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RESEARCH ARTICLE

Dissecting genetic variability and yield trait interplay in a diversity panel of *Brassica juncea* (L.) Czern. & Coss.

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Abstract

Enhancing yield and adaptability in *Brassica juncea* (L.) Czern. & Coss. requires a clear understanding of agro-morphological variability and genetic control of key traits under diverse environmental conditions. This study evaluated 150 diverse genotypes along with three checks at Ludhiana and Abohar during 2021–22 and 2022–23 (two locations × two years) using augmented design. Significant phenotypic variation was observed across environments, particularly for traits such as number of primary branches (PB), number of siliquae per plant (NOS) and seed yield per plant (SY/P). High heritability along with high genetic advance for traits including days to 50 % flowering (DF50), plant height (PH), main shoot length (MSL) and SY/P suggest a predominance of additive genetic effects and strong potential for selection gains. In contrast, traits like days to maturity (DM) and silique length (SL) exhibited moderate heritability and greater environmental sensitivity, indicating the need for location-specific breeding strategies. Genotype-by-environment interactions were significant for most traits, reinforcing the importance of multi-environment evaluation. Path coefficient analysis revealed that MSL, SL and seeds per silique (S/S) exerted strong direct effects on SY/P, offering valuable secondary selection criteria. The integration of genetic parameter estimation with path analysis provides a robust framework for identifying high-performing, stable genotypes and optimizing trait combinations. These findings support the development of targeted, environment-specific breeding programs aimed at improving yield potential and resilience in Indian mustard.

Keywords: *Brassica juncea*; genetic variability; heritability; path analysis; yield improvement

Introduction

The growing global demand for food and nutritional security necessitates continual enhancement of crop productivity through the development of high-yielding and resilient cultivars. Indian mustard (*Brassica juncea* (L.) Czern. & Coss.) is a major oilseed crop of economic importance in India, valued for edible oil production and its potential as a biofuel feedstock. It ranks as the second most important oilseed crop in the country after groundnut, contributing significantly to the agricultural economy (1). At the national level, India cultivated rapeseed–mustard over 8.63 million ha during 2024–25, producing approximately 12.61 million tonnes with an average yield of 1461 kg ha^{-1}. The crop is predominantly grown in Rajasthan (37.44 lakh ha; 56.67 lakh t), Uttar Pradesh (12.56 lakh ha; 18.57 lakh t), Madhya Pradesh (11.44 lakh ha; 17.26 lakh t), Haryana (7.16 lakh ha; 12.98 lakh t) and West Bengal (6.42 lakh ha; 8.00 lakh t), which together account for around 88 % of the entire national production (2). Despite the availability of varieties with a yield potential of 2000–2500 kg ha^{-1}, national mean productivity remains around 1190 kg ha^{-1}, well below the global average (1900 kg ha^{-1}) and yields reported in developed nations (2500–3000 kg ha^{-1}). This yield gap is largely attributable to cultivation on marginal lands, frequently rainfed or poorly irrigated and the limited availability of varieties tolerant to key biotic and abiotic stresses across diverse agro-ecological regions. These constraints highlight the need for deeper insight into the genetic control of yield-related traits to support the development of regionally adapted stress-resilient mustard genotypes. Agro-morphological traits such as days to 50 % flowering, plant height, branch number and seed yield per plant are critical determinants of crop productivity and adaptability (3). These complex, quantitative traits are shaped by both genetic and environmental effects and their interactions can strongly influence yield stability and expression (4). Dissecting their genetic architecture, including heritability and variance components, is therefore central to designing efficient breeding strategies in *B. juncea*.

Substantial genetic variability within mustard germplasm has been reported, providing a foundation for genetic improvement via selection (5, 6). Genetic parameters such as heritability and genetic advance help predict response to selection by estimating the proportion of phenotypic variance attributable to genotype and the expected gain under selection pressure (7). When high heritability is accompanied by high genetic advance, additive gene action is often implicated and selection is likely to be effective (8). Selection is complicated, however, by genotype × environment (G × E) interactions, which cause genotypes to respond differently across environments (9). Multi-environment evaluation is therefore required to identify

stable, high-performing material and to guide region-specific cultivar development (10). The present study evaluates a large and diverse panel of *B. juncea* genotypes across four environment-year combinations over two consecutive growing seasons. By integrating phenotypic assessment with heritability and related genetic parameters, the study aims to identify stable, high-yielding genotypes and yield-contributing traits that can be exploited in targeted breeding. The findings provide a genetic framework to support environment-specific improvement strategies and to enhance the productivity, adaptability and resilience of Indian mustard under variable production conditions. The main objectives of the study were: to evaluate agro-morphological variability among diverse *B. juncea* genotypes across environments and to estimate genetic parameters and path analysis for key yield-related traits.

Materials and Methods

Experimental sites and seasons

The study was conducted over two consecutive rabi seasons (2021–22 and 2022–23) at two agro-ecologically distinct locations in Punjab, India: Punjab Agricultural University (PAU), Ludhiana and the PAU Regional Research Station, Abohar. The multi-location, multi-season structure generated four environment-year combinations: Y1L1, Y1L2, Y2L1 and Y2L2.

Plant material and experimental design

A genetically diverse panel of 150 *B. juncea* accessions, along with three check varieties, were evaluated. Genotype names are provided in Supplementary Table 1. Field trials were established in augmented design: 15 entries + 1 Check per block (layout in Supplementary Table 2). Each experimental unit consisted of two uniform rows per entry. Recommended agronomic practices were applied uniformly across environments to minimize non-genetic variation.

Trait measurement

Twelve traits were recorded: days to 50 % flowering (DF50), days to maturity (DM), plant height (PH), main shoot length (MSL), number of primary branches (PB), number of secondary branches (SB), silique length (SL), seeds per silique (S/S), number of siliques per plant (NOS), seed yield per plant (SY/P), 1000-seed weight (TSW) and oil content (OC). DF50 and DM were recorded on a plot basis. All other traits were measured on five randomly selected representative plants per plot and averaged.

Statistical analysis

All analyses were performed in R. Descriptive statistics (mean, range), standard error (SE), coefficient of variation (CV) and least significant difference (LSD) were computed to describe variability and test genotype differences. Genotypic variance (GV), phenotypic variance (PV) and genotype × environment interaction variance (GIV) was estimated for each trait. Broad-sense heritability (H^2) was calculated as H^2 = GV / PV. Expected response to selection was evaluated using genetic advance (GA) and genetic advance as percent of the mean (GAM).

Genotypic and phenotypic coefficients of variation (GCV, PCV) were computed as:

$$GCV = \left(\frac{\sigma_g}{\bar{X}}\right) \times 100$$

$$PCV = \left(\frac{\sigma_p}{\bar{X}}\right) \times 100$$

where σ_g and σ_p are genotypic and phenotypic standard deviations and $\bar{X}$ is the trait mean.

Path coefficient analysis

To identify the traits most influential on yield, path coefficient analysis was performed (11). Genotypic and/or phenotypic correlation matrices were partitioned into direct and indirect effects on SY/P, enabling interpretation of complex trait interrelationships and refinement of selection strategies.

Results

Phenotypic variation across environments

Substantial phenotypic variation was observed for SY/P and associated traits across both seasons. As shown in Table 1, CV values ranged from 0.7 % for OC in Y1L1 to 13.88 % in Y1L2 for PB. High CVs also occurred for NOS (12.01) in Y1L1, SB (10.19) in Y1L2 and SY/P (13.48) in Y1L2, indicating broad phenotypic dispersion and ample scope for selection. DM varied widely across environments, ranging from (129.8 days) at Y1L1 in genotype V71; while in V26 (160.2 days) at Y2L2. Trait frequency distributions (Fig. 1) were generally unimodal and approximately normal, with color-coded checks and environment overlays aiding visual comparison. Data structure and distribution characteristics supported the suitability of the dataset for variance component and selection analyses.

Mean SY/P differed across environments: 16.28 g (Y1L1), 15.22 g (Y1L2), 16.93 g (Y2L1) and 17.35 g (Y2L2), indicating an upward trend in the second season that may reflect improved environmental expression of genetic potential. As shown in Table 1; genotype V131 recorded the highest mean SY/P (34.77 g) at Y1L1, whereas V103 produced the lowest (4.3 g) at Y2L1, illustrating the breadth of yield expression in the diversity panel. Across traits, DF50 averaged 65.37 days (range: 49.9–79.6) at Y1L1, with minimal environmental divergence. Minimum DM averaged 143.5 days (129.8–153.4) at Y1L2, confirming wide maturity variation. PH ranged from 65.66 at Y2L1 to 198.66 cm (mean 146.17 cm) at Y2L1, highlighting strong structural diversity. MSL averaged 61.66 cm (39.83–74.27) at Y1L1 and was slightly right-skewed, indicating a subset of tall-axis genotypes. Both PB (13.88 % CV) at Y1L2 and SB (13.03 % CV) at Y2L2 showed marked dispersion, suggesting breeding opportunity for canopy architecture. SL (mean 4.99 cm) at Y2L2 was observed. SY/P showed strong right skew (4.30 at Y2L1–34.77 g at Y1L1), pointing to a small number of very high-yielding entries useful as selection parents. In contrast, at Y2L1 both TSW (mean 5.08 g) and OC (mean 37.70 %) were relatively stable across environments, suggesting stronger genetic control and making them reliable selection targets. Collectively, multi-environment evaluation confirmed substantial genetic diversity within the *B. juncea* panel. High variability in SY/P, PB, NOS and PH, coupled with normal or near-normal trait distributions, provides a strong platform for trait-targeted genetic improvement.

Table 1. An overview of the agro-morphological traits recorded for each year – (a) Y1L1, (b) Y1L2, (c) Y2L1, (d) Y2L2

(a) Y1L1

Parameters	Mean	Range				SE (m)	CV	LSD	No. of genotypes above trial mean
		Min. value	Genotype	Max. value	Genotype				
DF50	65.37	49.89	V85	79.56	V145	0.45	2.12	5.53	77
DM	145.31	132.22	V74	156.89	V18	0.42	0.72	5.19	81
PH	147.3	87.84	V92	199.44	V129	1.52	8.31	18.78	77
MSL	55.46	34.33	V77	86.53	V96	0.85	6.29	10.55	70
NOS	44.24	19.61	V103	72.58	V4	0.72	12.01	8.97	66
PB	5.48	2.79	V59	9.71	V35	0.1	10.43	1.25	71
SB	12.19	5.79	V120	19.38	V65	0.23	7.3	2.81	70
SL	4.31	2.97	V77	7.01	V4	0.06	7.27	0.72	13
S/S	18.87	14.42	V97	24.07	V104	0.17	4.03	0.72	71
SY/P	16.28	4.65	V77	34.77	V131	0.54	9.28	0.72	70
TSW	5.04	3.94	V147	6.18	V4	0.04	4.55	0.72	71
OC	37.65	33.83	V82	42.7	V97	0.17	1.06	0.72	75

SE(m) is the standard error of mean; CV is coefficient of variation and LSD is least square difference.

(b) Y1L2

Parameters	Mean	Range				SE (m)	CV	LSD	No. of genotypes above trial mean
		Min. value	Genotype	Max. value	Genotype				
DF50	69.32	58.56	V113	80.22	V35	0.41	1.84	5.13	60
DM	143.54	129.78	V71	153.44	V26	0.36	1.23	4.46	82
PH	197.03	127.22	V14	232.22	V34	1.19	1.06	14.73	74
MSL	61.66	39.83	V138	74.27	V53	0.62	4.5	7.65	84
NOS	52.43	27.82	V95	66.62	V13	0.54	8.64	6.64	75
PB	3.39	1.88	V86	8.14	V47	0.09	13.88	1.14	69
SB	9.55	0.99	V5	16.72	V72	0.26	10.19	3.19	82
SL	4.83	3.24	V138	6.17	V73	0.05	4.94	0.57	75
S/S	17.73	12.44	V3	23.11	V98	0.18	7.31	2.17	70
SY/P	15.22	4.48	V118	31.35	V145	0.48	13.48	5.93	77
TSW	4.44	3.01	V121	5.93	V37	0.06	3.5	0.73	75
OC	37.4	31.39	V3	43.72	V4	0.18	0.7	2.22	77

SE(m) is the standard error of mean; CV is coefficient of variation and LSD is least square difference.

(c) Y2L1

Parameters	Mean	Range				SE (m)	CV	LSD	No. of genotypes above trial mean
		Min. value	Genotype	Max. value	Genotype				
DF50	66.41	53.81	V144	78.56	V143	0.42	3.5	5.15	74
DM	145.78	134.78	V75	156.44	V15	0.38	1.71	4.64	69
PH	146.17	65.66	V135	198.66	129	1.53	6.42	18.89	77
MSL	55.17	32.55	V100	83.72	V96	0.83	7.05	10.31	70
NOS	44.49	24	V103	70.5	V4	0.7	11.14	8.63	70
PB	5.42	3.02	V59	9.3	V35	0.1	6.67	1.19	68
SB	12.3	5.5	V120	19.33	V93	0.23	9.09	2.79	80
SL	4.33	2.98	V95	6.5	V4	0.05	5.52	0.6	74
S/S	18.74	15.11	V88	23.78	V104	0.17	6.29	2.05	79
SY/P	16.93	4.3	V103	34.17	V131	0.55	9.88	6.78	68
TSW	5.08	3.86	V103	6.05	V4	0.04	4.43	0.51	68
OC	37.7	33.67	V47	42.65	V103	0.15	1.22	1.85	77

SE(m) is the standard error of mean; CV is coefficient of variation and LSD is least square difference.

(d) Y2L2

Parameters	Mean	Range				SE (m)	CV	LSD	No. of genotypes above trial mean
		Min. value	Genotype	Max. value	Genotype				
DF50	66.8	58.28	V138	76.61	V82	0.34	3.01	4.16	70
DM	146.39	136.72	V143	160.22	V26	0.42	2.4	5.25	75
PH	172.67	129.5	V71	240.17	V7	1.56	5.05	19.29	71
MSL	60.34	38.22	V95	72.96	V135	0.61	9.91	7.53	79
NOP	51.87	30.96	V52	69.96	V89	0.64	4.43	7.94	78
PB	3.39	1.56	V54	7.72	V41	0.09	8.6	1.13	65
SB	8.35	3	V8	14.83	V102	0.2	13.03	2.47	72
SL	4.99	3.02	V138	6.37	V96	0.06	3.15	0.74	80
S/S	16.78	9.33	V3	23.07	V133	0.23	9.96	2.8	74
SY/P	17.35	5.57	V92	33.74	V131	0.5	9.08	6.2	76
TSW	4.69	3.11	V45	6.04	V70	0.06	3.92	0.72	139
OC	37.46	30.58	V45	44.08	V103	0.18	1.2	2.25	73

DF50: days to 50 % flowering; DM: days to maturity; PH: plant height; MSL: main shoot length; PB: number of primary branches; SB: number of secondary branches; SL: silique length; S/S: seeds per silique; NOS: number of siliques per plant; SY/P: seed yield per plant, TSW: 1000-seed weight; OC: oil content.

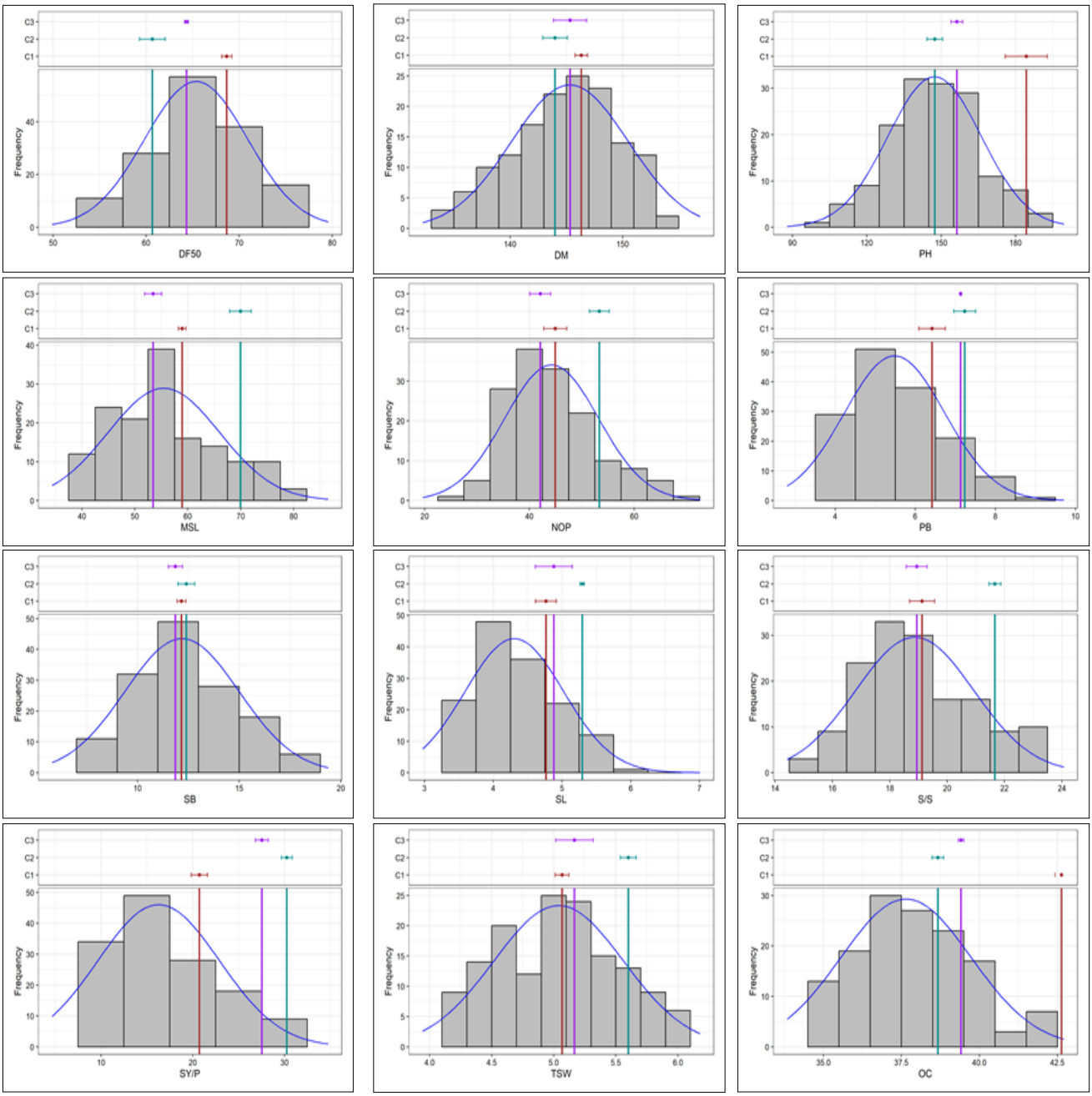

Fig. 1. Histogram illustrating the distribution of various agro-morphological traits within the diversity panel.

Heritability and genetic parameters

Genetic parameter analysis across the four environments (Y1L1, Y1L2, Y2L1, Y2L2) revealed wide differences among traits in the magnitude of genetic control and expected response to selection (Table 2; Fig. 2). Partitioning of phenotypic variance into GV, GIV and residual error enabled evaluation of the relative genetic contribution to be observed variability. Most traits showed moderate to high H^2 (≥ 0.60) across environments, consistent with the scale of Robinson (12). DF50 expressed H^2 values from 0.45 to 0.93; associated PCV and GCV ranges (5.6–8.14 % and 4.73–7.86 % respectively) indicate good selection potential. DM showed inconsistent H^2 (0–0.95) and lower GA, demonstrating environmental sensitivity and underscoring the need for environment-specific selection. PH recorded high H^2 (0.43–0.98) and broad variance, making it a structurally relevant and selectable trait. MSL expressed moderate to high H^2 (0.33–0.89) across environments; its variability supports use as a supporting architectural trait in yield improvement. NOS showed H^2 of 0.55–0.92, indicating favourable selection prospects. PB and SB expressed moderate to high H^2 (0.32–0.88 and 0.64–0.90, respectively) but also showed sizable PCV–GCV gaps, suggesting environmental contributions to expression. SL exhibited a broad H^2 span (0.13–0.96), indicating that selection efficiency will depend on environmental uniformity. S/S showed H^2 of 0.34–0.84, implying moderate selection efficiency in more stable environments.

SY/P showed consistently high H^2 in individual seasons (0.89–0.91 in Year 1; 0.84–0.93 in Year 2). In pooled analyses, H^2 was reduced due to increased G × E contribution, indicating that environmental modulation must be considered in yield-focused selection schemes. TSW expressed moderate to high H^2 (0.59–0.95) and relatively low environmental variance, making it a robust supporting trait. OC was highly heritable across all environments (0.94–0.99), accompanied by moderate GA, confirming strong genetic control. Across traits, all genotypic main effects were significant ($P < 0.01$) and all showed significant G × E in pooled analysis, confirming differential environmental responses. PH showed the largest GCV and PCV (46.43 % and

Table 2. Assessment of genetic parameters and variability across environments (a) Y1L1, (b) Y1L2, (c) Y2L1, (d) Y2L2

(a)

Characters	Y1L1			Pooled analysis										
	GV	SE	Hbs	GV	SE	GIV	SE	Hbs	MEAN	PV	GCV	PCV	GA	GAM
DF50	26.887	2.165	0.92	26.42	2.165	1.91	2.825	0.93	65.37	28.33	7.86	8.14	10.2	15.7
DM	20.43	2.275	0.88	20.87	2.275	1.09	0.98	0.95	145.3	21.96	3.14	3.23	9.19	6.32
PH	134.351	12.36	0.43	155.2	12.36	152.5	12.162	0.50	147.3	307.7	8.46	11.9	18.3	12.4
MSL	98.508	4.787	0.89	101	4.787	12.4	5.892	0.89	55.46	113.4	18.1	19.2	19.6	35.3
NOS	45.454	6.082	0.59	50.64	6.082	28.49	4.333	0.64	44.24	79.13	16.1	20.1	11.7	26.6
PB	1.045	0.763	0.73	1.11	0.763	0.34	0.38	0.76	5.48	1.45	19.2	22	1.9	34.7
SB	7.038	1.182	0.90	7.25	1.182	0.79	0	0.90	12.19	8.04	22.1	23.3	5.27	43.3
SL	0.041	0.267	0.13	0.23	0.267	0.1	0.21	0.69	4.31	0.33	11.2	13.4	0.83	19.4
S/S	3.431	1.063	0.84	3.59	1.063	0.58	1.09	0.86	18.87	4.17	10	10.8	3.63	19.2
SY/P	35.943	2.617	0.91	39.2	2.617	2.54	3.797	0.94	16.28	41.73	38.5	39.7	12.5	76.9
TSW	0.195	0.31	0.76	0.21	0.31	0.05	0.22	0.79	5.04	0.26	9.02	10.1	0.84	16.6
OC	4.074	0.596	0.96	4.13	0.596	0.16	1.442	0.96	37.65	4.29	5.4	5.5	4.11	10.9

(b)

Characters	Y1L2			Pooled analysis										
	GV	SE	Hbs	GV	SE	GIV	SE	Hbs	MEAN	PV	GCV	PCV	GA	GAM
DF50	21.151	2.186	0.89	22.75	2.186	1.61	2.862	0.93	69.32	24.36	6.88	7.12	9.51	13.7
DM	12.745	2.647	0.73	14.37	2.647	3.15	1.572	0.82	143.5	17.51	2.64	2.92	7.08	4.93
PH	193.334	3.412	0.98	184.4	3.412	4.25	12.876	0.98	197	188.7	6.89	6.97	27.7	14.1
MSL	49.662	3.738	0.86	49.52	3.738	7.69	5.796	0.87	61.66	57.21	11.4	12.3	13.5	21.9
NOS †	24.213	4.66	0.55	23.96	4.66	20.4	4.397	0.54	52.43	44.38	9.34	12.7	7.42	14.2
PB	0.849	0.619	0.78	0.83	0.619	0.26	0.965	0.76	3.39	1.09	26.8	30.8	1.64	48.3
SB	4.787	1.863	0.64	6.61	1.863	0.99	0	0.87	9.55	7.59	26.9	28.9	4.95	51.8
SL	0.279	0.304	0.84	0.31	0.304	0.06	0.066	0.84	4.83	0.36	11.5	12.5	1.05	21.7
S/S †	1.309	1.307	0.35	2.11	1.307	1.71	1.196	0.55	17.73	3.82	8.19	11	2.23	12.6
SY/P	27.687	3.007	0.84	30.91	3.007	4.6	2.108	0.87	15.22	35.52	36.5	39.2	10.7	70.3
TSW	0.502	0.234	0.95	0.5	0.234	0.02	0.186	0.95	4.44	0.52	15.9	16.3	1.42	32
OC	4.81	0.444	0.99	4.95	0.444	0.07	1.23	0.99	37.4	5.02	5.95	5.99	4.56	12.2

(c)

Characters	Y2L1			Pooled analysis										
	GV	SE	Hbs	GV	SE	GIV	SE	Hbs	MEAN	PV	GCV	PCV	GA	GAM
DF50	20.549	2.983	0.79	20.81	2.983	5.4	0.564	0.79	66.41	26.21	6.87	7.71	8.39	12.6
DM	15.23	2.972	0.71	15.41	2.972	6.22	2.802	0.71	145.8	21.64	2.69	3.19	6.84	4.69
PH	251.193	11.675	0.73	253.2	11.675	89.8	12.198	0.74	146.2	343	10.9	12.7	28.2	19.3
MSL	91.859	5.127	0.86	95.07	5.127	15.4	5.878	0.86	55.17	110.5	17.7	19.1	18.7	33.8
NOS	43.069	5.798	0.61	49.06	5.798	24.9	4.141	0.66	44.49	73.9	15.7	19.3	11.8	26.5
PB	1.186	0.534	0.88	1.2	0.534	0.14	0.45	0.89	5.42	1.34	20.2	21.3	2.14	39.5
SB	6.094	1.527	0.81	6.51	1.527	1.26	0.561	0.84	12.3	7.77	20.8	22.7	4.82	39.2
SL	0.241	0.343	0.76	0.27	0.343	0.06	0.288	0.82	4.33	0.33	11.9	13.2	0.96	22.2
S/S	2.589	1.372	0.64	2.81	1.372	1.4	0.678	0.67	18.74	4.22	8.95	11	2.83	15.1
SY/P	37.114	2.832	0.89	40.25	2.832	3.1	3.93	0.93	16.93	43.35	37.5	38.9	12.6	74.5
TSW	0.126	0.323	0.59	0.16	0.323	0.05	0.232	0.76	5.08	0.22	7.98	9.14	0.73	14.4
OC	3.087	0.652	0.94	3.08	0.652	0.21	1.393	0.93	37.7	3.29	4.65	4.81	3.5	9.28

(d)

Characters	Y2L2			Pooled analysis										
	GV	SE	Hbs	GV	SE	GIV	SE	Hbs	MEAN	PV	GCV	PCV	GA	GAM
DF50	6.185	2.605	0.45	10	2.605	4.02	0.923	0.71	66.8	14.01	4.73	5.6	5.51	8.25
DM †	0	0	0	8.32	0	12.4	1.983	0.40	146.4	20.67	1.97	3.11	3.78	2.58
PH	142.963	11.955	0.50	208.4	11.955	74.6	1.96	0.74	172.7	283.1	8.36	9.74	25.6	14.8
MSL †	18.507	4.929	0.35	17.44	4.929	35.6	5.507	0.33	60.34	53.01	6.92	12.1	4.94	8.19
NOS	54.959	3.401	0.90	57.96	3.401	5.27	3.753	0.92	51.87	63.23	14.7	15.3	15	29
PB	0.237	0.569	0.32	0.67	0.569	0.09	0.584	0.88	3.39	0.77	24.3	25.9	1.59	46.9
SB	3.852	1.499	0.71	4.37	1.499	1.26	0	0.78	8.35	5.62	25	28.4	3.8	45.5
SL	0.525	0.23	0.96	0.54	0.23	0.02	0.217	0.96	4.99	0.57	14.7	15.1	1.48	29.7
S/S	2.14	1.679	0.34	4.14	1.679	2.86	0.983	0.59	16.78	7	12.1	15.8	3.23	19.2
SY/P	32.915	2.496	0.91	34.76	2.496	2.69	2.129	0.93	17.35	37.45	34	35.3	11.7	67.5
TSW	0.441	0.301	0.90	0.45	0.301	0.03	0.173	0.93	4.69	0.48	14.3	14.8	1.33	28.4
OC	4.709	0.68	0.96	4.84	0.68	0.21	1.158	0.96	37.46	5.04	5.87	6	4.44	11.9

GV: Genotypic variance; SE: standard error; GIV: genotypic–year interaction variance; PV: phenotypic variance; Hbs: heritability in broad-sense estimated over each season and pooled data along with pooled mean values; GCV and PCV: genetic and phenotypic coefficients of variation; GA: genetic advance and GAM: genetic advance as percentage of mean. DF50: days to 50 % flowering; DM: days to maturity; PH: plant height; MSL: main shoot length; PB: number of primary branches; SB: number of secondary branches; SL: silique length; S/S: seeds per silique; NOS: number of siliques per plant; SY/P: seed yield per plant, TSW: 1000-seed weight; OC: oil content.

SE(m) is the standard error of mean, CV is coefficient of variation and LSD is least square difference.

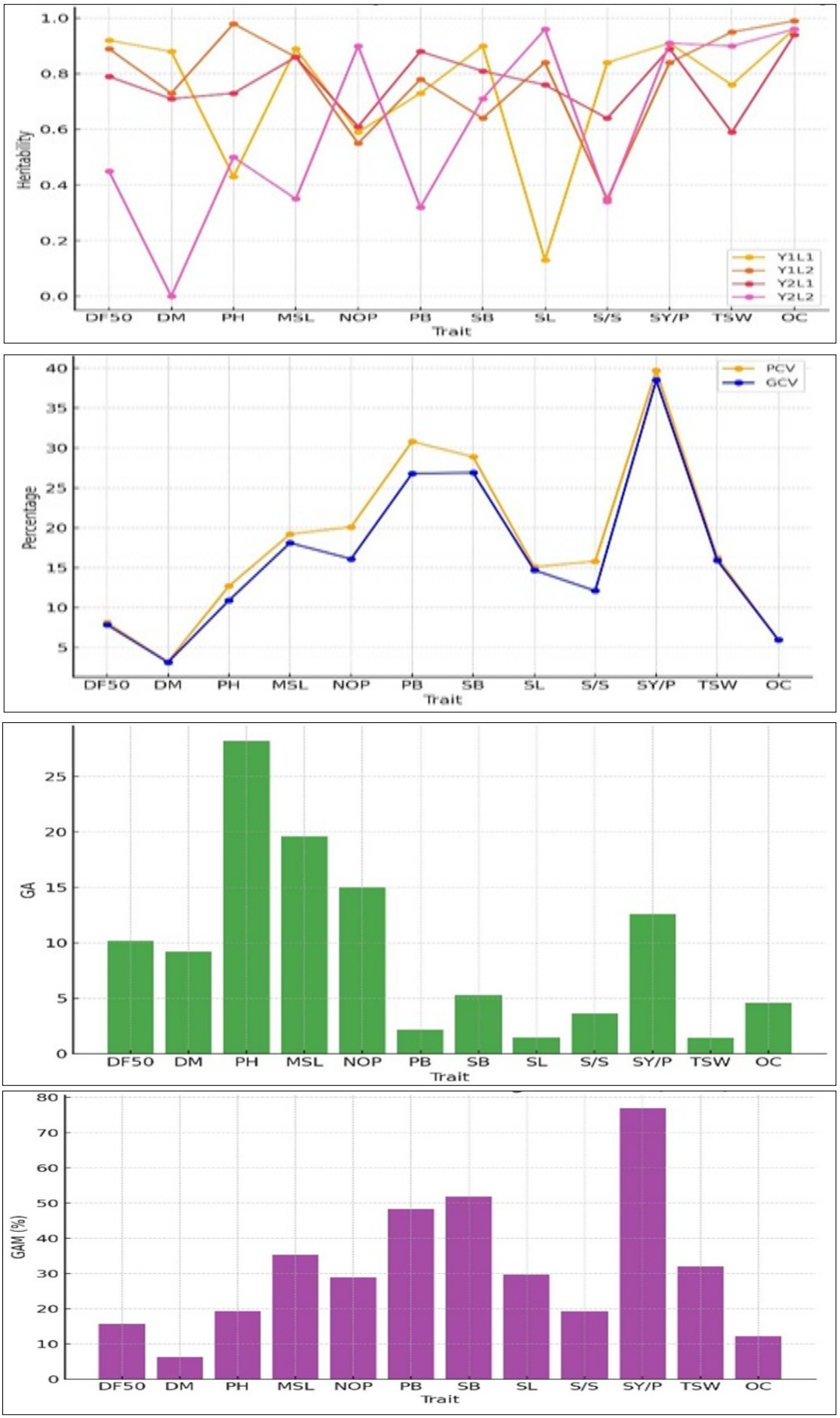

Fig. 2. Comparative analysis of genetic parameters and heritability of *Brassica* traits across different environments: (a) Heritability across environments; (b) Comparison of phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV); (c) Genetic advance; (d) Genetic advance as percentage of mean (GAM).

DF50: days to 50 % flowering; DM: days to maturity; PH: plant height; MSL: main shoot length; PB: number of primary branches; SB: number of secondary branches; SL: silique length; S/S: seeds per silique; NOS: number of siliques per plant; SY/P: seed yield per plant, TSW: 1000-seed weight; OC: oil content.

64.38 %), reflecting pronounced phenotypic plasticity; DM recorded the smallest (GCV 4.09 %, PCV 5.01 %), indicating relative stability. Narrow GCV–PCV gaps for DF50, DM, PH and MSL suggest limited environmental disruption of genetic expression and good potential for direct selection. Wider gaps for PB, SB and SY/P indicate stronger environmental influence; here, selection gains may improve when stratified by environment. GAM values ranged from 2.58 % (DM) to 76.9 % (SY/P), demonstrating trait-specific selection opportunity. Selection among the top 5 % of genotypes could improve DF50 by ~15.7 % and SY/P by > 70 %, illustrating strong breeding leverage. Taken together, DF50, PH, PB and SY/P combined high H^2, GCV, PCV and GAM, strong evidence of additive genetic control and suitability for direct selection in *B. juncea* improvement programs.

Path analysis: Yield-influencing traits

Path coefficient analysis clarified direct and indirect effects of measured traits on SY/P (Table 3). Direct contribution to SY/P was strongest for the yield path itself (0.30), followed by MSL (0.17) and SL (0.22), indicating that taller main axes and longer siliquae are associated with enhanced yield. PH showed a negative direct effect (–0.12), suggesting that increased stature may detract from yield, potentially via altered partitioning or lodging susceptibility. PB (–0.08) and SB (–0.23) also showed negative direct effects, indicating that excessive branching may not translate into yield gains under the tested conditions. Indirect effects revealed additional selection pathways. SL and S/S contributed strongly and positively to SY/P through indirect relationships (total effects 0.43 and 0.39 respectively), indicating that improvements in reproductive structure can cascade into yield benefits even when direct effects are modest. OC exerted a negative indirect effect (–0.23), pointing to a possible physiological trade-off between oil accumulation and seed yield. DF50 (total 0.06) and DM (total 0.09, with near-zero direct effect) influenced yield mainly through mediated pathways. Trait-level insights were reinforced by genotype performance. V131 recorded the highest SY/P across environments. Although V103 had the lowest SY/P, it also showed favourable values for MSL and NOS, suggesting utility as a donor for yield component improvement. V4, with desirable SL and S/S expression and V131 together represent strong candidates for hybridization strategies that combine complementary yield attributes. Overall, the path analysis identifies MSL, SL and S/S as high-priority traits, either direct or indirect contributors, to yield formation in mustard. At the same time, it cautions against indiscriminate selection for extreme PH or branching without considering yield trade-offs. Multi-trait selection schemes that integrate these insights can accelerate the development of structurally balanced, high-yielding cultivars.

Discussion

Evaluation across four contrasting environments provided a robust test of genetic vs. environmental contributions to trait expression in *B. juncea*. Several traits, most notably DF50, PH, MSL and SY/P, displayed consistently high H^2, confirming strong genetic control and good selection efficiency. These traits therefore offer immediate targets for cultivar development. DF50, with high H^2 and large GAM in pooled analyses, appears strongly influenced by additive genes, making it a reliable selection trait for optimizing crop phenology under variable production systems (13). Earlier flowering can accelerate crop maturity, improve fit in rotations and enhance adaptation under climate variability. PH also showed high GV and H^2, particularly in Y1L2 and Y2L1, underscoring its genetic tractability; its manipulation can produce ideotypes suited to mechanization and specific agro-ecological niches (3). MSL was highly heritable and expressed strong GAM in several environments (notably Y1L1, Y2L1), suggesting that canopy axis length can be improved through selection and may confer additional agronomic advantages, such as improved plant balance, reduced lodging risk, or enhanced source–sink alignment (4). SY/P, a key economic trait, was consistently heritable across environments, indicating that much of the observed variation among genotypes reflects true genetic differences. This trait should remain central in mustard yield improvement programs (14).

Not all traits were as stable. DM and SL showed moderate to high H^2 in some environments but were also environmentally responsive. For example, the lower H^2 and GA for DM in Y2L2 reflect environmental modulation of maturity expression, emphasizing the importance of environment-specific selection (10). Where wide adaptation is required, breeders may need to identify genotypes with buffered maturity responses. Significant G × E interactions for several traits (especially DM and PH) further illustrate selection complexity. Multi-environment testing remains essential for identifying regionally adapted cultivars with stable performance (8).

Table 3. Path coefficient analysis showing direct and indirect effects of agro-morphological traits on seed yield per plant (SY/P) in *Brassica*

Traits	Indirect effects to SY/Plant											Total effects		Total correlation of SY/Plant (r)
	DF50	DM	PH	MSL	NOP	PB	SB	SL	S/S	TSW	OC	Direct effects	Indirect effects	
DF50		-0.003	0.005	0.015	0.000	0.011	-0.001	0.011	-0.005	0.030	-0.001	0.00	0.06	0.06
DM	0.000		-0.016	0.007	0.000	0.003	0.001	0.017	0.038	0.045	-0.001	-0.01	0.09	0.08
PH	0.000	-0.002		0.007	0.000	0.007	-0.006	0.009	0.028	0.024	0.000	-0.12	0.07	-0.05
MSL	0.000	-0.001	-0.005		0.000	0.007	0.000	0.142	0.153	0.139	-0.002	0.17	0.43	0.60
NOP	0.000	0.000	-0.009	0.103		0.013	-0.009	0.142	0.146	0.145	-0.001	0.00	0.53	0.53
PB	0.000	-0.001	-0.015	0.020	0.000		-0.026	0.050	0.040	0.045	0.000	0.06	0.11	0.17
SB	0.000	0.000	-0.009	0.000	0.000	0.018		-0.022	-0.015	-0.042	0.000	-0.08	-0.07	-0.15
SL	0.000	-0.001	-0.005	0.108	0.000	0.013	0.008		0.153	0.157	-0.002	0.22	0.43	0.65
S/S	0.000	-0.002	-0.013	0.102	0.000	0.009	0.005	0.133		0.157	-0.002	0.25	0.39	0.64
TSW	0.000	-0.002	-0.009	0.077	0.000	0.008	0.011	0.113	0.131		-0.001	0.30	0.33	0.63
OC	0.000	0.002	-0.009	-0.055	0.000	0.001	-0.002	-0.059	-0.073	-0.030		0.01	-0.23	-0.22

DF50: days to 50 % flowering; DM: days to maturity; PH: plant height; MSL: main shoot length; PB: number of primary branches; SB: number of secondary branches; SL: silique length; S/S: seeds per silique; NOS: number of siliques per plant; SY/P: seed yield per plant, TSW: 1000-seed weight; OC: oil content.

Because heritability measures genetic proportion of variance, it must be interpreted with GA and with the scale of G × E; pooled H^2 reductions in the present study mirror patterns reported in sorghum (8), where G × E partitions reduced across-environment heritability relative to single-site estimates. The combined behaviour of DF50, PH, S/S and SY/P, high H^2, high GAM and elevated GCV, supports their direct use in selection pipelines (6, 15, 16). Pooled H^2 for SY/P reached 63 %, with GA > 60 %, indicating strong additive control and good repeatability across selection cycles (2, 4, 14).

Trait-specific heritability values ranged broadly (22 %–85 %). Flowering traits, PH and S/S combined high H^2 with high GA, patterns that align with reports of major QTLs affecting mustard yield components (17, 18). PH showed high H^2 but moderate GA, suggesting incremental progress under selection. PB and SY/P expressed high GA with moderate H^2, implying contributions from both additive and non-additive gene action; meaningful gains remain achievable where selection is well managed (19). Importantly, no trait combined low H^2 with low GA, indicating that genetic progress is possible across the trait set if selection environments are appropriate. Environmental influence on trait expression was further reflected in the generally higher PCV relative to GCV for most traits, confirming that phenotypic expression integrates genetic and environmental components (10). Large PCV–GCV gaps for PH, SB and SY/P point to heightened environmental sensitivity and reinforce the value of multi-environment testing and stratified selection.

Path analysis findings complement variance-based inferences and help prioritize yield-contributing traits. TSW, MSL and S/S were positively correlated with and showed moderate direct effects on SY/P, supporting their use as indirect selection criteria for yield (20). PH showed a negative direct effect on SY/P, indicating that extremely tall architectures may reduce yield under some production scenarios (21). Indirect contributions from total yield components (including S/S) also influenced SY/P, underscoring the need to consider trait networks rather than single-trait selection (22). DF50, PH and SL contributed to yield primarily through mediated pathways, reflecting the complex interdependence of developmental and reproductive traits (23). Together, the breadth of variability, high heritability in key traits and supportive path relationships identify this germplasm panel as a valuable resource for mustard improvement. Combining high-SY/P genotypes with favourable component traits (e.g. V131 × V4 or inclusion of MSL/NOS donors such as V103) represents a practical multi-trait strategy for breeding progress.

Conclusion

This multi-environment study demonstrated substantial genetic variability among *B. juncea* genotypes and identified several high-heritability traits; DF50, PH, MSL and SY/P as strong candidates for direct selection. Environmentally responsive traits such as DM and SL will benefit from environment-specific selection schemes. Significant G × E across traits highlights the need for multi-location testing to ensure stability. Path analysis identified MSL and S/S as important contributors, directly or indirectly, to SY/P, broadening the range of effective selection targets. Collectively, these results provide a genetic and analytical framework for developing high-yielding, adaptable mustard varieties across variable production environments.

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Authors' contributions

SP contributed to writing the original draft, conceptualization, data curation, formal analysis, investigation and methodology. IR was involved in writing, reviewing and editing, data curation, formal analysis, investigation and methodology. MS contributed to writing, reviewing and editing, data curation, formal analysis, supervision and visualization.

Compliance with ethical standards

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References

1. Meena HS, Kumar A, Ram B, Singh VV, Meena PD. Genetic variability and inter-relationship among yield and yield contributing traits in Indian mustard (*Brassica juncea* L. Czern. & Coss.). J Oilseed Brassica. 2017;8(1):1–7.
2. Kumar V, Sharma AK, Yogi RK, Singh VV. Rapeseed-mustard cultivation in India: National overview and regional insights with reference to Madhya Pradesh. J Oilseed Brassica. 2015;16(2):149–57. https://doi.org/10.56093/job.v16i2.172304
3. Joshi S, Shrivastava AN, Bhargava A. Genetic variability and association analysis in Indian mustard (*Brassica juncea* L. Czern. & Coss.). J Oilseed Brassica. 2009;1(2):90–93.
4. Kumar V, Kumar M, Shahi JP. Genetic analysis of yield and yield contributing traits in Indian mustard (*Brassica juncea* L. Czern. & Coss.). J Oilseed Brassica. 2019;10(2):130–34. https://doi.org/10.31901/24566535.2019/10.1-2.122
5. Ali N, Javidfar F, Mirza MY. Selection criteria for improved seed yield in *Brassica juncea* L. J Agric Res. 2003;41(1):11–18.
6. Kumar R, Misra S. Studies on genetic variability, heritability and genetic advance in *Brassica juncea* L. Indian J Plant Genet Resour. 2007;20(2):134–36.
7. Khan H, Rehman SU, Khan I. Genetic variability, heritability and correlation for yield and yield components in chickpea (*Cicer arietinum* L.). J Agric Res. 2008;46(1):109–16.
8. Phuke RM, Kavi Kishor PB, Satish Y. Genetic variability, heritability and genetic advance in sorghum (*Sorghum bicolor* L. Moench) for yield and yield contributing traits. Electron J Plant Breed. 2017;8 (1):57–63.
9. Gunasekara D, De Costa WAJM, Liyanage LP. Genotype by environment interactions in seed yield of sesame (*Sesamum indicum* L.) in Sri Lanka. Trop Agric Res Ext. 2006;9(1):43–48.
10. Kumar V, Singh BK, Sharma P, Kumar M. Genetic variability and character association in Indian mustard (*Brassica juncea* L. Czern. & Coss.). J Oilseed Brassica. 2012;3(2):86–89.
11. Dewey DR, Lu KH. A correlation and path-coefficient analysis of components of crested wheatgrass seed production. Agron J. 1959;51(9):515–18. https://doi.org/10.2134/agronj1959.00021962005100090002x
12. Robinson HF. Quantitative genetics in relation to breeding on the

centennial of Mendelism. Indian J Genet Plant Breed. 1966;26:171–87.

13. Shivanna H. Path coefficient analysis for oil yield and its attributes in Indian mustard (*Brassica juncea* L. Czern. & Coss.). Res J Agric Sci. 2008;2(1):57–59.

14. Tiwari A, Mishra P, Lal G. Genetic variability and association studies for yield and its contributing traits in Indian mustard (*Brassica juncea* L. Czern. & Coss.). J Oilseed Brassica. 2017;8(1):64–70.

15. Yadava DK, Bhushan B, Chander S. Genetic variability and trait association in Indian mustard (*Brassica juncea* L. Czern. & Coss.). J Oilseed Brassica. 2011;2(2):93–96.

16. Tripathi S, Kumari S, Tiwari P. Genetic variability and heritability in Indian mustard (*Brassica juncea* L. Czern. & Coss.). J Oilseed Brassica. 2013;4(2):84–88.

17. Kaur N, Banga SS. Genetic architecture of yield and its component traits in Indian mustard (*Brassica juncea* L. Czern. & Coss.). J Oilseed Brassica. 2015;6(1):22–29.

18. Akhatar M, Singh DP, Pant DC. Genetic variability, correlation and path analysis in Indian mustard (*Brassica juncea* L.). J Agric Sci. 2021;13(2):117–24.

19. Belete Y, Shumet T, Tulu L. Genetic variability, heritability and genetic advance for yield and yield-related traits in bread wheat (*Triticum aestivum* L.) genotypes. J Agron. 2011;10(5):99–104.

20. Albayrak S, Tongel O. Path coefficient analysis of yield and yield components in some Turkish genotypes of forage pea (*Pisum sativum* ssp. *arvense* L.). J Agron. 2006;5(4):505–10.

21. Kardam RP, Singh VV. Correlation and path coefficient analysis for seed yield and yield components in Indian mustard (*Brassica juncea* Czern. & Coss.). J Oilseeds Res. 2005;22(1):76–77.

22. Lenka D, Misra B. Path coefficient analysis of yield in rice varieties. Indian J Agric Sci. 1973;43:376–79.

23. Maphumulo PH, Chiduza C, Nyakurwa CS. Genetic variability, heritability and correlation coefficients of agronomic traits in mustard genotypes. J Agric Sci. 2015;7(4):34–42.

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