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Genetic variability and trait association studies in Indian mustard (*Brassica juncea* L. Czern & Coss)

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Abstract

Indian mustard (*Brassica juncea* L. Czern & Coss) is a crucial oilseed crop in India, contributing 13-15% of total edible oil production. Despite its importance, productivity remains below global averages, necessitating genetic improvement through breeding programs. To assess genetic variability, heritability, genetic advance, and trait associations among 24 Indian mustard genotypes to identify superior genotypes and key selection criteria for yield improvement. Twenty four mustard genotypes were evaluated in a Randomized Block Design with three replications during Rabi 2024-2025 at Sam Higginbottom University, Prayagraj. Eleven quantitative traits were recorded including days to 50% flowering, plant height, number of primary branches per plant, number of siliquae per plant, days to maturity, siliqua length, number of seeds per siliqua, seed index, biological yield per plant, harvest index, and seed yield per plant. Genetic parameters, correlation coefficients, and path analysis were computed. Analysis of variance revealed significant genotypic differences for most traits. High heritability was observed for number of siliquae per plant (80.01%), biological yield per plant (58.23%), and seed yield per plant (58.08%). Genetic advance as percentage of mean was highest for number of siliquae per plant (26.28%), followed by seed yield per plant (15.16%). Strong positive correlations were found between seed yield and biological yield ($r = 0.94$), and harvest index ($r = 0.75$). Path analysis identified biological yield per plant (0.745) and harvest index (0.371) as having the highest direct effects on seed yield. CS-60 recorded the highest seed yield (10.09 g) and biological yield (27.44 g), while Brijraj showed the highest harvest index (39.93%). Biological yield per plant and harvest index are the primary determinants of seed yield in mustard. Genotypes CS-60 and Brijraj are promising for breeding programs. High heritability estimates for key traits indicate good scope for genetic improvement through selection.

Keywords: Indian mustard, genetic variability, heritability, correlation, path analysis, yield improvement

1. Introduction

Indian mustard (*Brassica juncea* L. Czern & Coss) stands as one of India's most significant oilseed crops, playing a crucial role in the nation's agricultural economy and food security. As the primary source of edible oil for millions of Indians, mustard contributes approximately 13-15% of the country's total edible oil production. The crop is predominantly cultivated during the winter season (rabi) across diverse agroclimatic zones, occupying around 6.86 million hectares and producing nearly 9.12 million tonnes of seeds annually, with an average productivity of 1,331 kg per hectare.

Despite India's position as a leading global producer of rapeseed-mustard, the country's productivity remains significantly below the world average of 1,974 kg per hectare. This substantial yield gap represents both a challenge and an opportunity for agricultural scientists and breeders to enhance crop productivity through genetic improvement and advanced breeding strategies. The strategic importance of mustard is further amplified by India's heavy dependence on edible oil imports, which currently account for over 50% of domestic consumption, creating vulnerability to global price fluctuations and emphasizing the need for enhanced domestic production.

The genetic foundation for crop improvement lies in the availability of genetic variability within the crop species. Indian mustard, being an amphidiploid species (2n=36) with A and B genomes derived from Brassica rapa and Brassica nigra respectively, possesses considerable genetic diversity accumulated through centuries of cultivation and natural selection across varied environments. This genetic wealth, preserved in indigenous landraces, traditional cultivars, and modern breeding lines, provides the raw material essential for developing superior varieties with enhanced yield potential, improved quality traits, and resilience to biotic and abiotic stresses.

Understanding the relationships among yield components is equally crucial for designing effective breeding strategies. Seed yield, being a complex polygenic trait, results from the intricate interactions of multiple component traits. Correlation studies help identify traits that are positively or negatively associated with yield, enabling breeders to design appropriate selection strategies. Path coefficient analysis further dissects these relationships by partitioning correlations into direct and indirect effects, providing deeper insights into the relative importance of different traits in determining final yield.

Recent advances in statistical genetics and breeding methodologies have provided powerful tools for characterizing genetic variability and understanding trait relationships. Parameters such as genotypic and phenotypic coefficients of variation, heritability, and genetic advance help quantify the extent of genetic variability and predict the effectiveness of selection. High heritability estimates indicate that observed variation is primarily due to genetic factors rather than environmental influences, suggesting good prospects for genetic improvement through selection.

The present investigation was undertaken to evaluate genetic variability, estimate genetic parameters, and study trait associations in a diverse set of 24 Indian mustard genotypes. The specific objectives were: (1) to assess the extent of genetic variability, heritability, and genetic advance for various quantitative traits, (2) to determine phenotypic and genotypic correlations among different traits, and (3) to estimate direct and indirect effects of yield component traits on seed yield through path coefficient analysis.

2. Review of Literature

2.1 Genetic Variability, Heritability and Genetic Advance

Genetic variability forms the foundation of any successful plant breeding program. Verma *et al.* (2015) [12] studied 30 genotypes of Indian mustard and reported significant genotypic variability for traits such as plant height, number of branches per plant, siliquae per plant, 1000-seed weight, and seed yield per plant. High heritability and genetic advance were noted for seed yield and number of siliquae per plant, suggesting additive gene action and potential for improvement through selection.

Similarly, Bisht *et al.* (2016) [1] evaluated 40 genotypes and found wide variability for siliqua length, seeds per siliqua, and seed yield per plant. High genotypic and phenotypic coefficients of variation were recorded for siliquae per plant and seed yield, along with high heritability and genetic advance, indicating the possibility of yield enhancement through direct selection.

Kumar and Chauhan (2017) [6] analyzed 52 accessions of Indian mustard and observed significant variation among genotypes. Traits such as number of siliquae per plant, biological yield, and seed yield showed high GCV, heritability, and genetic advance, indicating these are governed mainly by additive gene effects and are suitable for improvement through selection.

More recent studies have continued to demonstrate the presence of substantial genetic variability in mustard germplasm. Tripathi *et al.* (2022) [11] used multivariate analysis and variability studies on 55 genotypes and observed that siliquae per plant, seed yield per plant, and 1000-seed weight contributed majorly to total variation. These traits showed high GCV, heritability, and genetic advance, making them suitable for yield improvement.

2.2 Correlation Studies

Correlation analysis provides valuable information about the degree and direction of association between different traits. Yadava *et al.* (2015) [16] studied correlation among yield and its components in 40 Indian mustard genotypes and reported that seed yield per plant had strong positive correlation with number of siliquae per plant, biological yield, and harvest index. Days to maturity showed negative correlation with seed yield.

Meena *et al.* (2016) [8] analyzed 45 genotypes and found significant positive correlation of seed yield with number of primary branches, number of siliquae per plant, and test weight. Negative correlation was observed with days to 50% flowering and plant height, suggesting that early flowering and moderate plant height are associated with higher yields.

Kumar *et al.* (2019) [7] studied 60 Indian mustard genotypes and found that seed yield per plant was positively and significantly correlated with number of primary and secondary branches, siliquae per plant, and oil content. Negative correlation was reported with days to maturity, indicating the advantage of early-maturing varieties.

2.3 Path Coefficient Analysis

Path coefficient analysis helps in understanding the direct and indirect effects of different traits on yield. Singh *et al.* (2015) [10] conducted path coefficient analysis in 30 genotypes and found that biological yield per plant had the highest positive direct effect on seed yield followed by number of siliquae per plant. Indirect effects through 1000-seed weight and plant height were also significant.

Verma *et al.* (2017) [13] analyzed path coefficients in 42 genotypes and observed that biological yield had the highest direct contribution to seed yield followed by number of seeds per siliqua. Days to flowering had a negative direct effect but positive indirect effects via siliquae per plant.

Recent studies have consistently shown the importance of biological yield and harvest index in determining seed yield. Choudhary *et al.* (2021) [2] observed high positive direct effects of biological yield, siliquae per plant, and harvest index on seed yield. Days to maturity and number of secondary branches contributed indirectly through biological yield and siliquae per plant.

3. Materials and Methods

3.1 Experimental Site and Design

The present investigation was conducted at the Crop Research Farm, Department of Genetics and Plant Breeding, Naini Agricultural Institute, Sam Higginbottom University of Agriculture, Technology and Sciences, Prayagraj, Uttar Pradesh during the rabi season of 2024-2025.

The experiment was laid out in a Randomized Block Design (RBD) with three replications. Each plot consisted of 4 rows of 3 m length with a spacing of 45 cm between rows and 15 cm between plants within rows. The recommended package of practices was followed to raise a healthy crop, including the application of fertilizers at the rate of 60:30:40 kg/ha of N:P:K.

3.2 Plant Material

The experimental material comprised 24 genotypes of Indian mustard obtained from the Department of Genetics and Plant Breeding, SHUATS. The genotypes included both released varieties and advanced breeding lines representing diverse genetic backgrounds and geographical origins.

3.3 Meteorological Conditions

The weather conditions during the crop growing period were favorable for mustard cultivation. The average temperature ranged from 15°C to 30 °C during the crop season. Humidity levels varied from 28% to 75%, with minimal rainfall during the critical growth stages.

3.4 Data Collection

Data were recorded for eleven quantitative traits:

Pre-harvest observations

1. Days to 50% flowering (DF50)
2. Plant height in cm (PH)
3. Number of primary branches per plant (NPB/P)
4. Number of siliquae per plant (NSLQ/P)
5. Days to maturity (DM)

Post-harvest observations

1. Siliqualength in cm (SLQL)
2. Number of seeds per siliqua (Seeds/SLQ)
3. Seed index/1000-seed weight in g (SI)
4. Biological yield per plant in g (BY/P)
5. Harvest index in % (HI)
6. Seed yield per plant in g (SY/P)

All observations except days to flowering and maturity were recorded on five randomly selected plants per plot, and the mean values were used for statistical analysis.

3.5 Statistical Analysis

The data were subjected to the following statistical analyses:

- **Analysis of Variance (ANOVA):** Performed according to the method described by Fisher (1918) [4] to test the significance of differences among genotypes.
- **Genetic Parameters:** Genotypic and phenotypic coefficients of variation (GCV and PCV), heritability in broad sense, and genetic advance were calculated following standard formulas.
- **Correlation Analysis:** Phenotypic and genotypic correlation coefficients were computed according to the method given by Johnson *et al*. (1955) [5].
- **Path Analysis:** Direct and indirect effects of different traits on seed yield were calculated using path coefficient analysis as described by Dewey and Lu (1959) [3].

4. Results and Discussion

4.1 Analysis of Variance

The analysis of variance revealed significant differences among the 24 mustard genotypes for most of the traits studied Highly significant ($p \leq 0.01$) mean sum of squares were observed for days to 50% flowering (16.115), number of primary branches per plant (0.126), number of siliquae per plant (170.660), days to maturity (18.318), seed index (0.408), biological yield per plant (9.409), harvest index (9.051), and seed yield per plant (2.107). Plant height (320.752) and siliqua length (0.190) showed significant differences at $p \leq 0.05$ level.

The significant genotypic differences observed for most traits indicate the presence of sufficient genetic variability among the genotypes, which is essential for any breeding program. These results are in agreement with earlier findings of Verma *et al*. (2018) [14] and Meena *et al*. (2019) [9], who reported significant genotypic variations for yield and yield-attributing traits in Indian mustard.

Table 1: Analysis of Variance among 24 Mustard genotypes for 11 quantitative traits

S. No	Source of variance	Mean sum of squares (MSS)		
	Degrees of freedom	Genotype	Replication	Error
		23	2	46
1	Days to 50% flowering	16.115**	518.389	5.867
2	Plant height	320.752*	4239.639	155.941
3	No of primary branches	0.126**	0.107	0.036
4	No of siliquae per plant	170.660**	14.691	13.120
5	Days to maturity	18.318**	683.556	5.990
6	Siliquae length	0.190*	0.491	0.105
7	Number of seeds per siliquae	1.975*	0.732	1.074
8	Seed index	0.408**	0.488	0.144
9	Biological yield per plant	9.409**	6.679	1.816
10	Harvest index	9.051**	11.323	3.560
11	Seed yield per plant	2.107**	2.381	0.409

4.2 Mean Performance of Genotypes

The mean performance of the 24 genotypes for all traits is presented in Days to 50% flowering ranged from 72.33 days (CS-60) to 81.00 days (RH-761), with a grand mean of 77.40 days. The coefficient of variation was low (3.13%), indicating good precision in data recording and minimal environmental influence on this trait.

Plant height varied widely from 99.05 cm (Pusa Mahak) to 142.27 cm (RB-50), with a mean of 117.02 cm. The high coefficient of variation (10.67%) suggests considerable environmental influence on this trait. Number of primary branches per plant ranged from 1.27 (JM-1) to 2.13 (Durgamani), with a mean of 1.60.

For the most important trait, seed yield per plant, genotype CS-60 recorded the highest yield (10.09 g), followed by RGN-298 (8.42 g) and RH-761 (8.76 g). The lowest seed yield was observed in Pusa Vijay (6.53 g). The wide range in seed yield (6.53-10.09 g) indicates substantial genetic diversity among the genotypes.

Table 2: Mean Performance Of 24 Mustard Genotypes For 11 Quantitative Parameters

Genotype	DF50	PH	NPB/P	NSLQ/P	DM	SLQL	Seeds/SLQ	SI	BY/P	HI	SY/P
Patan Mustard	77.667	125.720	1.733	48.940	108.000	4.847	11.267	4.267	22.723	34.336	7.783
Radhika	74.333	117.880	1.533	51.360	104.667	5.060	11.267	4.603	24.697	35.400	8.750
CS-60	72.333	128.393	1.667	46.450	105.333	4.630	11.867	4.883	27.437	36.746	10.090
RGN-298	76.667	129.113	1.733	48.177	105.667	4.827	10.400	3.880	23.283	36.138	8.417
Krishna	73.667	122.860	1.533	60.630	103.333	4.943	11.267	3.940	20.963	35.337	7.397
Rajat	78.333	122.013	1.467	64.407	109.333	5.100	10.867	4.087	19.400	34.492	6.710
Shivani	78.667	118.361	1.800	52.067	111.667	4.660	11.333	4.353	21.287	36.827	7.857
RH-761	81.000	125.253	1.667	55.150	111.000	4.680	11.133	3.747	23.620	36.909	8.757
Rohini	77.000	113.940	1.667	44.843	107.333	4.817	11.933	3.860	21.583	37.147	8.017
Pusa Vijay	78.000	111.273	1.600	68.307	109.667	4.900	11.333	4.647	19.913	32.848	6.527
RH-819	79.667	116.600	1.467	50.607	109.667	5.007	10.267	4.300	22.723	36.566	8.290
Seeta	74.667	109.560	1.733	61.163	107.333	5.140	11.267	3.853	20.247	32.407	6.577
Jm-1	77.333	105.893	1.267	46.673	106.667	4.853	10.800	4.173	22.120	34.729	7.687
PDZ-1	77.333	110.280	1.800	47.277	109.333	4.787	11.000	3.620	23.023	37.007	8.523
Jm-2	78.000	107.447	1.467	54.207	106.000	4.413	10.400	4.300	21.410	35.547	7.603
NRCDR-02	78.333	109.673	1.867	36.697	109.333	5.167	13.467	4.553	21.793	36.165	7.890
Narendra Rai	79.000	127.013	1.800	43.333	111.333	4.567	11.800	3.773	20.503	33.289	6.830
DRMR-150-35	80.667	128.660	1.400	46.370	110.333	5.180	12.067	4.660	20.863	34.487	7.210
RB-50	77.333	142.267	1.467	52.493	111.333	5.360	12.533	4.360	20.173	33.518	6.790
Ashirwad	74.333	105.900	1.333	43.130	107.000	4.633	11.533	4.640	20.177	37.224	7.507
Brijraj	77.333	104.060	1.400	42.933	106.667	4.900	12.733	4.627	21.997	39.931	8.757
RH-406	80.333	118.840	1.400	56.793	108.667	5.213	12.000	3.750	21.593	35.233	7.607
Pusa Mahak	75.333	99.047	1.400	44.067	106.000	4.720	10.133	3.820	23.280	33.407	7.780
Durgamani	80.333	108.387	2.133	53.437	112.667	5.347	12.133	4.047	21.120	36.292	7.660
Minimum	72.333	99.047	1.267	36.697	103.333	4.413	10.133	3.620	19.400	32.407	6.527
Maximum	81.000	142.267	2.133	68.307	112.667	5.360	13.467	4.883	27.437	39.931	10.090
Grand Mean	77.403	117.018	1.597	50.813	108.264	4.906	11.450	4.198	21.914	35.499	7.792
SEm	1.398	7.210	0.109	2.091	1.413	0.187	0.598	0.219	0.778	1.089	0.369
SEd	1.978	10.196	0.155	2.957	1.998	0.265	0.846	0.309	1.100	1.541	0.522
CD 5%	3.981	20.524	0.311	5.953	4.023	0.533	1.703	0.623	2.215	3.101	1.051
CD 1%	5.314	27.397	0.416	7.947	5.370	0.711	2.274	0.831	2.956	4.140	1.402
CV	3.129	10.672	11.866	7.128	2.261	6.609	9.052	9.027	6.149	5.315	8.203

4.3 Genetic Parameters

The estimates of genetic parameters for all traits are presented in The phenotypic coefficient of variation (PCV) was higher than the genotypic coefficient of variation (GCV) for all traits, indicating the influence of environment on trait expression. However, the differences between PCV and GCV were relatively small for most traits, suggesting that the observed variation was primarily due to genetic factors.

High GCV (>20%) was observed for number of siliquae per plant (14.26%), indicating substantial genetic variability for this trait. Moderate GCV (10-20%) was recorded for number of primary branches per plant (10.84%) and seed yield per plant (9.66%).

Heritability estimates in broad sense were high (>60%) for number of siliquae per plant (80.01%), biological yield per plant (58.23%), and seed yield per plant (58.08%). These high heritability values indicate that selection for these traits would be effective as a large proportion of the observed variation is due to genetic factors.

Genetic advance as percentage of mean was highest for number of siliquae per plant (26.28%), followed by seed yield per plant (15.16%) and number of primary branches per plant (15.05%). High genetic advance coupled with high heritability for these traits suggests that improvement through selection would be effective.

Table 3: Genetic variability for 11 quantitative characters in Mustard genotypes

S. No	Trait	Phenotypic coefficient of variation (%)	Genotypic coefficient of variation (%)	Heritability Broad Sense (%)	Genetic advance	Genetic Advance as percent of mean
1	Days to 50% flowering	3.936	2.388	36.798	2.310	2.984
2	Plant height	12.410	6.334	26.052	7.793	6.660
3	Number of primary branches	16.069	10.835	45.471	0.240	15.052
4	Number of siliquae per plant	15.944	14.261	80.011	13.353	26.279
5	Days to maturity	2.935	1.872	40.688	2.664	2.460
6	Siliquae length	7.443	3.423	21.151	0.159	3.243
7	Seeds per siliquae	10.239	4.785	21.839	0.527	4.606
8	Seed index	11.468	7.073	38.044	0.377	8.988
9	Biological yield per plant	9.514	7.260	58.227	2.501	11.412
10	Harvest index	6.540	3.811	33.952	1.624	4.574
11	Seed yield per plant	12.669	9.655	58.076	1.181	15.157

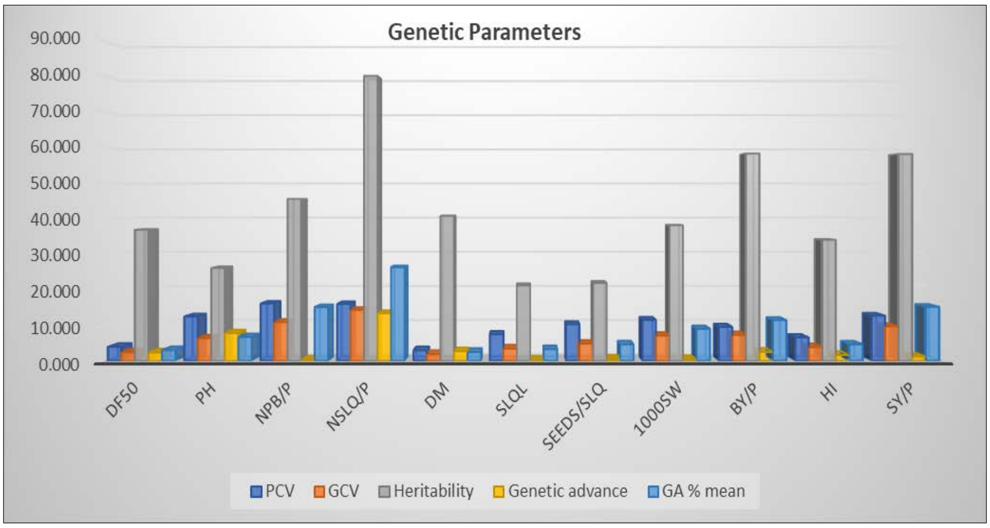

Fig 1: Bar diagram depicting GCV, PCV, heritability and genetic advance as % of mean for 11 quantitative characters Mustard

4.4 Correlation Analysis

4.4.1 Phenotypic Correlations

The phenotypic correlation coefficients among different traits are presented in Seed yield per plant showed highly significant positive correlations with biological yield per plant (0.878) and harvest index (0.673). Significant negative correlations were observed with number of siliquae per plant (-0.364), days to maturity (-0.239), and siliqua length (-0.261). The strong positive correlation between seed yield and biological yield indicates that genotypes producing higher total biomass tend to have higher seed yield. Similarly, the positive correlation with harvest index suggests that efficient partitioning of biomass to economic parts is crucial for high seed yield.

Table 4: Estimation of Phenotypic correlation coefficient for seed yield and its related traits in 24 Mustard genotypes

Trait	DF50	PH	NPB/P	NSLQ/P	DM	SLQL	Seeds/SLQ	SI	BY/P	HI	SY/P
DF50	1	-0.0396	0.0294	0.0171	0.6483 **	0.1231	0.028	-0.1227	-0.2193	-0.0001	-0.1619
PH		1	-0.0158	0.1166	0.1005	0.1801	0.0613	0.0309	0.0554	-0.1126	-0.002
NPB/P			1	-0.0577	0.3041 **	0.0213	0.0831	-0.0324	0.0168	-0.0034	0.0197
NSLQ/P				1	-0.0418	0.1687	-0.2152	-0.1113	-0.2698 *	-0.3341 **	-0.3642 **
DM					1	0.1534	0.1385	-0.0882	-0.3026 **	-0.0343	-0.2394 *
SLQL						1	0.3877 **	0.074	-0.2601 *	-0.1333	-0.2607 *
Seeds/SLQ							1	0.0744	-0.1137	0.2645 *	0.0423
SI								1	0.0937	0.1315	0.1347
BY/P									1	0.2411 *	0.8784 **
HI										1	0.6728 **
SY/P											1

**1% Level of significance *5% Level of significance

4.4.2 Genotypic Correlations

Genotypic correlations were generally higher in magnitude than phenotypic correlations, indicating strong genetic associations among traits Seed yield per plant showed highly significant positive genotypic correlations with biological yield per plant (0.939) and harvest index (0.747). The negative correlations of seed yield with number of siliquae per plant (-0.504), days to maturity (-0.432), and siliqua length (-0.419) indicate trade-offs that need to be carefully managed in breeding programs. These results suggest that while increasing the number of siliquae might seem beneficial, it could lead to reduced individual siliqua filling and ultimately lower seed yield.

Table 5: Estimation of Genotypical correlation coefficient for grain yield and its related traits in 24 mustard genotypes

Trait	DF50	PH	NPB/P	NSLQ/P	DM	SLQL	Seeds/SLQ	SI	BY/P	HI	SY/P
DF50	1	0.3385	0.3323	0.1073	0.9398 **	0.4513 *	0.2989	-0.3788	-0.4791 *	0.0634	-0.3383
PH		1	0.2395	0.1882	0.4075 *	0.229	0.3424	0.038	0.1177	-0.3654	-0.0263
NPB/P			1	-0.0068	0.5456 **	0.1935	0.5076 *	-0.4742 *	0.1423	0.1107	0.1575
NSLQ/P				1	0.1485	0.3267	-0.4769 *	-0.2029	-0.4136 *	-0.5321 **	-0.5042 *
DM					1	0.5344 **	0.5866 **	-0.1391	-0.4955 *	-0.1935	-0.4322 *
SLQL						1	0.5705 **	-0.0199	-0.369	-0.38 NS	-0.4191 *
Seeds/SLQ							1	0.8464 **	-0.2244	0.1352	-0.0908
SI								1	0.2006	0.2511	0.2516
BY/P									1	0.4739 *	0.9392 **
HI										1	0.7473 **
SY/P											1

**1% Level of significance *5% Level of significance

4.5 Path Coefficient Analysis

4.5.1 Phenotypic Path Analysis

The results of phenotypic path analysis are presented Biological yield per plant had the highest positive direct effect (0.762) on seed yield, followed by harvest index (0.490). These results confirm that biological yield and harvest index are the most important determinants of seed yield in mustard. Number of siliquae per plant showed a small negative direct effect (-0.008) on seed yield, despite having a significant negative correlation. This suggests that the negative association is primarily through indirect effects via other traits, particularly biological yield and harvest index.

Table 6: Direct and Indirect effects of yield component characters for seed yield in 24 genotypes of Mustard at Phenotypic level

Trait	DF50	PH	NPB/P	NSLQ/P	DM	SLQL	Seeds/SLQ	SI	BY/P	HI	SY/P
DF50	0.00315	-0.00051	-0.00009	-0.00011	0.00337	-0.00022	0.00003	-0.00033	-0.16713	-0.00005	-0.1619
PH	-0.00012	0.01289	-0.00004	-0.00189	0.00052	-0.00041	0.00006	-0.0001	0.04222	-0.05513	-0.002
NPB/P	0.00004	0.00006	-0.00796	-0.00002	0.00015	-0.00012	0.00005	0.00022	0.11714	0.00935	0.0197
NSLQ/P	0.00004	0.00308	-0.00002	-0.00758	-0.00011	-0.00036	0.00019	0.00022	-0.04847	-0.05048	-0.3642 **
DM	0.00204	0.0013	-0.00023	0.00017	0.0052	-0.00032	0.00013	-0.00027	-0.23062	-0.01679	-0.2394 *
SLQL	0.00033	0.00248	-0.00045	-0.00132	0.00077	-0.00215	0.00039	-0.00025	-0.17529	-0.0495	-0.2607 *
Seeds/SLQ	0.00009	0.00079	-0.00043	-0.00156	0.00072	-0.00089	0.00094	-0.00019	-0.08665	0.1295	0.0423
SI	0.0005	0.00062	0.00085	0.00083	0.00069	-0.00027	0.00009	-0.00205	-0.04718	0.0211	0.1347
BY/P	-0.00069	0.00071	-0.00123	0.0005	-0.00157	0.0005	-0.00011	0.00013	0.76212	0.11804	0.8784 **
HI	0	-0.00145	-0.00015	0.00081	-0.00018	0.00022	0.00025	-0.00009	0.18375	0.48954	0.6728 **
	Residual=0.0025										

**1% Level of significance *5% Level of significance

4.5.2 Genotypic Path Analysis

Genotypic path analysis revealed similar trends to phenotypic analysis. Biological yield per plant (0.745) and harvest index (0.371) had the highest positive direct effects on seed yield. The residual effect was low (0.014), indicating that the traits included in the analysis explained most of the variation in seed yield.

These results are consistent with earlier findings of Singh *et al.* (2015) [10] and Verma *et al.* (2017) [13], who reported biological yield as the most important trait contributing directly to seed yield in mustard.

Table 7: Direct and Indirect effects of yield component characters for seed yield in 24 genotypes of Mustard at Genotypic level.

Trait	DF50	PH	NPB/P	NSLQ/P	DM	SLQL	Seeds/SLQ	SI	BY/P	HI	SY/P
DF50	0.062407	0.005225	0.014577	0.002114	-0.07066	-0.00627	0.002584	-0.01472	-0.35702	0.023491	-0.3383
PH	0.021125	0.015436	0.010507	0.003707	-0.03064	-0.00318	0.002961	0.001478	0.087735	-0.13545	-0.0263
NPB/P	0.020735	0.003697	0.043872	-0.00013	-0.04102	-0.00269	0.004389	-0.01843	0.106046	0.04104	0.1575
NSLQ/P	0.006698	0.002905	-0.0003	0.019701	-0.01116	-0.00454	-0.00412	-0.00789	-0.30821	-0.19727	-0.5042 *
DM	0.05865	0.006291	0.023938	0.002925	-0.07519	-0.00742	0.005072	-0.00541	-0.36927	-0.07175	-0.4322 *
SLQL	0.028165	0.003535	0.008488	0.006435	-0.04018	-0.01389	0.004933	-0.00077	-0.27499	-0.14087	-0.4191 *
Seeds/SLQ	0.018653	0.005285	0.022269	-0.0094	-0.0441	-0.00793	0.008647	0.032905	-0.16722	0.050115	-0.0908
SI	-0.02364	0.000587	-0.0208	-0.004	0.010458	0.000276	0.007319	0.038875	0.149485	0.093079	0.2516
BY/P	-0.0299	0.001817	0.006243	-0.00815	0.037256	0.005126	-0.00194	0.007798	0.745226	0.175679	0.9392 **
HI	0.003955	-0.00564	0.004857	-0.01048	0.014552	0.005279	0.001169	0.009761	0.35317	0.370702	0.7473 **
	Residual=0.0143										

**1% Level of significance *5% Level of significance

4.6 Superior Genotypes

Based on the overall performance across traits, genotype CS-60 emerged as the most promising, recording the highest seed yield (10.09 g), biological yield (27.44 g), and seed index (4.88 g). This genotype also showed early flowering (72.33 days) and moderate days to maturity (105.33 days).

Genotype Brijraj recorded the highest harvest index (39.93%) and good seed yield (8.76 g), making it valuable for breeding programs aimed at improving harvest index. RGN-298 also showed good performance with high seed yield (8.42 g) and harvest index (36.14%).

5. Conclusions

1. **Genetic Variability:** Significant genetic variability was observed among the 24 mustard genotypes for most traits studied, providing good scope for crop improvement through breeding.
2. **Heritability and Genetic Advance:** High heritability estimates were recorded for number of siliquae per plant (80.01%), biological yield per plant (58.23%), and seed yield per plant (58.08%). High genetic advance as percentage of mean for these traits indicates good potential for improvement through selection.
3. **Trait Associations:** Strong positive correlations of seed yield with biological yield (0.939) and harvest index (0.747) indicate these as key selection criteria for yield improvement. Negative correlations with days to maturity suggest the importance of developing early-maturing varieties.
4. **Path Analysis:** Biological yield per plant (0.745) and harvest index (0.371) had the highest direct effects on seed yield, confirming their primary importance in determining final yield.
5. **Superior Genotypes:** CS-60 emerged as the most promising genotype with highest seed yield (10.09 g) and biological yield (27.44 g), while Brijraj showed the highest harvest index (39.93%).
6. **Breeding Implications:** The study suggests that breeding programs should focus on improving biological yield and harvest index for sustainable yield

enhancement in mustard. The identified superior genotypes can serve as parents in hybridization programs or be directly released as varieties after multi-location testing.

These findings contribute valuable information for mustard breeders and provide a foundation for developing high-yielding varieties through systematic breeding approaches. The high heritability estimates for key traits and identification of superior genotypes offer promising prospects for genetic improvement of Indian mustard.

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