4.49*	3.06**	34.01**	82.88**	27.42**	1.27
	E2	2.19	31.43**	37.22**	74.58**	27.55**	1.69
Plant Height (cm)	E1	765.53**	408.16**	336.30**	4474.81**	297.67**	82.96
	E2	1037.88**	360.23**	307.42**	2809.62**	297.62**	89.20
Number of Primary branches/ plant	E1	0.37	0.46*	0.09	6.89**	0.40	0.29
	E2	0.26	0.39	0.18	4.42**	0.35	0.31
Number of Secondary branches / plant	E1	8.89*	10.90**	1.30	249.2**	6.64**	2.51
	E2	10.65*	9.86**	1.54	241.50**	5.32**	2.10
Number of Siliqua / plant	E1	684.07	1632.97**	387.67	5881.53**	2001.76**	584.63
	E2	286.47	1910.69**	392.43	11857.31	2195.95**	669.88
Siliqua length(cm)	E1	0.13	0.17**	0.19**	0.10	0.17**	0.05
	E2	0.09	0.15**	0.12*	0.20*	0.16**	0.05
Point to primary branches(cm)	E1	7.6459	58.12**	51.94**	132.70**	58.10**	16.15
	E2	39.40*	65.44**	93.42**	260.69**	47.13**	15.35
Main shoot length(cm)	E1	304.07**	107.82**	65.31	372.30**	116.29**	35.09
	E2	359.11**	91.5*	67.80	89.11	101.53**	53.67
Days to maturity	E1	0.22	18.18**	17.41**	64.68**	16.89**	0.80
	E2	0.98	20.20**	19.86**	48.25**	19.37**	2.19
Number of seeds / Siliqua	E1	0.92	1.29**	1.34**	0.13	1.31**	0.41
	E2	1.17	1.55**	1.69**	0.24	1.54**	0.38
1000 seed weight(g)	E1	0.01	1.67**	1.15**	1.18**	1.91**	0.03
	E2	0.06	1.69**	1.00**	3.74**	1.92**	0.03
Seed yield / plant(g)	E1	1.89*	7.03**	10.23**	50.09**	4.23**	0.51
	E2	3.20**	6.71**	9.69**	58.46**	3.69**	0.54

*and ** Significant at 5% and 1% probability levels, respectively

Table 2. Mean, range, genotypic and phenotypic coefficient of variability, heritability (% in broad sense) and genetic advance in % of mean for different characters in Indian mustard under timely (E1) and late sown condition (E2)

Estimates	Environment	Days to 50% flowering	Plant Height (cm)	Number of Primary branches/plant	Number of Secondary branches/plant	Number of Siliqua/plant	Siliqua length (cm)	Point to primary branches (cm)	Main shoot length(cm)	Days to maturity	Number of seeds/Siliqua	1000 seed weight(g)	Seed yield / plant(g)
Range	E1 (Min)	45	106.83	3.33	3.33	118.6	3.71	12.8	54.4	107	12.71	1.7	2.52
	E1 (Max)	62	160.6	4.73	10	237.53	4.75	32.61	81.77	119.67	15.03	5.7	9.3
	E2 (Min)	44.67	107.5	3	2.97	120.03	3.91	16.2	55.33	104.67	11.78	1.74	2.24
	E2 (Max)	57.33	157.27	4.7	9.8	232.01	4.83	34.3	79.33	117.67	14.72	5.83	9.03
Mean	E1	53.52	132.92	3.85	6.16	153.98	4.29	23.35	67.98	114.19	13.77	3.9	5.37
	E2	52.72	130.05	3.79	6.04	155.58	4.32	23.01	68.2	111.27	13.5	3.89	5.21
GCV%	E1	5.83	7.81	6.25	27.17	12.14	4.78	16.08	7.21	2.11	3.93	19.24	27.26
	E2	5.96	7.29	4.34	26.62	13.07	4.26	17.81	5.19	2.20	4.64	19.33	27.28
PCV%	E1	6.20	10.38	15.30	37.43	19.85	6.97	23.60	11.27	2.25	6.07	19.69	30.27
	E2	6.45	10.27	15.40	35.82	21.16	6.63	24.68	11.89	2.57	6.51	19.83	30.65
h²%	E1	88.48	56.65	16.66	52.70	37.41	46.92	46.41	40.86	87.92	42.05	95.44	81.09
	E2	85.41	50.32	79.50	55.24	38.17	41.27	52.10	19.07	73.26	50.82	95.02	79.19
GAM%	E1	11.30	12.11	5.25	40.64	15.30	6.74	22.56	9.49	4.07	5.26	38.71	50.56
	E2	11.35	10.65	2.52	40.77	16.64	5.64	26.49	4.67	3.88	6.82	38.81	50.01

E1= Timely sown condition (TS) and E2= Late sown condition (LS)

3.3 Genetic Divergence

Timely sown: On the basis of D^2 values, all the 43 genotypes (30 F1 hybrids and 13 parents) were grouped in 9 clusters (Table 3) under timely sown condition. Cluster I had highest number of genotypes 28 followed by cluster II which had 5 genotypes, respectively. Cluster, III, IV and V consisted of 2 genotypes each and cluster VI, VII, VIII and IX consisted of one genotype each. The intra and inter-cluster distance among different clusters are given in Table 4. The intra-cluster D^2 values ranged from 0.00 (cluster 6,7,8 and 9) to 68.49 (cluster 5). The inter cluster D^2 values indicated that the most diverse groups were VI and IX (672.69) followed by VI and VIII (583.34). The minimum inter cluster value was found between I and II (194.948) indicates that these groups are less diverse. The mean performance of all the characters in different clusters is presented in Table 5. Cluster I showed highest mean for days to 50%flowering (57.67), plant height (142.93) and 1000 seed weight (4.4). Cluster II exhibited highest mean for Silqua length (4.39). Cluster III showed highest mean for number of primary branches / plant (4.87), number of secondary branches / plant(10.47) and number of siliqua / plant (226.13). Cluster V exhibited highest mean for days to maturity (119.44). Cluster VIII showed highest mean for main shoot length (76.51) and number of seeds / siliqua (14.51). Cluster IX exhibited highest mean

for point to primary branches (24.16) and seed yield / plant (7.00).

Late sown (E2): Forty three genotypes were grouped into 7 clusters (Table 6) under late sown condition (E2). Cluster I consisted of maximum number of genotypes (27) followed by cluster II which had 9 genotypes. Cluster III consisted of 3 genotypes where as, cluster IV,V,VI and VII consisted of only one genotype. The intra and inter- cluster distance among different clusters are given in Table 7. The intra-cluster D^2 values ranged from 0.00 (cluster IV,V VI and VII) to 67.83(cluster III). The inter-cluster D^2 values indicated that the most diverse groups were IV and VI (806.46) followed by III and VI (453.86). The minimum inter-cluster value was found between II and V (95.05) which indicates that these groups are less diverse. The mean /formance for all the morphological characters in different clusters is presented in Table 8. Cluster I showed highest mean for number of primary branches / plant(4.18), number of primary branches / plant(8.65), number of siliqua / plant (203.11) and seed yield / plant(5.93). Cluster II exhibited highest mean for number of seeds / siliqua (13.66). Cluster IV showed highest mean value for days to 50% floweing(55.89) and 1000 seed weight(4.42). Cluster V exhibited highest mean for siliqua length (4.45), and point to primary branches (27.75). Cluster VI showed highest mean for main shoot length (113.40). Cluster VII exhibited highest mean for plant height (141.43).

Table 3. Distribution of 43 genotypes of Indian mustard in different clusters under timely sown condition (E1)

Clusters	No. of genotypes	Genotypes
I	28	LES 39 X NPJ 112, TN 3 X NPJ 112, DRMRIJ 12-48 X NPJ 112, DRMRMJA 35 x BBM-1,DRMRMJA 35 x Shivani , RE 8 x BBM-1, DRMRIJ 31 x Shivani, DRMRIJ 12-40 x Shivani, M 34 X NPJ 112, Shivani,DRMRMJA 35 X NPJ 112, RLC 3 x BBM-1, TN 3 x Shivani, DRMRMJA 35,DRMRIJ 12-40, DRMRIJ12-48, RE 8 x Shivani, DRMRIJ 31 X NPJ 112, LES 39 x Shivani, M 34 x Shivani, IC 597880 x BBM-1, IC 597880 X NPJ 112, DRMRIJ 12-40 X NPJ 112, RE 8 X NPJ 112, BBM1, RLC 3, RLC 3 x Shivani, RLC 3 X NPJ 112
II	5	DRMRIJ 12-40 x BBM-1,LES 39 x BBM-1, M 34 ,TN 3 x BBM-1,DRMRIJ 12-48 x BBM-1
III	2	IC 597880, RE 8
IV	2	TN 3, NPJ 112
V	2	M 34 x BBM-1, LES 39
VI	1	IC 597880 x Shivani
VII	1	DRMRIJ 12-48 x Shivani
VIII	1	DRMRIJ 31
IX	1	DRMRIJ 31 x BBM-1

Table 4. Intra-cluster and inter-cluster D² values among 9 clusters in Indian mustard under timely sown condition (E1)

Clusters	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII	Cluster VIII	Cluster IX
Cluster I	53.87	123.30	96.18	190.35	104.57	215.96	97.55	157.87	265.43
Cluster II		66.65	243.54	329.86	135.96	435.38	263.88	137.60	84.53
Cluster III			47.32	158.86	128.27	104.46	115.57	349.33	430.13
Cluster IV				64.48	284.92	332.30	260.24	354.37	527.88
Cluster V					68.49	205.38	131.38	252.76	209.98
Cluster VI						0.00	130.06	583.34	672.69
Cluster VII							0.00	228.40	463.41
Cluster VIII								0.00	225.32
Cluster IX									0.00

Bold figures indicate intra-cluster D² values

Table 5. Cluster mean for 12 morphological characters in Indian mustard under timely sown condition (E1)

Clusters	Days to 50% flowering	Plant Height (cm)	Number of Primary branches/plant	Number of Secondary branches/plant	Number of Siliqua/plant	Siliqua length(cm)	Point to primary branches (cm)	Main shoot length(cm)	Days to maturity	Number of seeds / Siliqua	1000 seed weight(g)	Seed yield / plant(g)
Cluster I	57.67	142.93	3.33	4.71	129.42	4.32	24.15	69.49	119.08	14.24	4.40	4.47
Cluster II	51.33	126.49	4.12	7.07	169.77	4.39	21.05	71.27	116.93	13.86	3.86	6.23
Cluster III	55.00	135.80	4.87	10.47	226.13	3.81	15.73	65.80	114.33	13.87	1.80	4.35
Cluster IV	51.72	116.72	3.53	4.77	153.99	4.25	22.44	66.74	118.11	13.36	3.99	5.00
Cluster V	50.11	118.56	3.62	4.14	129.84	4.36	22.62	61.40	119.44	13.88	3.64	4.63
Cluster VI	53.50	127.70	4.57	8.03	188.16	4.24	19.02	71.16	116.50	14.22	3.71	6.89
Cluster VII	51.24	132.52	3.68	5.59	143.41	4.31	23.89	67.73	118.88	13.75	4.06	6.68
Cluster VIII	52.56	140.31	4.10	9.24	185.40	4.33	23.38	76.51	118.89	14.51	4.05	6.87
Cluster IX	52.47	142.13	3.95	7.29	162.28	4.26	24.16	69.79	116.40	14.09	3.27	7.00

Bold figures indicate highest mean value

Table 6. Distribution of 43 genotypes of Indian mustard in different clusters under late sown condition (E2)

Clusters	No. of genotypes	Genotypes
I	27	IC 597880 x BBM-1, RE 8 x Shivani, Shivani, DRMRIJ 12-40, DRMRMJA 35 x Shivani, DRMRIJ 31 X NPJ 112, M 34 X NPJ 112, DRMRMJA 35, BBM-1, RLC 3 X NPJ 112, RE 8, TN 3 x Shivani, LES 39 x Shivani, DRMRIJ 12-48 x Shivani, DRMRMJA 35 X NPJ 112, IC 597880 X NPJ 112, M 34 x Shivani, RLC 3 x Shivani, DRMRIJ 12-40 x Shivani, DRMRIJ 31 x Shivani, DRMRIJ 12-48 X NPJ 112, RE 8 X NPJ 112, DRMRIJ 12-48, RLC 3 x BBM-1, DRMRIJ 12-48 x BBM-1, TN 3, M 34 x BBM-1
II	9	RE 8 x BBM-1, TN 3 X NPJ 112, DRMRIJ 12-40 X NPJ 112, DRMRMJA 35 x BBM-1, LES 39 x NPJ 112, DRMRIJ 12-40 x BBM-1, DRMRIJ 31, LES 39 x BBM-1, M 34
III	3	IC 597880, RLC 3, LES 39
IV	1	IC 597880 x Shivani
V	1	DRMRIJ 31 x BBM-1
VI	1	TN 3 x BBM-1
VII	1	NPJ 112

Table 7. Intra-cluster and inter-cluster D² values among 7 clusters in Indian mustard under late sown condition (E2)

Clusters	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII
Cluster I	48.59	97.94	92.00	217.53	212.63	249.64	98.42
Cluster II		49.64	207.12	438.44	95.05	100.52	179.89
Cluster III			67.83	124.95	313.52	453.81	142.06
Cluster IV				0.00	621.06	806.46	301.08
Cluster V					0.00	100.10	333.84
Cluster VI						0.00	310.36
Cluster VII							0.00

Bold figures indicate intra-cluster D² value

Table 8. Cluster mean for 12 morphological characters in Indian mustard under late sown condition (E2)

Clusters	Days to 50% flowering	Plant Height (cm)	Number of Primary branches/plant	Number of Secondary branches / plant	Number of Siliqua/ plant	Siliqua length (cm)	Point to primary branches (cm)	Main shoot length(cm)	Days to maturity	Number of seeds per Siliqua	1000 seed weight(g)	Seed yield per plant(g)
Cluster I	53.94	135.41	4.18	8.65	203.11	4.22	21.76	74.03	109.89	13.58	3.55	5.93
Cluster II	51.60	122.43	4.05	7.47	172.03	4.40	20.48	71.89	110.47	13.66	4.16	5.84
Cluster III	51.37	121.84	3.58	4.84	148.45	4.29	22.00	66.73	111.44	13.56	3.89	4.68
Cluster IV	55.89	134.87	3.60	4.80	124.57	4.27	23.93	75.72	112.33	13.35	4.42	4.63
Cluster V	52.73	136.67	3.51	4.60	138.62	4.45	27.75	63.29	112.53	12.91	4.22	5.44
Cluster VI	51.80	117.36	3.61	4.20	126.61	4.34	23.39	63.21	113.40	13.56	3.53	4.39
Cluster VII	53.70	141.43	3.91	6.87	157.52	4.29	22.80	68.16	110.13	13.59	3.69	5.62

Bold figures indicate highest mean value

The genetic divergence estimates for the majority of the traits examined align with previous findings. Research by Ratnesh et al. [12], Neelam et al. [13], Vanukuri and Pandey [14], Gupta et al. [9] and Kumar et al. [15] has similarly explored genetic diversity in Indian Mustard [16-18].

4. CONCLUSION

The analysis of variance (ANOVA) revealed significant variations across all traits among the genotypes, underscoring a broad spectrum of genetic diversity. This diversity offers a promising opportunity for effective selection. Furthermore, the observed phenotypic coefficient of variation (PCV) surpassed the genotypic coefficient of variation (GCV) for every character evaluated, suggesting that environmental factors exerted a relatively minor influence on the traits' expression. A high heritability coupled with high genetic advance as a percentage of the mean was observed 1000 seed weight and seed yield / plant in both TS and LS conditions. These traits exhibit strong potential for selection and improvement. Consequently, future breeding programs, should concentrate on these key characteristics, as their enhancement could significantly advance the development of Brassica varieties. Cluster analysis demonstrated that the greatest inter-cluster distance in TS was between clusters IV and IX. In LS, the maximum inter-cluster distance was observed between clusters IV and VI. These findings highlight significant genetic diversity among the genotypes, suggesting distinct genetic variations and potential for targeted breeding strategies.

DISCLAIMER (ARTIFICIAL INTELLIGENCE)

Author(s) hereby declare that NO generative AI technologies such as Large Language Models (ChatGPT, COPILOT, etc) and text-to-image generators have been used during writing or editing of this manuscript.

ACKNOWLEDGEMENTS

We extend our sincere gratitude to the Chairman of the Department of Genetics and Plant Breeding at Birsa Agricultural University, Ranchi, for the crucial logistical support that enabled the successful completion of this research. We are also profoundly grateful to Dr. Arun Kumar for his continuous assistance throughout every phase of the study—from planning and trial execution to the analysis of results. His expertise and

steadfast support were instrumental in the success of this research.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

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